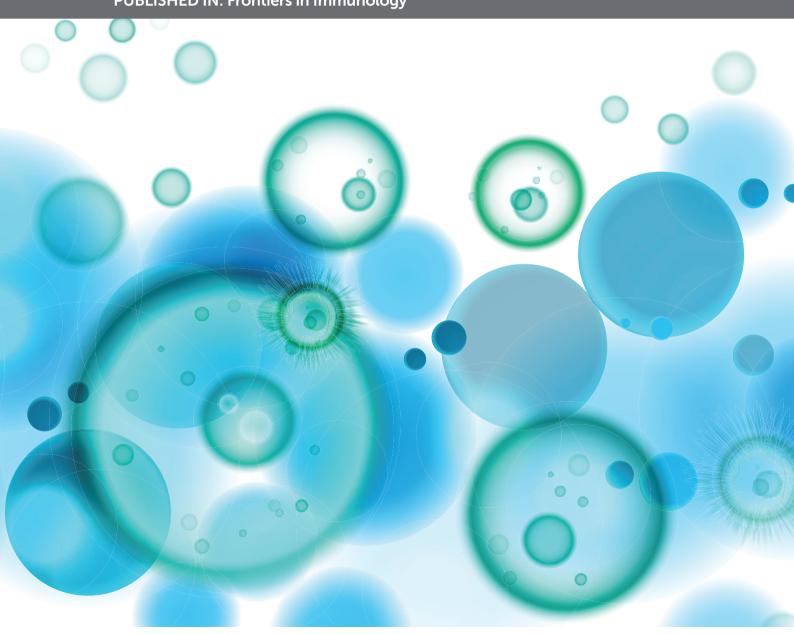
IMMUNITY AND IMMUNOPATHOGENESIS TO HERPESVIRUSES

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IMMUNITY AND IMMUNOPATHOGENESIS TO HERPESVIRUSES

Topic Editors:

Susmit Suvas, Wayne State University, United States **Richard D. Dix,** Georgia State University, United States

Herpesviruses are a large group of double-stranded DNA viruses, which have evolved strategies to persist and disseminate widely throughout the human population. Unlike RNA viruses which have the ability to alter their antigenic expression profile to evade host immune responses, herpesviruses can establish life-long latency in the infected host. Herpesviruses are divided into alpha, beta and gamma herpesviruses sub-families. The human members of the alpha-herpesvirinae subfamily is comprised of herpes simplex virus-1 and 2 (HSV-1 and HSV-2) and of varicella-zoster virus (VZV). These viruses are considered neurotropic, as they can (i) infect nerve endings; (ii) traffic via neuronal axons and (iii) establish latency in neuronal nuclei. On the other hand, the members of the beta-herpesvirinae subfamily such as human cytomegalovirus (HCMV), human herpesviruses 6 and 7 (HHV-6 and HHV-7) are known to establish latent infections in immune cell types such as monocytes and T cells. Epstein-Barr Virus (EBV) is a member of gamma-herpesvirinae subfamily that establishes latency in B lymphocytes. Additionally, HHV-8 also known as Kaposi's Sarcoma-Associated Herpes virus (KSHV) is a γ-herpes virus which establishes latency in monocytes, dendritic cells, B lymphocytes and endothelial cells of the host.

Although members of the herpesviridae family share few properties, they differ significantly in terms of the expression of viral genes during the latent infection period, incidence of viral reactivation, the molecular mechanisms by which they evade the host immunity to establish latency, and the pathogenesis associated with viral reactivation. A better understanding of the virological and immunological events associated with herpesviruses infection should help in the development of prophylactic and therapeutic approaches to better manage these viral infections in patients worldwide.

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Role of Herpes Simplex Virus Type 1 (HSV-1) Glycoprotein K (gK) Pathogenic CD8⁺ T Cells in Exacerbation of Eye Disease

Ujjaldeep Jaggi¹, Shaohui Wang¹, Kati Tormanen¹, Harry Matundan¹, Alexander V. Ljubimov² and Homayon Ghiasi^{1*}

¹ Department of Surgery, Center for Neurobiology and Vaccine Development, Cedars-Sinai Medical Center, Los Angeles, CA, United States, ² Eye Program, Cedars-Sinai Medical Center, and David Geffen School of Medicine, Board of Governors Regenerative Medicine Institute, University of California, Los Angeles, Los Angeles, CA, United States

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Richard D. Dix, Georgia State University, United States

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Lbachir Benmohamed, University of California, Irvine, United States Clinton Jones, Oklahoma State University, United States

*Correspondence:

Homayon Ghiasi ghiasih@cshs.org

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HSV-1-induced corneal scarring (CS), also broadly referred to as Herpes Stromal Keratitis (HSK), is the leading cause of infectious blindness in developed countries. It is well-established that HSK is in fact an immunopathological disease. The contribution of the potentially harmful T cell effectors that lead to CS remains an area of intense study. Although the HSV-1 gene(s) involved in eye disease is not yet known, we have demonstrated that gK, which is one of the 12 known HSV-1 glycoproteins, has a crucial role in CS. Immunization of HSV-1 infected mice with gK, but not with any other known HSV-1 glycoprotein, significantly exacerbates CS, and dermatitis. The gK-induced eye disease occurs independently of the strain of the virus or mouse. HSV-1 mutants that lack gK are unable to efficiently infect and establish latency in neurons. HSV-1 recombinant viruses expressing two additional copies of the gK (total of three gK genes) exacerbated CS as compared with wild type HSV-1 strain McKrae that contains one copy of gK. Furthermore, we have shown that an 8mer (ITAYGLVL) within the signal sequence of gK enhanced CS in ocularly infected BALB/c mice, C57BL/6 mice, and NZW rabbits. In HSV-infected "humanized" HLA-A*0201 transgenic mice, this gK 8mer induced strong IFN-y-producing cytotoxic CD8+ T cell responses, gK induced CS is dependent on gK binding to signal peptide peptidase (SPP). gK also binds to HSV-1 UL20, while UL20 binds GODZ (DHHC3) and these quadruple interactions are required for gK induced pathology. Thus, potential therapies might include blocking of gK-SPP, gK-UL20, UL20-GODZ interactions, or a combination of these strategies.

Keywords: ocular, eye disease, virus replication, corneal scarring, peptide, SPP, GODZ

ROLE OF HSV-1 GLYCOPROTEINS IN PROTECTION AND DISEASE

HSV-1 encodes at least 85 genes (1) and 12 of these genes code for glycoproteins (1–6). These glycoproteins (gB, gC, gD, gE, gG, gH, gI, gJ, gK, gL, gM, and gN) are the major inducers and targets of humoral and cell-mediated immune responses following infection (4, 7–10). We have constructed recombinant baculoviruses expressing high levels of each of the 10 HSV-1 glycoprotein

genes (3–6, 11–20). Based on immunization studies in mice, we have classified these 10 baculovirus-expressed genes into four groups: (i) Immunization with gB, gC, gD, gE, or gI completely protects mice against lethal challenge (11–15); (ii) No significant protection was seen with gH, gJ, and gL (5, 6, 16–18); (iii) Immunization with gK leads to severe exacerbation of eye disease (3, 19, 20); and (iv) Immunization with gG also showed a tendency to be harmful (6, 16).

HERPES STROMAL KERATITIS (HSK)

HSV-1-induced CS, also broadly referred to as herpes stromal keratitis (HSK), can lead to blindness. HSV-1 is the leading cause of corneal blindness due to an infectious agent in developed countries (21–26). In the U.S., \sim 30,000 people suffer recurrent ocular HSV episodes annually, requiring doctor visits, medication, and in severe cases, corneal transplants. It is estimated that 70-90% of American adults have antibodies to HSV-1 and/or HSV-2, and about 25% of these individuals have clinical symptoms upon routine clinical exam (21-26). HSV-1 is responsible for >90% of ocular HSV infections. The global incidence of Herpes Keratitis is roughly around 1.5 million including 40,000 new cases of severe visual impairment and blindness each year (27). A significant proportion (15-50%) of primary genital herpes is caused by HSV-1, and recent studies indicate that the proportion of first clinical episode genital herpes due to HSV-1 is increasing (28-30). Despite the frequent recurrence of ocular herpes, there are no vaccines available for HSV infections (31). In addition, no drug has been FDA approved for the prevention of ocular recurrences.

HERPES INFECTION AS AN IMMUNE-MEDIATED EVENT

Viral infections trigger the host immune response in a way that the immune system gets highly compromised (32). Chronic viral infections have evolved different mechanisms by which they escape the response of protective immune response presenting a serious challenge to the infected host (32). Many factors come into play, which are responsible for causing the spread of the disease and, if not properly managed, it can pose a serious threat to the host (33). Current therapies for treatment of ocular HSV-1 infection include the use of antiviral drugs and corticosteroids which can minimize the lesions but often lead to certain side effects (34); therefore, new measures need to be adopted. Studies on mouse models of ocular HSV-1 infection have unraveled many insights into the disease pathogenesis paving ways to future innovative therapies (35, 36). It is well-documented that HSV-1 pathology is a consequence of the immune response mounted by the host after virus infection and therefore, it is considered an immunopathological disease (37). During the course of HSV-1 infection, a series of events take place involving the replication of virus in the epithelial cells and formation of new blood vessels which accounts for the angiogenic response (33). The infectious virus is cleared from the eye by day 6-7 post infection, but secondary effects lead to the induction of strong cellular immune response with the appearance of immune cell infiltrates in the cornea resulting in damage to the eye (38, 39). Recent studies done in mice showed that HSV-1 infection also leads to corneal nerve damage/retraction, which results in loss of corneal sensitivity and blink reflexes and promotes HSK pathogenesis (40).

In this review, we will discuss the role of gK in HSV-1-induced CS and will propose new potential therapeutic approaches to reduce or control gK-induced CS.

gK AND ITS ROLE IN HERPES INFECTION

gK encoded by the UL53 gene is one of the HSV-1 glycoproteins and is expressed on the virions (1, 3, 41). gK is a highly hydrophobic 338-amino acid protein with a predicted molecular mass of 37 kDa (1). gK has a cleavable 30-amino-acid NH2terminal signal sequence and is N-glycosylated on amino acids 48 and 58 (1, 42, 43). In HSV-1 infected cells, gK is expressed as a 39 kDa high-mannose precursor polypeptide, designated precursor gK (pgK), which is further glycosylated to produce a 41 kDa mature glycoprotein (41). When we expressed gK using a recombinant baculovirus, four gK-related baculovirus-expressed polypeptides of 29-, 35-, 38-, and 40-kDa were detected (3). The 35-, 38-, and 40-kDa species were susceptible to tunicamycin treatment revealing that they were N-glycosylated. The 35kDa protein represented the cleaved and partially glycosylated peptide, whereas the 29-kDa protein represented the cleaved unglycosylated peptide. gK translated in vitro had a molecular mass of 36 kDa with four possible membrane-spanning regions (43, 44). Studies using insertion/deletion mutants have shown the importance of gK in virion morphogenesis and egress (45-47). Deletion of gK results in the formation of extremely rare microscopic plaques indicating that gK is required for virus replication, a concept that is supported by the observation that gK-deficient virus can only be propagated on complementing cells that express gK (45, 46).

gK shares 100% amino acid homology between different strains of HSV-1 (1, 48, 49). Similar to HSV-1 gK, HSV-2 is also 338 amino acids long but with ~84% amino acid homology (1, 50, 51). In addition to HSV-1 and HSV-2, gK is also present in other members of alphaherpes viruses. The gK homologies between different alphaherpes viruses are shown in Figure 1. Protein sequence alignment is illustrated using clustal omega, in which we show that gK from Macacine Herpes Virus 1 (McHV-1), Bovine Herpes Virus 1 (BoHV-1) and Varicella zoster virus (HH3, VZV), share 66, 33 and 28% sequence homology with HSV-1 gK, respectively (Figure 1). Kousoulas' group reported that HSV-1 gK is a structural component of virion particles and demonstrated that gK is a Golgi complex-dependent glycosylated species (52). Previously, it was shown that HSV-1 UL20 is required to interact with gK for HSV-1 infection (53). Also, a similar study with Bovine herpes virus type 1 (BoHV-1), a member of the alphaherpes virus family, demonstrated that BoHV-1 gK and UL20 proteins function together in a manner similar to HSV-1 gK and UL20 in virus spread and infection. UL20 has a role in cell surface expression of gK but is not required

```
HSV-1
            -MLAVRSLOHLSTVVLITAYGLVLVWYTVFGASPLHRCIYAVRPTGTNNDTALVWMKMNO 59
HSV-2
            -mlavrslqhlttvifitayglvlawyivfgasplhrciyavrpagahndtalvwmkinq
HHV3
            MQALGIKTEHFIIMCLLSGHAVFTLWYTA-RVKFEHECVYATTV---INGGPVVWGSYNN
McHV-1
            -mlavrslrhlttlclvtayglvlgwyvvfganpahrciyavrpvgagndtapawmrtnk
BoHV-1
            -mllggrtvnlaalalltahlalalwval-aarcq-rcacvrat---arngslrwelrsp 54
                     :: :::::: *
HSV-1
            TLLFLGAPTHPP-NGGWRNHAHICYANLIAGRVVPFQVPPDAMNRRIMNVHEAVNCLETL 118
HSV-2
            tllflgpptapp-ggawtpharvcyaniiegravslpaipgamsrrvmnvheavncleal
HHV3
            SLIYVTFVNHSTFLDGLSGYDYSCRENLLSGDTMVKTAISTPLHDKIRIVLGTRNCHAYF
McHV-1
            sllflsggrp-p-aedprdptalcrgdvigghavslpaappgsgprvmivqeavnclaal
BoHV-1
            gavyvwggann----atlaadapcrhavvqhippglldgdealhgrvravagardcrayl
                                                        :: * ::*
            WYTRVRLVVVGWFLYLAFVALHQRRCMFGVVSPAHKMVAPATYLLNYAGRIVSSVFLQYP 178
HSV-1
HSV-2
            wdtqmrlvvvgwflylafvalhqrrcmfgvvspahsmvapatyllnyagrivssvflqyp 178
HHV3
            WCVOLKMIFFAWFVYGMYLOFRRIRRMFGPFRSSCELISPTSYSLNYVTRVISNILLGYP
McHV-1
            wdtqvrliavswflylafvtlhqrrcmfgvvspahkmvapatyllnyagrvvssvllryp 177
BoHV-1
            wcaqarggllawllyvafvylrqerrmfglcrndadflspggytlnyaaaalaavvghgp 170
                    ..*::* :: ::: * ***
                                              . . . . *
HSV-1
            YTKITRLLCELSVQRQNLVQLFETDPVTFLYHRPAIGVIVGCELMLRFVAVGLIVGTAFI 238
HSV-2
            ytkitrllcelsvqrqtlvqlfeadpvtflyhrpavgvivgcelllrfvalglivgtali
HHV3
            YTKLARLLCDVSMRRDGMSKVFNADPISFLYMHKGVTLLMLLEVIAHISSGCIVLLTLGV
McHV-1
            ytkitrllcelsvqrqslveifeadpvtflyhrpaigtavgceillrvasqgliastaiv
                                                                         237
BoHV-1
            ytklarlmcelsarrralavdfrldplgcawrpraalpl-laegfarlgariaaagsv-g 228
            ***::**:*: * : *. **: :
                                                      * : :. :
HSV-1
            SRGACAITYPLFLTITTWCFVSTIGLTELYCILRRGPAPKNADKA--AAPGRSKGLSGVC 296
HSV-2
            srgacaithplfltittwcfvsiialtelyfilrrgsapknaepa--aprgrskgwsgvc
HHV3
            AYTPCALLYPTYIRILAWVVVCTLAIVELISYVRPKPTKDNHL----NHINTGGIRGIC
McHV-1
            pwgacaiayplflniitwcfvsaillaeayfvargesappgsekg--prppkrgglagic
BoHV-1
            ithpcaaayplylkiwawvhvalfaglelvsllyrkprrrggtcagdggdggesgirkvc
                ** :* :: * :* *. :
HSV-1
            GRCCSIILSGIAVRLCYIAVVAGVVLVALHYEQEIQRRLFDV-----
                                                                338
HSV-2
            grccsiilsgiavrlcyiavvagvvlvalryeqeiqrrlfdl------
                                                                338
HHV3
            TTCCATVMSGLAIKCFYIVIFAIAVVIFMHYEQRVQVSLFGESENSQKH
                                                                340
McHV-1
                                                                337
            grccsiilsgiavrlcyvaivavvvvvafryeqeiqrrifdt-----
BoHV-1
            vnccstllagllvkalylaaivggviallhyehnlrlrllgaqt-----
                                                                332
              **: :::*: :: *:. .. *: ::**:.:: ::.
```

FIGURE 1 | gK protein sequence alignment in different strains of alphaherpes viruses. Protein sequence was aligned by clustal omega and percentage of amino acid homology was compared among different groups of Herpes viruses. HSV-1 has 85% homology with HSV-2, 66% homology with McHV-1, 34% homology with BoHV-1, and 28% homology with VZV. Stars (*) indicate that the amino acids sequences are the same.

for gK-mediated cell fusion (54). It has also been demonstrated that UL20 plays a critical role in virion envelopment, and virions lacking either gK or UL20 fail to form an envelope. A similar role has been assigned to HSV-1 UL37 protein in cytoplasmic virion envelopment, and it was shown that UL37 interacts with gK-UL20 protein complex in infected cells and facilitates in virion cytoplasmic envelope (55).

Recently, we reported that HSV-1 UL20 binds to and is palmitoylated by GODZ (also known as DHHC3), a Golgi apparatus-specific Asp-His-His-Cys (DHHC) zinc finger protein and an essential component of virus infectivity (56). Palmitoylation of UL20 is critical for gK cell surface localization. Thus, the use of GODZ dominant-negative mutant or GODZ shRNA can be a potential way of inhibiting the binding of UL20 to GODZ, which can affect gK localization and viral replication.

We further showed the importance of GODZ in HSV-1 infection using knockout mice. $GODZ^{-/-}$ mice ocularly infected with HSV-1 had reduced ocular virus replication and reduced latency-reactivation as compared with wild type control mice. Our study also showed that the absence of GODZ resulted in blocking of palmitoylation of UL20 and affected the localization of gK along with the reduced expression levels of UL20, gK, and gB transcripts in the corneas of HSV-1 infected $GODZ^{-/-}$ mice (57).

Recently, it was shown that intramuscular injection with HSV-1 (F) mutant virus, which lacks the expression of gK conferred significant protection against either virulent HSV-1 strain McKrae or HSV-2 strain G intravaginal challenge in mice (58). To test if disruption of gK/UL20 interactions with gB would lead to reduced viral load, a recombinant virus (VC2) was

constructed with specific mutations in gK and its binding protein UL20. Intramuscular injection with VC2 indeed protected 100% of mice against virulent HSV-1 strain McKrae or HSV-2 strain G challenges by providing cross-reactive humoral and cellular immunity (59).

Additionally, gK binds with different affinity in different cell types (Figure 2) to signal peptide peptidase (SPP) also known as minor histocompatibility antigen H13 (60). To illustrate this binding, recombinant gKV5DI, gKV5DII, gKV5DIII, and gKV5DIV viruses were constructed expressing V5 epitope tags in frame within domains I, II, III, and IV of gK, respectively (52, 61). We infected rabbit skin (RS), HeLa and Vero cells with each virus and evaluated the co-localization of V5-gK and endogenous SPP. There was a strong co-localization in all the cell lines (RS, HeLa and Vero) when the V5 tag was expressed on cytoplasmic domains (II and III) compared to when it was expressed on extracellular domain (I and IV) (Figure 2). Binding of gK to SPP can be blocked by SPP inhibitors like aspirin, ibuprofen, L685, 458, (Z-LL)₂ ketone, and DAPT (62). These inhibitors significantly reduced viral replication in HSV-1 infected eye and reduced pathology. Thus, blocking the binding of SPP to gK can be one of the potential approaches toward treating HSV-1 induced CS (62).

gK AND VIRUS ENTRY

HSV-1 induced CS begins with the binding of viral glycoproteins to the host cell entry receptors. There are at least seven known receptors including herpes virus entry mediator (HVEM) as well as nectin-1, nectin-2, 3-O-sulfated heparan sulfate (3-OS-HS), paired immunoglobulin-like type 2 receptor (PILR α), nonmuscle myosin heavy chain IIA (NMHC-IIA), and myelin-associated glycoprotein (MAG) (2, 63–72). For gK to potentiate its disease severity, the amino terminal of gK binds to the amino terminal of gB, which leads to the virus entry and disease progression (73). gB binds to Akt-1 during virus entry and it induces Akt phosphorylation and intracellular calcium release. A recent study done by Kousoulas' group showed that deletion of

amino acids 31-68 within the amino terminus of gK inhibits gB binding to Akt-1 and thus blocks virus entry and its progression (74). Studies by the same group showed that both gK and PlLRα (paired immunoglobulin-like type 2 receptor α) bound gB in infected cells and that the association between gB-PILRα protein complex regulates membrane fusion of virus and the host cell which aids in virus penetration (75). Along with the role of amino terminus of gK in virus entry, a recent study described the role of two conserved N-linked glycosylation sites (N48 and N58) of gK in virus-induced cell fusion and replication (76). Mutation at N58 to alanine (N58A) resulted in extensive virus-induced cell fusion. The same group showed that mutation of cysteine residues within the amino terminus of gK, C37, and C114, led to significant reduction in virus production (76). In addition, gK plays a vital part in the recruitment of other viral glycoproteins into intracellular virus assembly. A recent study found that gM plays a major role in synergy with gK/UL20 in the incorporation of gD and gH/gL into mature virions (74).

ROLE OF gK-INDUCED CELLULAR RESPONSES

Adaptive immune responses play a major role in HSV-1 pathogenesis. The role of CD8⁺ T cells in HSV-1 pathogenesis is currently unclear and needs deeper investigation. There are studies reporting that CD8+ T cells play a protective role, whereas other studies show that CD8+ T cells exacerbate the disease pathogenesis (77, 78). There is evidence supporting that gK is the only HSV-1 glycoprotein responsible for exacerbation of HSV-1 induced corneal scarring (CS). Research done by our team shows that a virus construct of HSV-gK³ which is derived from the virulent HSV-1 strain McKrae mediates critical effects on HSV-1 pathogenicity in mice (79). Mice infected with HSVgK³ showed severe CS compared with control mice infected with wild type virus. HSV-gK³ infected mice had elevated levels of virus replication and also had significantly higher number of CD8⁺ T cells (79). Depletion of CD8⁺ T cells and not CD4⁺ T cells reduced CS in HSV-gK³ infected mice to the level of wild

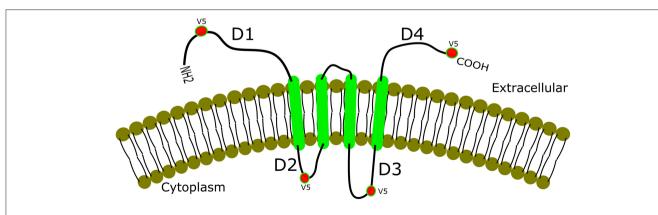


FIGURE 2 | Co-localization of gK and SPP. gK is a highly hydrophobic protein with four transmembrane domains. Epitope-tagging of four different domains of gK is shown with a strong co-localization of the two cytoplasmic domains (labeled D2 and D3 in the figure). Extracellular domains (D1 and D4), on the other hand, show weak or no co-localization with SPP in RS. HeLa, and Vero cell lines.

type infected mice. Overall, we have shown that exacerbation of eye disease in response to gK immunization or following ocular infection with recombinant viruses expressing additional copies of gK is associated with CD8 $^+$ T cell and not CD4 $^+$ T cell responses. Other studies have shown that CD4 $^+$ T cells are involved in HSK (80–83). Thus, in the context of CD8 $^+$ -induced gK pathogenicity the role of CD4 $^+$ T cells to disease or protection cannot be ruled out.

We previously looked into what region of gK participates in T cell proliferation and subsequently IFN-γ production (84). To this end, a panel of 33 overlapping peptides spanning all 338 amino acids of the gK polypeptide were produced. Splenocytes from mice were stimulated with each peptide individually both in vivo and in vitro. We found that out of 33 peptides, peptide 2 was involved in T cell proliferation and IFN-y production in vivo and in vitro and accounted for 52% of CTL activity in vivo. The percentages of IFN-γ production by both CD4⁺ T and CD8⁺T cells in vivo and the CTL responses are illustrated in Table 1. In vitro results showed that CD8⁺ T cells produced more IFN-γ compared to CD4⁺ T cells. Our study confirmed that both CD4⁺ and CD8⁺T cells produced IFN-γ when stimulated with peptide 2, but IFN-γ production by CD4⁺ T was CD8⁺ T cell-dependent. In connection with our mapping studies (3, 79), we identified a highly conserved gK epitope (ITAYGLVL) within the peptide STVVLITAYGLVLVW, which served as an immunodominant gK T cell stimulatory region both in vitro and in vivo (84). This peptide is highly conserved between HSV-1 and HSV-2 strains. To investigate its role in HSV-1 infection, the octamer (8mer) was administered as an eye drop an hour before ocular infection. This resulted in a significant increase in viral replication leading to enhancement of CS, along with strong cytotoxic CD8⁺ T cell responses and IFN-γ production (85). Mutations in the signal sequence of gK using recombinant viruses that expressed two additional copies of the mutated (MgK) or native (NgK) form of the gK blocked cell surface expression of gK in RS cells resulting in reduced reactivation and hence, less ocular disease when compared to RgK (revertant) virus. This study confirms the role of octamer within the signal sequence of gK in HSV-1 pathogenesis (86). Another study showed that the amino terminus of gK was essential for neuroinvasiveness and acute HSK using a recombinant HSV-1 (McK∆gK31-68), which was lacking the 38 amino acids from gK amino terminus. In McK∆gK31-68 mutant viral infection, there were no significant disease symptoms (87).

Hendricks's group looked at HSV-1-specific CD8⁺ T cell repertoire in C57BL/6 mice that respond to 376 predicted HSV-1 CD8⁺ T cell epitopes in C57BL/6 mice (88). Out of 376 HSV-1 CD8⁺ T cell epitopes, only 19 (gB₄₉₈₋₅₀₅ and 18 subdominant epitopes) stimulated CD8⁺T cells in spleen and TG of HSV-1 infected mice. The data in comparison to all these epitopes demonstrated that majority of the CD8⁺T cells in spleen and TG of HSV-1 infected mice responded to gB₄₉₈₋₅₀₅ HSV-1 epitope and as expected the authors showed that gK peptide corresponding to aa 54-62 was recognized by CD8⁺ effector T cells in TG and spleen of infected mice (88). So, collectively our study and Hendricks's group showed that CD8⁺ T cells in C57BL/6 mice recognize various HSV-1 epitopes, especially

TABLE 1 | IFN-γ production and CTL activity from both CD4⁺T and CD8⁺T cells when stimulated with gK synthetic peptides^a.

Peptide	gK aa	CD4 ⁺ IFN _γ ⁺	CD8 ⁺ IFNγ ⁺	CTL activity
1	MLAVRSLQHLSTVVL	2%	1%	9%
2	STVVLITAYGLVLVW	21%	8%	52%
3	LVLVWYTVFGASPLH	3%	2%	-
4	ASPLHRCIYAVRPTG	ND	ND	ND
5	VRPTGTNNDTALVWM	ND	ND	ND
6	ALVWMKMNQTLLFLG	ND	ND	ND
7	LLFLGAPTHPPNGGW	ND	ND	ND
8	PNGGWRNHAHICYAN	ND	ND	ND
9	ICYANLIAGRVVPFQ	ND	ND	ND
10	VVPFQVPPDAMNRRI	ND	ND	ND
11	MNRRIMNVHEAVNCL	ND	ND	ND
12	AVNCLETLWYTRVRL	ND	ND	ND
13	TRVRLVVVGWFLYLA	ND	ND	ND
14	FLYLAFVALHQRRCM	ND	ND	ND
15	QRRCMFGVVSPAHKM	ND	ND	ND
16	PAHKMVAPATYLLNY	ND	ND	ND
17	YLLNYAGRIVSSVFL	ND	ND	ND
18	SSVFLQYPYTKITRL	ND	ND	ND
19	KITRLLCELSVQRQN	ND	ND	ND
20	VQRQNLVQLFETDPV	ND	ND	ND
21	ETDPVTFLYHRPAIG	ND	ND	ND
22	RPAIGVIVGCELMLR	ND	ND	ND
23	ELMLRFVAVGLIVGT	ND	ND	ND
24	LIVGTAFISRGACAI	ND	ND	ND
25	GACAITYPLFLTITT	ND	ND	ND
26	LTITTWCFVSTIGLT	ND	ND	ND
27	TIGLTELYCILRRGP	ND	ND	ND
28	LRRGPAPKNADKAAA	ND	ND	ND
29	DKAAAPGRSKGLSGV	ND	ND	ND
30	GLSGVCGRCCSIILS	ND	ND	ND
31	SIILSGIAVRLCYIA	ND	ND	ND
32	LCYIAVVAGVVLVAL	ND	ND	ND
33	VLVALHYEQEIQRRL	ND	ND	ND

^aSplenocytes from naive BALB/c mice were prepared and tested for in vivo cytolytic activity as was reported (84). Cells were pulsed with respective peptides for 18 h and cytolytic activity was measured by FACS analysis. ND, Not detected.

gK but this is in contrast to human TG study in which it was indicated that the human TG is an immunocompetent environment for both CD4+ and CD8+ T cell recognition of diverse HSV-1 proteins expressed during latent infection (89). The infiltration of CD4+ and CD8+ T cells was measured in 15 TG of eight HSV-1 IgG seropositive donors by flow cytometry. It was found that there were equivalent numbers of CD4+ and CD8+ T cells, with a median ratio of CD4+ and CD8+ T cells of 0.99 (range 0.01–9.32). Also, peptide-specific CD8+ T cell responses were detected in two TG which recognized four HLA-A*0101-restricted peptides: gL_{66-74} , $gK_{201-209}$ and two VP16 peptides, VP16₉₀₋₉₉, and VP16₄₇₉₋₄₈₈. It was concluded that human intra-TG HSV-1-specific CD8+ T cell responses were directed to a relatively restricted number of viral proteins in

each person (89). CD8⁺ T cell depletion in gK immunized mice resulted in reduced severity of gK-induced CS in mice infected with wild type HSV-1 strain McKrae (90). The underlying mechanism of CD8⁺ T cell pathology in HSV-1 infected gK-immunized mice was confirmed by the presence of CD8⁺CD25⁺ regulatory T cells in cornea of gK immunized mice (78). Thus, similar to our results, the published studies confirmed our finding that gK induces CD8⁺ T cell responses and this response is contributing to enhancement of eye disease. This is probably the reason why depletion of CD8⁺ T cell but not CD4⁺ T cells reduced gK exacerbation of eye disease (79).

Previous studies revealed that gK sera caused antibody-dependent enhancement (ADE) of HSV-1 infection, which may explain the higher viral load in the corneas of gK-vaccinated mice (91). ADE differs from the usual process of virus entry where virus enters the host cells by binding of the viral glycoproteins to the cellular receptors. In ADE, IgG binds to a virus allowing the virus-antibody complex to attach to the host cells containing Fc receptors. A comparative study between HSK sera and non-HSK sera indicated that about 75% of found neutralizing antibodies were associated with gB, gC, gD, gE, and gI. It was shown by ELISA that sera from HSK group had significantly higher antigD and anti-gK antibodies than sera from non-HSK group.

Similarly, when mice were immunized with gD+gK, levels of neutralizing antibody titers in immunized mice were reduced by \sim 30% in comparison to mice immunized with gD alone. This is in agreement with data showing that mice immunized with gD showed $T_{\rm H}1$ response whereas mice immunized with gK exhibited a $T_{\rm H}1+T_{\rm H}2$ response. $T_{\rm H}1+T_{\rm H}2$ response in gK-immunized mice enhances the eye pathology (79).

ROLE OF gK IN HSV-1 CHRONIC INFECTION

One of the hallmarks of HSV-1 infection is the ability of the virus to establish latency in sensory neurons of an infected host (92–96). In neurons, expression of more than 80 genes of HSV-1 that occurs during lytic infection is drastically modified. The latency-associated transcript (LAT) is the only gene product consistently detected in abundance during latency in infected mice, rabbits, and humans (92–94, 97, 98). In mice, spontaneous reactivation occurs at extremely low levels and infectious virus is rarely detected. When mouse TGs are removed at autopsy and explant co-cultivated in tissue culture with indicator cells, latent virus reactivates and can be observed by the detection

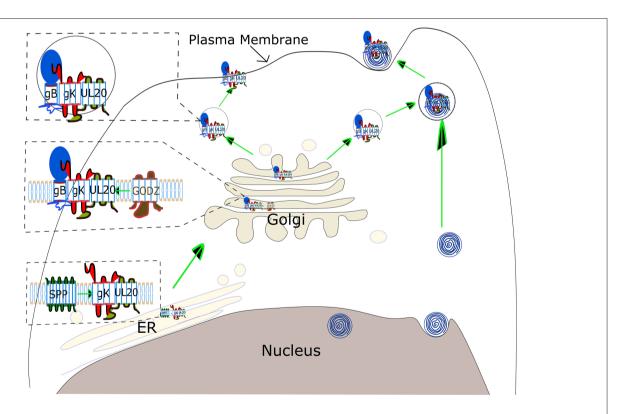


FIGURE 3 | Schematic view of gK transportation and its role in virus egress. gK binds to SPP in the ER, which is necessary for virus replication, although the precise binding domain between these two proteins has not been identified yet. gK has a signal sequence in its N-terminus, however, it is not clear if this gK signal peptide is cleaved by SPP. gK is then transported to the Golgi via a UL20-dependent pathway. UL20 is palmitoylated by the host *cis*-Golgi protein GODZ, and this post-translational modification by GODZ is necessary for transport of the gK, and UL20 complex to the plasma membrane and virus infectivity. The gK and UL20 complex is also required for gB transportation to the cell surface. The complex of three proteins, gB, gK, and UL20, is either assembled into virus capsid emerging from the nucleus in a vesicle derived from TGN (**Upper right**) or transported directly to the plasma membrane (**Upper left**).

of cytopathic effects (CPE) on the indicator cell monolayer. Reactivation from latency is not immediate, and typically CPE is not detected during the first 2-3 days of explant co-cultivation. In contrast, when cell-free lysates of latently infected TG are plated on indicator cells, CPE is not seen (20, 99). This indicates that there was no infectious virus present in the TGs and confirms that reactivation from latency by co-cultivation requires explant of intact neurons (100, 101). We previously reported that vaccination of BALB/c mice with the baculovirus-expressed gK or passive transfer of anti-gK purified IgG to naïve BALB/c mice causes severe exacerbation of HSV-1 induced CS following ocular challenge (3, 19). In addition, a productive chronic infection, rather than a latent infection, is found in most TGs (20). Similar to gK immunization or anti-gK IgG transfer, ocular challenge of naive $A_{\beta}^{-/-}$ but not $\beta_2 m^{-/-}$ mice with HSV-1 did not result in chronic infections. Surprisingly, however, when $A_{\textrm{B}}^{\textrm{O/O}}$ mice were vaccinated even with media alone or adjuvant alone prior to ocular challenge, a chronic, rather than a latent, infection was seen (102). When SCID mice which lack both T and B cells, are challenged ocularly with HSV-1, the surviving mice have a chronic, rather than a latent infection in their TG, with significant amounts of infectious virus (103). Thus, gK enhancement of eye disease may be associated with suppression of a certain protective arm of immune response, while enhancing the harmful arm.

From the studies done above, we can make an observation that both gK and LAT plays an important role in pathogenesis of CS. Where LAT is directly involved in reactivation of the virus which leads to pathogenicity, gK follows an indirect approach toward pathology by binding to SPP, which is known to cause virus infectivity and activation of CD8 $^+$ T cells which in turn produce high amounts of IFN- γ and cytotoxic effects. We have also studied that deletion of gK in neural cell cultures leads to inhibition of virus to undergo transport in anterograde or retrograde directions, in short inhibiting the reactivation of virus. gK is known to cause severe immunopathology including cornea scaring, its effect on nerve damage can be detrimental to the host. A recent report shows that deletion of gK can significantly attenuate nerve damage caused by HSV-1 infection (104).

POSSIBLE USE OF gK FOR CONTROL OF HSV-1 INDUCED CS

Many steps have been evaluated in resolving the lesions caused after HSV-1 infection such as administering anti-viral drugs and using corticosteroids, which provide limited control of viral

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replication and are also known to cause side effects (105). Drugs like trifluridine and ganciclovir are being extensively used for patients with HSV-1 infection along with topical acyclovir to control active viral replication (106). Therefore, we need effective measures to control virus reactivation. It would be more clinically beneficial if new means are developed to prevent the initiation of pathogenesis. As discussed above, HSV-1 gK binds to SPP and UL20, while UL20 binds to GODZ (56, 60). Therefore, blocking the binding of gK to SPP, gK to UL20, or UL20 to GODZ or their combinations could be used to block HSV infectivity and pathogenesis. For example, previously we have shown that blocking the binding of gK to SPP by using SPP inhibitors can reduce CS in infected mice.

CONCLUSIONS

The journey of combating HSV-1 induced CS has started long ago, although many areas of the path of virus pathogenesis still remain unexplored (107). Seroprevalence studies have illustrated that the majority of individuals in the United States are infected with HSV-1 (108). This review focused on the role of HSV gK in the progression of disease severity. Published studies have clearly demonstrated the participation of gK in the exacerbation of CS and the immune response to gK in this process as a major pathogenic mechanism. A model of gK activity is illustrated in Figure 3. gK interacts with SPP in the endoplasmic reticulum (ER), and this interaction may be necessary for transport of gK from the ER to the Golgi. In the Golgi, gK interacts with gB and UL20. Palmitoylation of UL20 by GODZ either facilitates transport of the gB- gK- UL20 complex to the plasma membrane or viral packaging (Figure 3). Research is in progress to inhibit the function of gK in causing HSV-1 induced CS but further studies are required. Clearly, an exciting approach would be inhibiting the binding of gK to SPP, gK to UL20, and UL20 interactions with GODZ supports the goal of controlling HSK pathogenesis.

AUTHOR CONTRIBUTIONS

UJ, KT, and HG writing and editing. SW, HM, and AL editing. SW and KT designing figures.

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Blockade of LAG-3 Immune Checkpoint Combined With Therapeutic Vaccination Restore the Function of Tissue-Resident Anti-viral CD8⁺ T Cells and Protect Against Recurrent Ocular Herpes Simplex Infection and Disease

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*Correspondence:

Lbachir BenMohamed Lbenmoha@uci.edu

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Soumyabrata Roy¹, Pierre-Grégoire Coulon¹, Ruchi Srivastava¹, Hawa Vahed¹, Grace J. Kim¹, Sager S. Walia¹, Taikun Yamada¹, Mona A. Fouladi¹, Vincent T. Ly¹ and Lbachir BenMohamed^{1,2,3*}

¹ Laboratory of Cellular and Molecular Immunology, School of Medicine, Gavin Herbert Eye Institute, University of California, Irvine, Irvine, CA, United States, ² Department of Molecular Biology and Biochemistry, University of California, Irvine, Irvine, CA, United States, ³ Institute for Immunology, School of Medicine, University of California, Irvine, Irvine, CA, United States

Recurrent viral diseases often occur after the viruses evade the hosts' immune system, by inducing exhaustion of antiviral T cells. In the present study, we found that functionally exhausted herpes simplex virus type 1 (HSV-1) -specific CD8+ T cells, with elevated expression of lymphocyte activation gene-3 (LAG-3), an immune checkpoint receptor that promotes T cell exhaustion, were frequent in symptomatic (SYMP) patients with a history of numerous episodes of recurrent corneal herpetic disease. Similarly, following UV-B induced virus reactivation from latency the symptomatic wild-type (WT) B6 mice that developed increase virus shedding and severe recurrent corneal herpetic disease had more exhausted HSV-specific LAG-3+CD8+ T cells in both trigeminal ganglia (TG) and cornea. Moreover, a therapeutic blockade of LAG-3 immune checkpoint with antagonist antibodies combined with a therapeutic immunization with gB₄₉₈₋₅₀₅ peptide immunodominant epitope of latently infected B6 mice significantly restored the quality and quantity of functional HSV-1 gB₄₉₈₋₅₀₅ specific CD8⁺ T cells in both TG and cornea and protected against UV-B induced recurrent corneal herpes infection and disease. In contrast to dysfunctional HSV-specific CD8+ T cells from WT B6 mice, more functional HSV-specific CD8⁺ T cells were detected in LAG-3^{-/-} deficient mice and were associated with less UV-B induced recurrent corneal herpetic disease. Thus, the LAG-3 pathway plays a fundamental role in ocular herpes T cell immunopathology and provides an important immune checkpoint target that can synergizes with T cell-based therapeutic vaccines against symptomatic recurrent ocular herpes.

Keywords: herpes simplex type 1, CD8⁺ T cells, LAG-3, immune check point, recurrent, therapeutic, animal model, humans

INTRODUCTION

A staggering 3.72 billion individuals worldwide are infected with herpes simplex virus type 1 (HSV-1), a prevalent human viral pathogen (1–3). Herpes infection and reactivation cause complications which range from mild, such as cold sores and genital lesion, to grave, such as permanent brain damage from encephalitis in adults and neonates, and blinding recurrent corneal herpetic disease (4). After a primary acute infection of the cornea, HSV-1 travels up sensory neurons to the trigeminal ganglia (TG) where it establishes lifelong latency in its host (5–9). Potentially blinding keratitis occurring from recurrent corneal herpetic disease results from the reactivation of latent virus from neurons of the TG, anterograde transportation to nerve termini, and re-infection of the cornea (8, 9).

Controlling the establishment of HSV-1 latency and preventing reactivation from TG involves dynamic crosstalk between the virus and CD8⁺ T cells within the latently infected TG microenvironment (5, 6, 8-10). However, the molecular mechanisms by which such interactions occur remain to be fully elucidated. HSV-specific CD8+ T cells are selectively activated and retained in the tissues of latently infected TG (6, 8, 9). On one hand, HSV-specific CD8+ T cells can significantly reduce reactivation in TG explant from latently infected mice (5, 9), apparently by interfering with virus replication and spread following the initial molecular events of reactivation (5, 8, 9). On the other hand, HSV-1 can manage to reactivate in the face of an often-sizable pool of virus-specific CD8⁺ T cells in the TG, apparently by interfering with the quality and quantity of CD8⁺ T cells that reside in the TG (6, 9, 11). Thus, the virus appears to keep CD8+ T cells "in check" using among several mechanisms, functional impairment of T cells (i.e., exhaustion), which is usually the result of prolonged exposure of T cell to high levels of viral antigens, as occurs during productive chronic infections (12, 13). Many viruses, including HSV-1, appear to reactivate from latency and sustain their productive infection by inducing functional exhaustion of antiviral CD8+ T cells (10, 12, 14-17).

Total or partial loss of T cell function occurs following repetitive HSV-1 latent/reactivation cycles, sporadic events that occur in latently infected trigeminal ganglia (TG) (10, 18, 19). T cell dysfunction requires two signals: (1) T cell receptors (TCR) engaged by MHC presenting an HSV epitope (16); and (2) T cell co-inhibitory receptors engaged by their ligands expressed on infected cells (e.g., infected sensory neurons of TG) (10, 20). When T cell dysfunction develops under conditions of repetitive exposure to viral antigens it is called exhaustion [reviewed in (21)]. This is usually linked with the expression of a long list of T cell co-inhibitory receptors including: programmed death-1 (PD-1), T cell immunoglobulin mucin-(TIM)-3, lymphocyte activation gene-3 (LAG-3, also known as CD223), T cell immunoreceptor with Ig and ITIM domains (TIGIT), Pselectin glycoprotein ligand-1 (PSGL-1), 2B4 (also known as CD244), glucocorticoid-induced TNFR-related protein (GITR, also known as TNFRSF18), CD160, cytotoxic T-lymphocyteassociated protein 4 (CTLA-4, also known as CD152), Band T-lymphocyte attenuator (BTLA also known as CD272), and V-domain immunoglobulin suppressor of T cell activation (VISTA) [reviewed in (16, 22)]. In humans, sporadic molecular reactivations of latent HSV-1 from sensory neurons of the TG is accompanied by chronic CD8⁺ T cell infiltrates (23-27). The cellular and molecular immune mechanisms that control the HSV-1 latency-reactivation cycle remain to be fully elucidated. Nevertheless, at least a portion of these virus reactivations in the TG appears to be controlled by CD8+ T cell-mediated mechanisms (8, 10, 28). Many of these gangliaresident CD8+ T cells express PD-1 (25). However, there is not much information: (i) on the exhaustion states of HSVspecific CD8⁺ T cells that reside in the TG of HSV-1 seropositive individuals; nor (i) on the phenotypic and functional exhaustion characteristics of HSV-specific CD8⁺ T cells from symptomatic (SYMP) individuals (who develop frequent, recurrent herpetic disease) and asymptomatic (ASYMP) individuals (who never experience any recurrent herpetic disease despite being infected). Based on these collective observations, we hypothesized that: (i) HSV-1 latently infected TG, with spontaneous or UV-B induced sporadic virus reactivation, would harbor CD8+ T cells that express at least some of the T cell co-inhibitory receptors above and exhibit functional exhaustion; and (ii) therapeutic blockade of the highly expressed T cell inhibitory receptors, to restore the function of TG-resident anti-viral CD8⁺ T cells combined with a therapeutic vaccination to further boost the number and the function of HSV-specific CD8⁺ T cells that reside in TG would markedly improve clinical outcomes and protect against recurrent corneal herpes infection and

In the present study, we tested the above hypotheses by: (i) Comparing phenotypic and functional exhaustion of peripheral blood-derived HSV-specific CD8+ T cells from SYMP and ASYMP individuals; and (ii) Studying phenotypic and functional exhaustion of cornea and TG-derived HSV-specific CD8+ T cells using our established mouse model of recurrent ocular herpes. In this model, UV-B irradiation of the cornea of latently infected B6 mice induces HSV-1 reactivation from latently infected TG, as measured by shedding of reactivated virus in tears, in turn leading to recurrent herpetic corneal disease (29, 30). We found that: (i) Both PD-1 and LAG-3 co-inhibitory receptors were expressed at significantly higher levels on HSVspecific CD8+ T cells from SYMP individuals, with severe recurrent corneal disease, compared to ASYMP individuals with no disease; (ii) Higher prevalence of HSV-specific LAG-3+CD8+ T cells and PD-1+CD8+ T cells were present in SYMP individuals compared to ASYMP individuals; (iii) In the B6 mouse model of recurrent ocular herpes, following UV-B induced reactivation, most effector CD8⁺ T cells from the cornea and TG expressed higher levels of LAG-3 and PD-1; (iv) This phenotype correlated with functional exhaustion of HSV-specific CD8⁺ T cells and with increased virus reactivation, as measured by shedding of reactivated virus in tears, and severe recurrent cornea herpetic disease; and (v) Blockade of LAG-3 pathway combined with therapeutic immunization of latently infected B6albino mice reversed the exhaustion of HSV-specific CD8+ T cells, in both TG and cornea, associated with protection against UV-B induced recurrent corneal herpes infection and disease.

TABLE 1 | Cohorts of HLA-A*02:01 positive, HSV seropositive symptomatic and asymptomatic individuals enrolled in the study.

Subject-level characteristic	All subjects ($n = 39$)	
Gender [no. (%)]:		
Female	15 (51%)	
Male	14 (49%)	
Race [no. (%)]		
Caucasian	19 (66%)	
Non-Caucasian	10 (34%)	
Age [median (range) years]	39 (21-67 years)	
HSV status [no. (%)]		
HSV-1 seropositive	29 (100%)	
HSV-2 seropositive	0 (0%)	
HSV-1 and -2 seropositive	0 (0%)	
HSV seronegative	10 (100%)	
HLA [no. (%)]		
HLA-A*02:01 positive	24 (83%)	
HLA-A*02:01 negative	5 (17%)	
Herpes disease status [no. (%)]		
Asymptomatic (ASYMP)	19 (66%)	
Symptomatic (SYMP)	10 (34%)	

Definition of symptomatic and asymptomatic individuals are detailed in Materials and Methods.

Overall, our findings suggest that: (i) Besides PD-1, the LAG-3 pathway plays a fundamental role in controlling herpes T cell immunity; (ii) Blockade of the LAG-3 pathway provides an important immune checkpoint that can synergize with T cell-based therapeutic herpes vaccines to protect against recurrent ocular herpes.

MATERIALS AND METHODS

Human Study Population

All clinical investigations in this study were conducted according to the Declaration of Helsinki. All subjects were enrolled at the University of California, Irvine under approved Institutional Review Board-approved protocols (IRB#2003-3111 and IRB#2009-6963). Written informed consent was received from all participants prior to inclusion in the study.

During the last 15 years (i.e., January 2003 to July 2018), we have screened 875 individuals for HSV-1 and HSV-2 seropositivity. Patients were segregated into SYMP and ASYMP individuals based on the inclusion criteria as previously described (2, 32–33). Among the large cohort of SYMP and ASYMP individuals, 16 HLA-A*02:01 positive patients (8 ASYMP and 8 SYMP) were enrolled in this study (Table 1). SYMP and ASYMP groups were matched for age, gender, serological status, and race. The HLA-A2 status was confirmed by PBMC staining with 2 µl of anti-HLA-A2 mAb (clone BB7.2; BD Pharmingen Inc., San Diego, CA), at 4°C for 30 min. The cells were washed and analyzed by flow cytometry using a LSRII (Becton Dickinson, Franklin Lakes, NJ). The acquired data were analyzed with FlowJo software (BD Biosciences, San Jose, CA).

Human Peripheral Blood Mononuclear Cells (PBMC) Isolation

Individuals (negative for HIV, HBV, and with or without any HSV infection history) were recruited at the UC Irvine Institute for Clinical and Translational Science (ICTS). Between 40 and 100 mL of blood was drawn into Vacutainer® Tubes (Becton Dickinson). The serum was isolated and stored at -80° C for the detection of anti-HSV-1 and HSV-2 antibodies, as we have previously described (31). PBMCs were isolated by gradient centrifugation using leukocyte separation medium (Life Sciences, Tewksbury, MA). The cells were then washed in PBS and resuspended in complete culture medium consisting of RPMI1640, 10% FBS (Bio-Products, Woodland, CA) supplemented with 1x penicillin/streptomycin/L-glutamine, 1x sodium pyruvate, 1x non-essential amino acids, and 50 µM of 2-mercaptoethanol (Life Technologies, Rockville, MD). Freshly isolated PBMCs were also cryo-preserved in 90% FCS and 10% DMSO in liquid nitrogen for future testing.

Human T Cells Flow Cytometry Assays

The following anti-human antibodies were used for the flow cytometry assays: CD3 A700 (clone SK7; BioLegend, San Diego, CA), CD8 PE-Cy7 (clone SK1; BioLegend) PD-1 FITC (clone EH12.2H7; BioLegend), LAG-3 PerCPCy5.5 (clone 11C3C65; BioLegend), For the surface stain, mAbs against cell markers were added to a total of 1×10^6 cells in 1X PBS containing 1% FBS and 0.1% sodium azide (FACS buffer) for 45 min at 4°C. After washing twice with FACS buffer, cells were fixed in PBS containing 2% paraformaldehyde (Sigma-Aldrich, St. Louis, MO). For each sample, 100,000 total events were acquired on the BD LSRII. Ab capture beads (BD Biosciences) were used as individual compensation tubes for each fluorophore in the experiment. To define positive and negative populations, we used fluorescence minus controls for each fluorophore. Furthermore, we optimized gating by examining known negative cell populations for background expression levels similar to that used in our previous work (7). Briefly, we gated single cells, dump cells, viable cells (Aqua Blue), lymphocytes, CD3+ cells, and CD8⁺ cells before finally gating human epitope-specific CD8⁺ T cells using HSV-specific tetramers (Figure S1). Data analysis was performed using FlowJo software (BD Biosciences, San Jose, CA). Statistical analyses were done using GraphPad Prism version 5 (La Jolla, CA).

Tetramer/VP11/12 Peptide Staining

Fresh PBMCs were analyzed for the frequency of CD8⁺ T cells recognizing the VP11/12 peptide/tetramer complexes, as we previously described (32–35). The cells were incubated with VP11/12 peptide/tetramer complex for 30–45 min at 37°C. The cell preparations were then washed with FACS buffer and stained with FITC-conjugated anti-human CD8 mAb (BD Pharmingen). The cells were then washed and fixed with 1% paraformaldehyde in PBS and subsequently acquired on a BD LSRII. Data were analyzed using FlowJo version 9.5.6 (Tree Star).

Mice

Female B6(Cg)-*Tyrc*^{-2J}/J, or B6-albino mice and LAG-3-deficient mice (LAG-3^{-/-} mice) (6 to 8 weeks old; on the C57BL/6 background) and female C57BL/6 (B6) wild-type (WT) mice (6 to 8 weeks old) were purchased from the Jackson Laboratory (Bar Harbor, ME). Animal studies were performed conforming to the *Guide for the Care and Use of Laboratory Animals* (28). Experiments were conducted with the approval of the Institutional Care and Use Committee of University of California Irvine (Irvine, CA).

Virus Production and the Ocular Challenge of Mice With HSV-1

HSV-1 (strain McKrae) was grown and tittered on rabbit skin (RS) cells as described previously (20–22). All types of mice were ocularly infected with either with 2 \times 10 5 PFU (acute phase studies) or 1 \times 10 6 PFU (reactivation studies) of strain McKrae via eye drops. Following ocular infection, mice were monitored for ocular herpes virus infection and disease.

Immunization With Immunodominant gB₄₉₈₋₅₀₅ Peptide SSIEFARL

Age-matched female mice of each type were assorted in various groups ($n=10/\mathrm{group}$). As per the experimental plan, groups of mice were immunized subcutaneously (s.c.) with the immunodominant gB₄₉₈₋₅₀₅ peptide SSIEFARL delivered with the promiscuous CD4+ T helper (Th) epitope PADRE and CpG1826 adjuvant on day 18 post-infection (PI) followed by a booster dose on day 25 PI. All immunizations were carried out with 100 uM of each peptide.

UV-B Induced Reactivation of HSV-1 From Latency in Mice

Thirty-five days post-infection, when latency was fully established, reactivation of latent HSV-1 infection was induced following UV-B irradiation in all groups of mice (30). TM20 Chromato-Vu transilluminator (UVP, San Gabriel, CA), which emits UV-B at a peak wavelength of 302 nm was used for the purpose. Anesthetized [Intraperitoneal (IP) injection of ketamine/xylazine mouse cocktail 0.1 mL/20 g mouse containing 87.5 mg/kg ketamine and 12.5 mg/kg xylazine] mice were placed on the transilluminator, and each mouse was positioned on a piece of cardboard containing a hole the same size as the mouse's eye. This allowed just the eyes to be irradiated by the UV-B source. Each eye was irradiated with 250 mJ/cm² of UV-B light (60-s exposure on the transilluminator).

PD-1 and LAG-3 Blockade in Mice

Anti-PD-1 mAb (RMPI-14) and anti-LAG-3 mAb (C9B7W) were purchased from BioXcell (West Lebanon, NH). For acute phase studies, WT B6 mice were ocularly infected with 2×10^5 PFU of strain McKrae and treated on day 3, 5, and 7 with IP injection of 200 μg of anti-PD-1 mAb or anti-LAG-3 mAb during the acute phase. For reactivation studies, in some designated groups, UV-B irradiation was performed on day 35 and subsequently treated on day 37, 39, and 41 with IP injection of 200 μg of anti-LAG-3 mAb.

Monitoring of Ocular Herpes Infection and Disease in Mice

Virus shedding during the acute phase and that induced by UV-B irradiation was quantified in eve swabs collected every day during the acute phase and post-UV-B irradiation (up to day 8). Eyes were swabbed using moist type 1 calcium alginate swabs and frozen at -80° C until titrated on RS cell monolayers, as described previously (30-34). Animals were examined for signs of recurrent corneal herpetic disease by slit lamp camera (Kowa American Corporation, Torrance CA 90502), for 30 days post UV-B radiation; this was performed by investigators who were blinded to the treatment regimen of the mice and scored according to a standard 0-4 scale (0 = no disease; 1 = 25%; 2 = 50%; 3 = 75%; 4 = 100%) as previously described (30, 31). Total disease score of each day in each group of mice till 30-days post-UV-B exposure was noted. Cumulative graphs of eye disease were generated by dividing the total score of each day per group of mice by total number of eyes in each group and adding the value to that obtained in the succeeding day and continuing till day 30 post-UV-B. Similarly, cumulative graphs of the number of eves showing recurrent keratitis were done by dividing the total number of eyes showing disease per group of mice (irrespective of disease severity) by the total number of eyes in each group and adding the value to that obtained in the following day and continuing till 30-days post-UV-B. Average of the total score of each group for each of the 30 days post UV-B was calculated by dividing the total score of each day by the total number of eyes in each group.

Isolation of Lymphocytes

Mice from all groups were euthanized, and the spleen, cornea, and TG were individually harvested. Cornea and TG tissues were digested in complete medium containing 2.5-mg/ml collagenase type IV (Sigma Chemical Co., St. Louis, MO). Digestion was accomplished by incubation at 37°C with shaking for 30 min. After digestion, tissues and cells were filtered through a sterile gauze mesh and washed with RPMI 1640 medium. Spleen homogenates were prepared by pressing the tissue through a sterile mesh screen into 10 ml of PBS under aseptic conditions. Single-cell suspensions thus prepared from spleen, TG and cornea were analyzed using flow cytometry (Figure S1).

Mice Flow Cytometry Analysis

The following anti-mouse antibodies were used: CD3 FITC (clone17A2; Biolegend), CD8 PerCP (clone 53-6.7; BD), CD107a FITC (clone 1D4B; BD), CD107b FITC (clone Ha1/29; BD), IFN- γ -PE (clone XMG1.2; BioLegend), and Ki-67 PE/Cy7 (clone 16A8; BioLegend). Both surface and intracellular staining were performed similarly to the human study as described above.

Tetramer/gB₄₉₈₋₅₀₅ Staining

Cells harvested from spleen, TG and cornea were analyzed for the frequency of CD8 $^+$ T cells recognizing gB₄₉₈₋₅₀₅ peptide tetramer complex similarly to the human study as aforementioned

Statistical Analysis

Data for each assay were compared by ANOVA and Student's t-test using GraphPad Prism version 5 (La Jolla, CA). Differences between the groups were identified by ANOVA and multiple comparison procedures, as we previously described (33, 34). Data are expressed as the mean \pm SD. Results were considered statistically significant at P value of \leq 0.05.

RESULTS

HSV-Specific CD8⁺ T Cells, With Elevated Expression of PD-1 and LAG-3, Are Frequent in Symptomatic Patients With Recurrent Herpetic Disease

The characteristics of the symptomatic (SYMP) and asymptomatic (ASYMP) study population used in this present study, with respect to gender, age, HLA-A*02:01 frequency distribution, HSV-1/HSV-2 seropositivity and status of ocular and genital herpetic diseases are presented in Table 1 and detailed in the Materials and Methods section. Since HSV-1 is the main cause of ocular herpes, only individuals who are HSV-1 seropositive and HSV-2 seronegative were enrolled in the present study. HSV-1 seropositive individuals were divided into two groups: (i) ten HLA-A*02:01 positive, HSV-1-infected ASYMP individuals who have never had any clinically detectable herpes disease; and (ii) ten HLA-A*02:01 positive HSV-1-infected SYMP individuals with a history of numerous episodes of well-documented recurrent clinical herpes diseases, such as herpetic lid lesions, herpetic conjunctivitis, dendritic or geographic keratitis, stromal keratitis, and iritis consistent with rHSK, with one or more episodes per year for the past 5 years. Only SYMP patients who were not on Acyclovir or other anti-viral or anti-inflammatory drug treatments at the time of blood sample collections were enrolled. One patient had over two severe recurrent episodes during the last 10 years that necessitated multiple corneal transplantations.

We first sought to determine whether there is any differential frequency of HSV-specific CD8⁺ T cells expressing exhaustion markers PD-1 and LAG-3 between SYMP and ASYMP individuals. Blood-derived HSV-1 VP11/12₆₆₋₇₄ epitope specific $CD8^+$ T cells from SYMP and ASYMP (n = 8, each) individuals were analyzed by flow cytometry for the expression of LAG-3 and PD-1. A tetramer specific to the immunodominant VP11/12₆₆₋₇₄ epitope was used to decipher the expression of LAG-3 and PD-1 uniquely on HSV-specific T cell (instead of bulk CD8⁺ T cells). As shown in Figure 1A, there were no observed differences in the frequency of VP11/12₆₆₋₇₄ epitope-specific CD8⁺T cells between ASYMP (1.1%) and SYMP (1.5%) individuals. However, VP11/12₆₆₋₇₄ epitope-specific LAG-3⁺CD8⁺T cells and PD-1⁺CD8⁺T cells appeared to be more frequent in SYMP compared to ASYMP individuals (Figures 1B,C). Moreover, as shown in Figure 1D, elevated expression levels of LAG-3 and PD-1 were detected in VP11/12₆₆₋₇₄ epitope-specific CD8⁺T cells of SYMP patients compared to ASYMP healthy individuals, as depicted by a significant difference in mean fluorescent intensity (MFI) of LAG-3 and PD-1 expression.

Altogether these results indicate that both PD-1 and LAG-3 markers of exhaustion are highly expressed in HSV-specific CD8 $^+$ T cells from SYMP patients that are clinically diagnosed with the repetitive recurrent ocular herpetic disease. This data is in agreement with the functional impairment of VP11/12 $_{66-74}$ -specific CD8 $^+$ T cells we have previously reported on in SYMP individuals (2). Since LAG-3 and PD-1 markers are strong determinants of functional exhaustion, this denotes that exhaustion of antigen-specific CD8 $^+$ T cells in SYMP individuals may be a potential cause of the suboptimal immunity, often associated with symptomatic shedding.

Because of ethical and practical complexities in obtaining cornea- and trigeminal ganglia- (TG) derived CD8⁺ T cells in humans, we were limited to using blood-derived CD8⁺ T cells in humans. However, the phenotype and function of human blood-derived CD8⁺ T cells may not reflect tissue-resident CD8⁺ T cells. For these reasons, the remainder of this study utilized our established mouse model of acute and UV-B induced recurrent ocular herpes to determine the phenotypic and functional exhaustion of TG- and cornea-resident CD8⁺ T cells and their association with acute and recurrent ocular herpes. Since our results above on human blood-derived CD8⁺ T cells suggests high frequencies of HSV specific CD8⁺ T cells expressing LAG-3 and PD-1 in SYMP individuals; next, we determined the kinetics of LAG-3 and PD-1 expression in cornea and TG following HSV-1 infection in mice.

Increased Frequency and Number of HSV Specific LAG-3⁺CD8⁺ T Cells in the Cornea and TG of Ocular Herpes Infected Mice

A group of 40 mice were infected with 2×10^5 pfu of HSV-1 strain McKrae. Mice (n = 10) were sacrificed during acute and latent phases at five different time points (i.e., days 3, 8, 14, 23, and 41). Cornea and TG were harvested, and the frequencies of HSV specific (gB₄₉₈₋₅₀₅) CD8⁺ T cells expressing LAG-3 and PD-1 exhaustion markers were analyzed by FACS. The frequencies of HSV specific (gB₄₉₈₋₅₀₅) CD8⁺ T cells expressing LAG-3 appeared to increase starting on day 3 during acute infection in both cornea (33.1%) and TG (12.1%) (Figures 2A-E). The highest frequencies of HSV specific ($gB_{498-505}$) CD8⁺ T cells expressing LAG-3 were detected on day 23 during latency in both cornea (53.2%) and TG (27.2%), and those seem to persist until day 41 of latency (Figures 2B,C). Similarly, the frequencies of HSV specific (gB₄₉₈₋₅₀₅) CD8⁺ T cells expressing PD-1 increased in both the cornea and TG starting on day 3 during acute infection in both cornea (18.8%) and TG (13.3%) (Figures 2D,E). Further heightened expression of PD-1 was observed late in acute phase on day 14 in both cornea (41.2%) and TG (34.6%) and gradually diminished by day 41 during latency (**Figures 2D,E**). Intriguingly, high frequencies of LAG-3⁺CD8⁺ T cells, but not of PD-1⁺CD8⁺ T cells, were found in the cornea. In contrast, similar frequencies of LAG-3+CD8+ T cells and PD-1⁺CD8⁺ T cells were detected in the TG.

Altogether, these findings suggest that similar to HSV-1 infected SYMP humans: (i) HSV-specific CD8⁺ T cells in

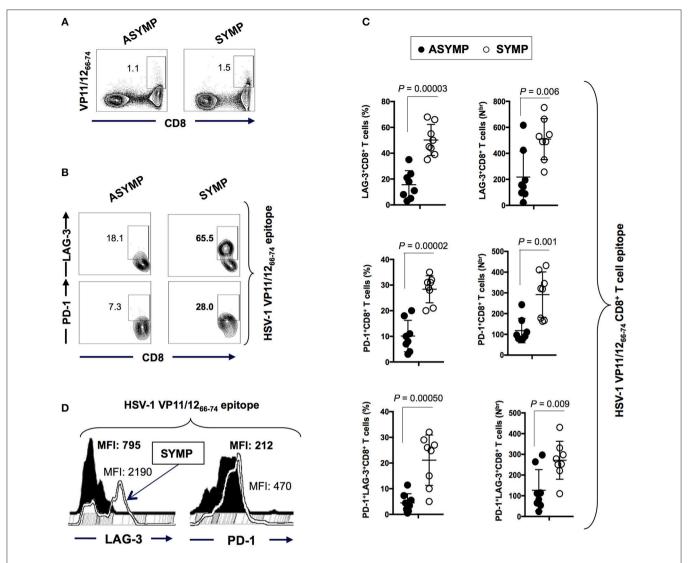


FIGURE 1 | Frequency of HSV-1 VP11/12₆₆₋₇₄ epitope-specific LAG-3+CD8+T cells and PD-1+CD8+T cells in ASYMP vs. SYMP individuals. (A) Representative FACS plot of the frequencies of HSV-1 VP11/12₆₆₋₇₄ tetramer-specific CD8+ T cells in ASYMP vs. SYMP individuals. (B) Representative FACS plot of the frequencies of LAG-3+CD8+T cells and PD-1+CD8+T cells in ASYMP and SYMP individuals. (C) Average percentages (left panels) and the absolute number (right panels) of HSV-1 VP11/12₆₆₋₇₄ tetramer-specific PD-1+ CD8+ T cells, LAG-3+ CD8+ T cells and PD-1+LAG-3+CD8+ T cells in ASYMP and SYMP individuals. (D) level of expression of LAG-3 and PD-1 receptors on CD8+ T cells from ASYMP vs. SYMP individuals, depicted as Mean fluorescent intensity (MFI). Results are representative of two independent experiments in each individual. The indicated P-values, calculated using the unpaired t-test, show statistical significance between SYMP and ASYMP individuals.

infected cornea and TG of mice show elevated expression of LAG-3 and PD-1 exhaustion markers; and (ii) a conspicuous involvement of the LAG-3 and PD-1 pathways in mediating CD8⁺ T cell exhaustion during the latent phase of symptomatic herpes infection.

Blockade of LAG-3 and PD-1 During Acute Phase Controls Herpes Infection and Disease and Strengthens the Anti-viral Immune Response

We next studied the effect of blocking LAG-3 and PD-1 using antagonist mAbs, on viral infection, disease, and anti-viral $\rm CD8^+$

T cell response during the acute phase of HSV-1 infection. A group of 40 WT B6 mice were infected with 2 \times 10⁵ pfu of HSV-1 strain McKrae. Mice were intraperitoneally (i.p.) injected with 200 μ g of anti-LAG-3 mAb (n=10) and 200 μ g of anti PD-1 mAb (n=10) at 3 different time points [i.e., days 3, 5, and 7 post-infection (PI)].

Following the blockade of both LAG-3 and PD-1, a significant decrease in viral replication and disease was evidenced (P < 0.05, **Figures 3A,B**, **4A,B**). This was associated with a significant decrease in the severity of primary ocular disease, as shown in average of 10 mice (**Figures 3B, 4B,** *right panels*) and in representative eye disease pictures (**Figures 3B, 4B,** *left panels*). Further the number and function of HSV-1 gB₄₉₅₋₅₀₅ specific

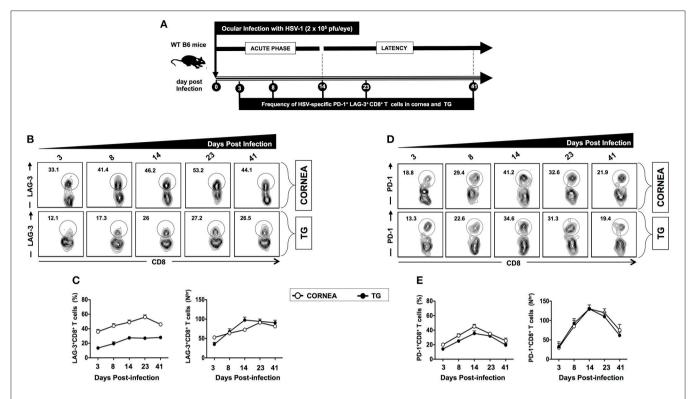


FIGURE 2 | Kinetics of LAG-3 and PD-1 expression on HSV-specific CD8+ T cells following ocular herpes virus infection. **(A)** Schematic representation of the timeline for HSV-1 infection and assays on phenotypic exhaustion of HSV-specific CD8+ T cells in WT B6 mice (6–8 weeks old, n=40), following ocular infection on day 0 with 2×10^5 pfu of HSV-1 strain McKrae, as described in *Materials* and *Methods*. A group of 10 mice were sacrificed on days 3, 8, 14 (acute phase), 23, and 41 (latent phase) post-infection (PI). Subsequently, cornea and TG were harvested, and the frequencies of the HSV specific (gB₄₉₈₋₅₀₅) CD8+ T cells expressing LAG-3 and PD-1 exhaustion markers were determined by FACS. **(B)** Representative FACS plot and **(C)** average percentages and absolute numbers of HSV-specific CD8+ T cells expressing PD-1 detected in cornea and TG at different time points. **(D)** Representative FACS plot, and **(E)** average percentages and absolute numbers of HSV-specific CD8+ T cells expressing PD-1 detected in cornea and TG at different time points. The results are representative of two independent experiments.

CD8⁺ T cells detected from αLAG-3 (**Figures 3C–J**) and αPD-1(Figures 4C-J) mAb treated mice revealed an increase in both the frequency and number of gB₄₉₈₋₅₀₅ specific CD8⁺ T cells, IFN-γ⁺CD8⁺ T cells, CD107⁺CD8⁺ T cells, and Ki-67⁺CD8⁺ T cells, as compared to isotype and mock treated control groups. Representative FACS plots showed heightened frequencies of gB₄₉₈₋₅₀₅ specific CD8⁺ T cells (αLAG-3: 10% vs. Isotype: 8%, Mock: 6.9%; αPD-1: 12% vs. Isotype: 8%, Mock: 6.9%), IFN- $\gamma^{+}CD8^{+}$ T cells ($\alpha LAG-3$: 15.6% vs. Isotype: 6%, Mock: 5.2%; αPD-1: 10.1% vs. Isotype: 6%, Mock: 5.2%), CD107⁺CD8⁺ T cells (αLAG-3: 13% vs. Isotype: 5.8%, Mock: 4.7%; αPD-1: 9.6% vs. Isotype: 6%, Mock: 5.2%) and Ki- 67^+ CD8 $^+$ T cells (α LAG-3: 10.8% vs. Isotype: 6.8%, Mock: 5.7%; αPD-1: 11.6% vs. Isotype: 6%, Mock: 5.2%) in αLAG-3 mAb (Figures 3C-J) and αPD-1 mAb (Figures 4C-J) treated groups in comparison to controls. The corresponding average percentage and average absolute number of $gB_{498-505}$ tetramer specific CD8⁺ T cells; IFN- γ ⁺ CD8⁺ T cells; CD107⁺CD8⁺ T cells and Ki-67⁺CD8⁺ T cells are also shown for αLAG-3 (Figures 3C-J) and αPD-1 (Figures 4C-J) treated groups in comparison to controls. No systemic or local side effect was detected following the blockade of both LAG-3 and PD-1 pathways.

Altogether, these results suggest that blockade of the LAG-3 and PD-1 pathways of exhaustion can be a promising strategy to combat ocular herpes. As PD-1 blockade is already widely reported to combat persistent pathogens including HSV and is the most thoroughly investigated immune checkpoint pathways, our results essentially reinforce the earlier studies, and henceforth we focused on the lesser investigated LAG-3 pathway to combat HSV reactivation.

Combination of a Therapeutic LAG-3 Blockade and Therapeutic Immunization Restored the Function of HSV-Specific CD8⁺ T Cells in Cornea and TG Associated With a Reduction in Recurrent Ocular Herpes

Subsequently, we determined whether LAG-3 blockade after HSV-1 reactivation from latently infected mice would reduce viral shedding and disease and restore antiviral immune response. We used our novel UV-B model of virus reactivation and preferred albino B6(Cg)- Tyr^{c-2J}/J mice over WT B6 mice, as they are known to be more susceptible to reactivation and recurrent corneal disease. Four groups of B6(Cg)- Tyr^{c-2J}/J mice (n = 10/group) were latently infected with 1×10^6 pfu of McKrae as described in the *Materials* and *Methods* and were

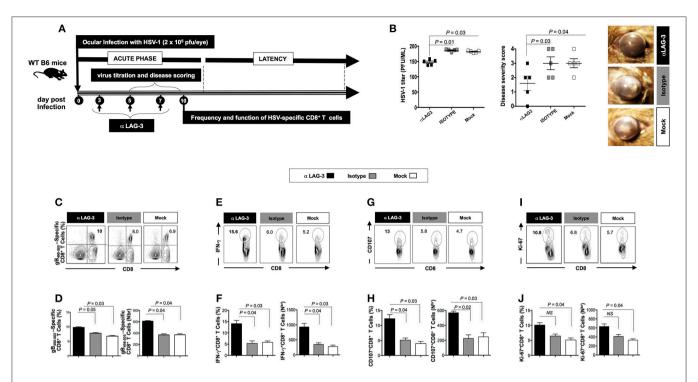


FIGURE 3 | Effects of the LAG-3 blockade on herpes infection, disease and antiviral CD8+ T cell response during the acute phase of ocular herpes infection. (A) Schematic representation of HSV-1 ocular infection, blockade LAG-3 mAb treatment, virological and immunological analyses in 30 WT B6 mice (6–8 weeks old) following ocular infection on day 0 with 2×10^5 pfu of HSV-1 (strain McKrae) as detailed in the *Materials* and *Methods* section. (B) Quantification of infectious virus particles in the eye swabs by standard plaque assay on RS cells and acute eye disease scoring on a scale of 1–4. Mean viral load (pfu/ml), mean disease score and representative eye disease pictures after the terminal day of the blockade (day 8) are shown. Representative FACS plots, average percentage and average absolute number of (C,D) HSV- specific (gB₄₉₈₋₅₀₅) CD8+ T cells (E,F) HSV-specific IFNy+CD8+ T cells (G,H) HSV-specific CD107+CD8+ T cells (I,J) HSV-specific Ki-67+CD8+ T cells in the spleen of mice from each group. The results are representative of two independent experiments. The indicated *P*-values, calculated using the unpaired t-test, show statistical significance between mAb treated and control groups.

then segregated as follows: (1) a group of $\alpha LAG-3 + gB_{498-505}$ mice was therapeutically immunized during latency on days 18 and 25 PI with gB₄₉₈₋₅₀₅ CD8⁺ T cell epitope mixed with the CD4⁺ T helper epitope PADRE and then treated three times with αLAG-3 on days 3, 5, and 7 post UV-B exposure (i.e., days 37, 39, and 41 PI, respectively); (2) a group of αLAG-3 alone, in which mice were non-immunized but therapeutically treated with $\alpha LAG-3$ as in 1; (3) a group of $gB_{498-505}$ alone, in which mice were only immunized with gB₄₉₈₋₅₀₅ CD8⁺ T cell epitope mixed with the CD4⁺ T helper epitope PADRE; and (4) a group of Mock controls, in which the mice were neither immunized nor treated with αLAG-3. All the three forms of therapeutic interventions: $\alpha LAG-3 + gB_{498-505}/PADRE$, $\alpha LAG-3$ alone, gB₄₉₈₋₅₀₅/PADRE alone significantly reduced the manifestation of UV-B induced recurrent disease compared to mock, but the combination therapy of $\alpha LAG-3 + gB_{498-505}/PADRE$ showed the most significant effect (Figures 5A-D). This is clear from both the cumulative reactivation score (Figure 5B) and the cumulative number of eyes with recurrent disease (Figure 5C). The average score of each day per group detected till day 30 post UV-B exposure also revealed significant difference between the combination therapy of $\alpha LAG-3 + gB_{498-505}$ vaccine vs. αLAG -3 alone (P = 0.05), $\alpha LAG-3+gB_{498-505}$ vaccine vs. $gB_{498-505}$

vaccine alone (P=0.04), and $\alpha LAG-3+gB_{498-505}$ vaccine vs. mock (P=0.03) (**Figure 5D**). Meanwhile, the average degree of viral shedding following the final $\alpha LAG-3$ treatment (day 8 post UV-B) showed significant difference between combination therapy of $\alpha LAG-3+gB_{498-505}$ vs. $\alpha LAG-3$ alone (P=0.04), $\alpha LAG-3+gB_{498-505}$ vs. $gB_{498-505}$ alone (P=0.03), and $\alpha LAG-3+gB_{498-505}$ vs. mock (P=0.02) (**Figure 5E**). Representative eye pictures showed significant differences in disease severity amongst all the groups (**Figure 5F**).

At the end of monitoring recurrent disease on day 30 post UV-B, we sacrificed the mice of all groups, harvested mononuclear cells (MNC's) from cornea and TG, as described in *Materials* and *Methods* and determined the number and function of HSV-specific CD8⁺ T cells. Representative FACS plots showed increased frequencies of gB₄₉₈₋₅₀₅ specific CD8⁺ T cells (Cornea: α LAG-3 + gB₄₉₈₋₅₀₅ vaccine: 25.4% vs. α LAG-3 alone: 20.3%, gB₄₉₈₋₅₀₅ vaccine alone: 18.5%, Mock: 12.8%; TG: α LAG-3+gB₄₉₈₋₅₀₅ vaccine: 28.9% vs. α LAG-3 alone: 18.1%, gB₄₉₈₋₅₀₅ vaccine alone: 21.3%, Mock: 15%), IFN- γ +CD8+ T cells (Cornea: α LAG-3 + gB₄₉₈₋₅₀₅ vaccine alone: 16%, Mock: 9%; TG: α LAG-3 + gB₄₉₈₋₅₀₅ vaccine: 40.1% vs. α LAG-3 alone: 34.5%, gB₄₉₈₋₅₀₅ vaccine alone: 29.1%, Mock: 20.2%), CD107+CD8+

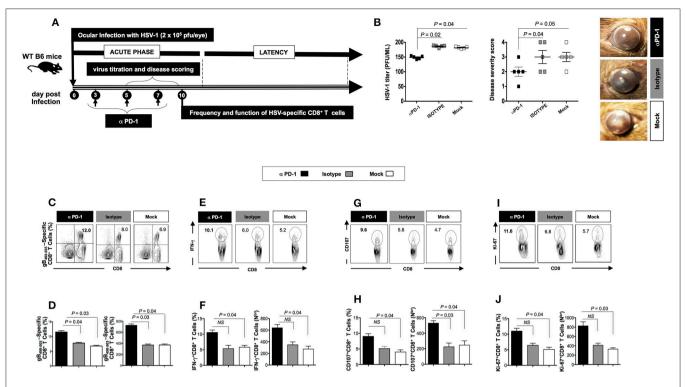


FIGURE 4 | Effect of the PD-1 blockade on herpes infection, disease and antiviral immune response during the acute phase of ocular herpes virus. **(A)** Schematic representation of HSV-1 ocular infection, blockade PD-1 mAb treatment, virological and immunological analyses in 30 WT B6 mice (6–8 weeks old) following ocular infection on day 0 with 2 × 10⁵ pfu of HSV-1 (strain McKrae) as detailed in the *Materials* and *Methods* section **(B)** Quantification of infectious virus particles in the eye swabs by standard plaque assay on RS cells and acute eye disease scored on a scale of 1–4. Mean viral load (pfu/ml), mean disease score and representative eye disease pictures after the terminal day of the blockade (day 8) are shown. Representative FACS plots, average percentage and average absolute number of **(C,D)** HSV- specific (gB_{498–505}) CD8+ T cells **(E,F)** HSV- specific IFNy+CD8+ T cells **(G,H)** HSV-specific CD107+CD8+ T cells **(I,J)** HSV-specific Ki-67+CD8+ T cells in the spleen of mice from each group. The results are representative of 2 independent experiments. The indicated *P*-values, calculated using the unpaired *t*-test, show statistical significance between mAb treated and control groups.

T cells (Cornea: $\alpha LAG-3 + gB_{498-505}$ vaccine: 24% vs. $\alpha LAG-$ 3 alone: 19%, gB₄₉₈₋₅₀₅ vaccine alone: 16.1%, Mock: 8.1%; TG: α LAG-3 + $gB_{498-505}$ vaccine: 34.2% vs. α LAG-3 alone: 28.2%, gB₄₉₈₋₅₀₅ vaccine alone: 24.2%, Mock: 13.1%), and Ki-67⁺CD8⁺ T cells (Cornea: α LAG-3 + $gB_{498-505}$ vaccine: 42% vs. αLAG-3 alone: 34.3%, gB₄₉₈₋₅₀₅ vaccine alone: 28%, Mock: 19%; TG: $\alpha LAG-3 + gB_{498-505}$ vaccine: 18% vs. $\alpha LAG-$ 3 alone: 13%, gB₄₉₈₋₅₀₅ vaccine alone: 10.2%, Mock: 5%) in combination therapy of $\alpha LAG-3 + gB_{498-505}$ vaccine group when compared with the other groups (Figures 6A,C). The corresponding average percentage and average absolute number of $gB_{498-505}$ tetramer specific CD8⁺ T cells; IFN- γ ⁺ CD8⁺ T cells; CD107+CD8+ T cells and Ki-67+CD8+ T cells are also shown for all the groups ($\alpha LAG-3+gB_{498-505}$ vaccine, $\alpha LAG-3$ alone, gB₄₉₈₋₅₀₅ vaccine alone, and mock) in cornea (**Figure 6B**) and TG (Figure 6D).

Taken together, these results suggest that the combined effect of the blockade and immunization (1) significantly combats the manifestation of disease severity during reactivation of HSV-1 from latency and (2) significantly restores HSV specific immunity in the resident tissues during latency that underscores the observed protection from recurrent ocular herpes.

Therapeutic Immunization Improves HSV-Specific CD8⁺ T Cell Response in the Cornea and TG and Protects Against Recurrent Ocular Herpes in LAG-3^{-/-} Mice

Two groups of mice (WT B6 and LAG-3^{-/-} deficient mice ($n=10/{\rm group}$) were latently infected with 1×10^6 pfu of McKrae. One group of WT B6 and one of LAG-3^{-/-} mice were immunized with the immunodominant ${\rm gB_{498-505}}$ peptide mixed with the promiscuous CD4⁺Th epitope PADRE and CpG₁₈₂₆ adjuvant as detailed in the *Materials* and *Methods* section (**Figure 7A**). The groups were then divided as follows: (1) LAG-3^{-/-} mice + ${\rm gB_{498-505}}$ vaccine; (2) LAG-3^{-/-} mice + Mock vaccine; (3) WT mice + ${\rm gB_{498-505}}$ vaccine; and (4) WT mice + Mock vaccine.

As shown in **Figures 7B–D**, the groups $LAG-3^{-/-} + gB_{498-505}$ vaccine, $LAG-3^{-/-} + Mock$ vaccine, $WT + gB_{498-505}$ vaccine showed significant reduction of recurrent disease compared to WT + Mock vaccine. Moreover, the group of mice that received the combination therapy of the $LAG-3^{-/-} + gB_{498-505}$ vaccine showed the most significant effect on recurrent corneal herpetic disease. This is evident from both the cumulative reactivation score (**Figure 7B**) and the cumulative number of eyes with recurrent disease (**Figure 7C**). As shown in **Figure 7D**

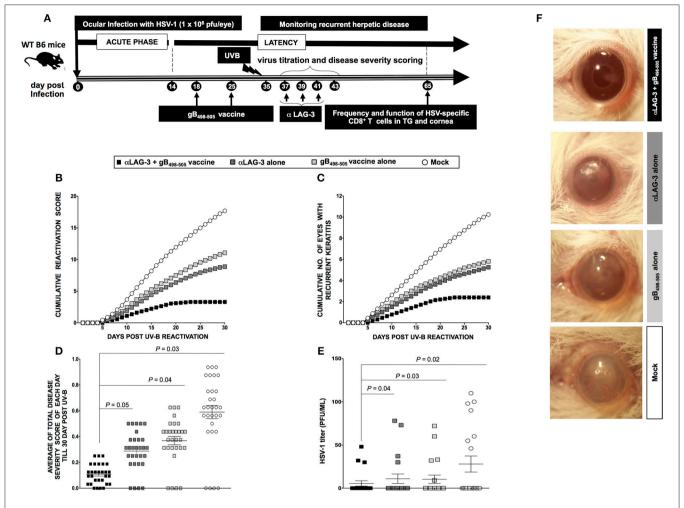


FIGURE 5 | Blockade of LAG-3 following UV-B induced HSV-1 reactivation reduces recurrent ocular herpes. (A) Schematic representation of UV-B induced reactivation, blockade by mAb treatment, virological and immunological analyses, and recurrent eye disease scoring in 40 B6(Cg)- Tyr^{C-2J} /J mice (6–8 weeks old) categorized into α-LAG-3 + $gB_{498-505}$, α-LAG-3 alone, $gB_{498-505}$ alone, and mock groups on the basis of different immunization strategies following ocular infection on day 0 with 1 × 10⁶ pfu of HSV-1 (strain McKrae). (B) Cumulative reactivation score till 30-day post UV-B. (C) The cumulative number of eyes showing recurrent disease till 30-day post UV-B. (C) Average viral shedding evaluation by plaque assay after the last day of LAG-3mAb treatment (day 8 post UV-B). (F) Representative eye pictures of recurrent disease. Results are representative of two independent experiments. The indicated P-values, calculated using the unpaired t-test, show statistical significance between α-LAG-3 + $gB_{498-505}$ and other groups.

the average of total score of each day per group, detected up to 30-day post UV-B induced reactivation, showed a significant difference between; LAG-3 $^{-/-}$ + gB₄₉₈₋₅₀₅ vaccine vs. LAG-3 $^{-/-}$ + Mock (P=0.04), LAG-3 $^{-/-}$ + gB₄₉₈₋₅₀₅ vaccine vs. WT + gB₄₉₈₋₅₀₅ vaccine (P=0.03), LAG-3 $^{-/-}$ + gB₄₉₈₋₅₀₅ vaccine vs. WT + Mock (P=0.02).

Significance differences in virus shedding were found between LAG-3 $^{-/-}$ + $\rm gB_{498-505}$ vaccine vs. LAG-3 $^{-/-}$ + Mock (P=0.03), LAG-3 $^{-/-}$ + $\rm gB_{498-505}$ vaccine vs. WT + $\rm gB_{498-505}$ vaccine (P=0.03), LAG-3 $^{-/-}$ + $\rm gB_{498-505}$ vaccine vs. WT + Mock (P=0.02) (**Figure 7E**). Recurrent disease was also significantly reduced in LAG-3 $^{-/-}$ + $\rm gB_{498-505}$ vs. all the other groups (**Figure 7F**).

On day 30 post UV-B exposure (i.e., at the end of monitoring recurrent disease) the mice of all groups were

sacrificed, mononuclear cells (MNC's) from cornea and TG were harvested and antiviral CD8⁺ T cell responses were compared between groups. From the representative FACS plots heightened frequencies for gB₄₉₈₋₅₀₅ specific CD8⁺ T cells (Cornea: LAG-3^{-/-} + gB₄₉₈₋₅₀₅ vaccine: 44% vs. LAG-3^{-/-} + Mock: 35.9%, WT + gB₄₉₈₋₅₀₅ vaccine: 35%, WT + Mock: 23%; TG: LAG-3^{-/-} + gB₄₉₈₋₅₀₅ vaccine: 35% vs. LAG-3^{-/-} + Mock: 29%, WT + gB₄₉₈₋₅₀₅ vaccine: 25%, WT + Mock: 17%), IFN- γ +CD8⁺ T cells (Cornea: LAG-3^{-/-} + gB₄₉₈₋₅₀₅ vaccine: 43% vs. LAG-3^{-/-} + Mock: 35%, WT + gB₄₉₈₋₅₀₅ vaccine: 27.6% vs. LAG-3^{-/-} + Mock: 20%; TG: LAG-3^{-/-} + gB₄₉₈₋₅₀₅ vaccine: 18%, WT + Mock: 13%), CD107⁺CD8⁺ T cells (Cornea: LAG-3^{-/-} + gB₄₉₈₋₅₀₅ vaccine: 68.4% vs. LAG-3^{-/-} + Mock: 60.2%, WT + gB₄₉₈₋₅₀₅ vaccine: 55.2%, WT + Mock: 42%; TG: LAG-3^{-/-} +

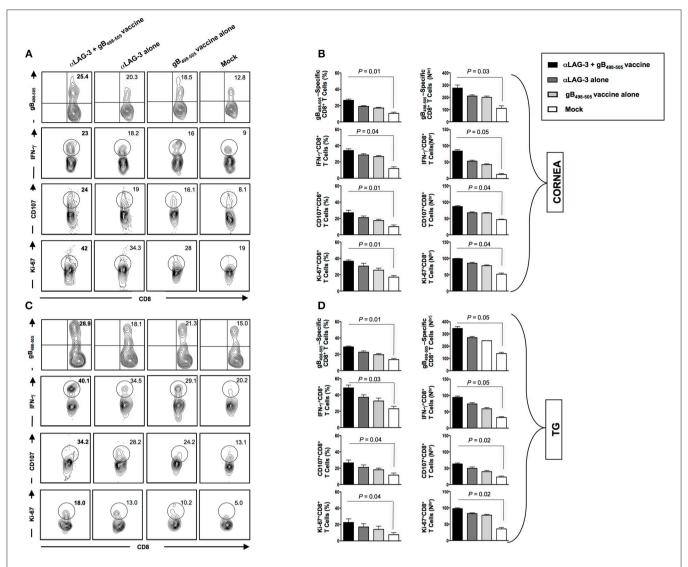


FIGURE 6 | Reduction in recurrent disease by blockade of LAG-3 is associated with better anti-viral immune response in cornea and TG. Representative FACS plots, average percentage and average absolute number of HSV- specific $(gB_{498-505})$ CD8+ T cells; HSV- specific IFNy+CD8+ T; HSV-specific CD107+CD8+ T cells; HSV-specific Ki-67+CD8+ T cells against four immunization strategies namely α-LAG-3 +gB₄₉₈₋₅₀₅ vaccine, α-LAG-3 alone, $gB_{498-505}$ vaccine alone, and mock in **A,B** cornea and **(C,D)** TG are shown. Results are representative of 2 independent experiments. The indicated *P*-values are calculated using the unpaired *t*-test, show statistical significance between α-LAG-3 + $gB_{498-505}$ vaccine and mock groups.

gB₄₉₈₋₅₀₅ vaccine: 56.2% vs. LAG-3^{-/-} + Mock: 47.3%, WT + gB₄₉₈₋₅₀₅ vaccine: 41.2%, WT + Mock: 32%), and Ki-67⁺CD8⁺ T cells (Cornea: LAG-3^{-/-} + gB₄₉₈₋₅₀₅ vaccine: 38% vs. LAG-3^{-/-} + Mock: 32.2%, WT + gB₄₉₈₋₅₀₅ vaccine: 25.6%, WT + Mock: 19%; TG: LAG-3^{-/-} + gB₄₉₈₋₅₀₅ vaccine: 28% vs. LAG-3^{-/-} + Mock: 21.3%, WT + gB₄₉₈₋₅₀₅ vaccine: 16.2%, WT + Mock: 11%) were observed in combination therapy of LAG-3^{-/-} + gB₄₉₈₋₅₀₅ vaccine group when compared with the other groups (**Figures 8A,C**). The corresponding average percentage and average absolute number of gB₄₉₈₋₅₀₅ tetramer specific CD8⁺ T cells; IFN-γ⁺ CD8⁺ T cells; CD107⁺CD8⁺ T cells and Ki-67⁺CD8⁺ T cells are also shown for all the groups (LAG-3^{-/-} mice + gB₄₉₈₋₅₀₅, LAG-3^{-/-} mice + Mock, WT mice +

gB₄₉₈₋₅₀₅, WT mice + Mock) in cornea (**Figure 8B**) and TG (**Figure 8D**). Taken together, these results essentially substantiate our earlier observations on the blockade of LAG-3.

DISCUSSION

An immune-surveillance role for the trigeminal ganglia-resident HSV-specific CD8⁺ T cells that decrease virus reactivations has been established (9, 10, 28, 36–38). However, the mechanisms of CD8⁺ T cell dynamics in recurrent ocular herpetic disease remain to be fully elucidated. Key knowledge gaps that remain include: (*i*) How CD8⁺ T cells protect from reactivation, virus shedding, and recurrent disease; and (*ii*) The immune evasion

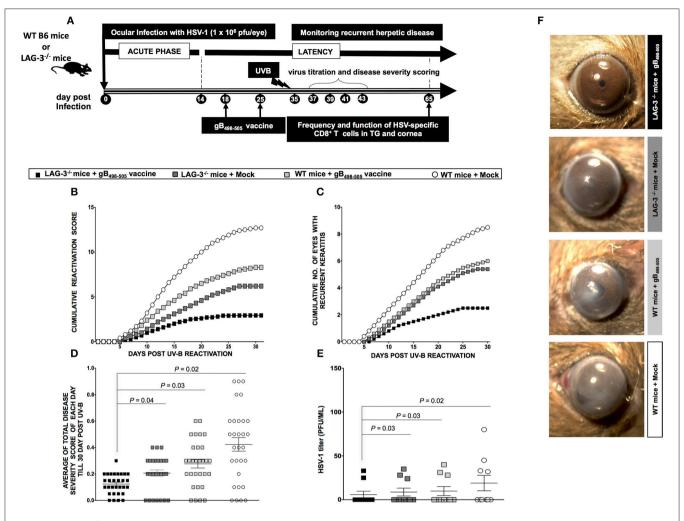


FIGURE 7 | LAG-3^{-/-} mice show less recurrent ocular herpes compared to WT B6 mice following UV-B induced HSV-1 reactivation. **(A)** Schematic representation of UV-B induced reactivation, virological and immunological analyses, following HSV-1 ocular infection of 20 WT B6 and 20 LAG-3^{-/-} mice (6–8 weeks old) on day 0 with 1 \times 10⁶ pfu of HSV-1 (strain McKrae). In one group; WTs B6 mice (n = 10) and LAG-3^{-/-} mice (n = 10) are immunized; while in the other group, WTs B6 (n = 10) and LAG-3^{-/-} (n = 10) mice remain non-immunized. **(B)** The cumulative reactivation score till day 30 post UV-B. **(C)** The cumulative number of eyes showing recurrent disease till day 30 post UV-B. **(D)** Average of total eye disease score of each day till day 30 post UV-B. **(E)** Average viral shedding measured by plaque assay at day 8 post UV-B. **(F)** Representative eye pictures of recurrent disease. Results are representative of 2 independent experiments. The indicated P-values, calculated using the unpaired t-test, show statistical significance between LAG-3^{-/-} + gB498-505 and other groups.

strategies evolved by the virus as a counter-defense against the host's CD8+ T cells. How does the virus evade CD8⁺ T cell immune surveillance to allow efficient reactivation from latency? This report shows that: (i) Humans with recurrent clinical ocular herpes upregulate expression of the inhibitory receptors PD-1 and LAG-3 on their HSV-specific CD8⁺ T cells; (ii) Compared to ASYMP individuals, SYMP individuals have a significant number of PD-1⁺CD8⁺ T cells and LAG-3⁺CD8⁺ T cells; (iii) HSV-1 specific CD8⁺ T cells from SYMP patients, but not from healthy ASYMP individuals, were functionally exhausted; (iv) In mice latently infected with HSV-1(strain McKrae), there is an increase in cornea- and TG-resident LAG-3⁺CD8⁺ and PD-1⁺CD8⁺ T cells. LAG-3⁺CD8⁺ T and PD-1⁺CD8⁺ T cells increased in both TG and cornea as early as 3 days of acute infection, and on day 14-post-infection (just after the acute infection has cleared),

there were significantly more LAG-3⁺CD8⁺ T cells and PD-1⁺CD8⁺ T cells in both the cornea and TG. However, on days 23 to 41, during latent infection, the number of both LAG-3⁺CD8⁺ T cells and PD-1⁺CD8⁺ T cells started to decline. To our knowledge, this is the first report showing: (*i*) LAG-3-related functional exhaustion of HSV-1 specific CD8⁺ T cells in both TG and cornea of latently infected mice; (*ii*) A significant increase in functionally exhausted LAG-3⁺CD8⁺ T cells in SYMP patients as well as in B6 mice that developed increased virus shedding and severe recurrent corneal herpetic disease following UV-B induced reactivation.

This study also confirms our previous finding showing that HSV-1 infection in B6 mice results in accumulation of virus-specific exhaustion CD8⁺T cells, expressing PD-1, in latently-infected trigeminal ganglia (TG) (10, 15, 28). More importantly,

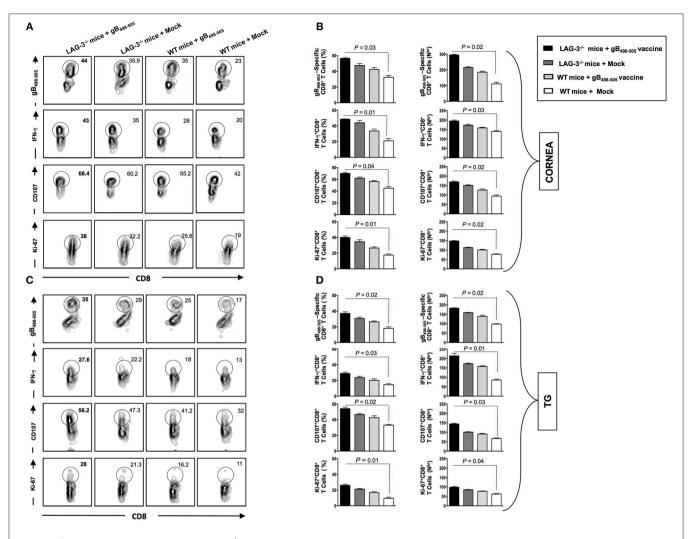


FIGURE 8 | Reduction in recurrent disease in LAG-3 $^{-/-}$ mice is associated with better anti-viral immune response in cornea and TG. The mice are monitored till day 30 post UV-B and subsequently sacrificed to process cornea, and TG for immunological analysis as mentioned in the *Materials and Methods*. Representative FACS plots, average percentage and average absolute number of HSV- specific (gB₄₉₈₋₅₀₅) CD8 $^+$ T cells; HSV- specific IFNy $^+$ CD8 $^+$ T; HSV-specific CD107 $^+$ CD8 $^+$ T cells; HSV-specific Ki-67 $^+$ CD8 $^+$ T cells detected in **A,B** cornea and **(C,D)** TG are shown. The results are representative of 2 independent experiments. The indicated P-values, calculated using an unpaired t-test, show statistical significance between LAG-3 $^{-/-}$ + gB₄₉₈₋₅₀₅ vaccine and mock groups.

we show that combination of a therapeutic LAG-3 blockade and therapeutic immunization restored the function of HSV-specific CD8⁺ T cells in cornea and TG associated with a reduction in recurrent ocular herpes, following UV-B induced reactivation in latently infected B6 mice. Thus, in addition to previously described immune evasion mechanisms (5, 8, 15, 28, 29, 29, 39–44), our data reveal a novel mechanism by which HSV-1 evades the protective host immune responses through dampening and dysregulating LAG-3⁺CD8⁺ T cell function. Moreover, the LAG-3 pathway plays a fundamental role in ocular herpes T cell immunity, thus providing an important immune checkpoint target that can be combined with T cell-based therapeutic vaccines to improve protection against recurrent ocular herpes.

A protective CD8⁺ T cell response to viral infection depends upon T cell receptor (TCR) stimulation along with costimulatory signals (45). Dysregulation in positive and negative

co-stimulatory signals affects the magnitude of CD8⁺ T cell response (45–47). The LAG-3 receptor is a negative T cell costimulatory molecule that is highly expressed on dysfunctional virus specific CD8⁺ T cells and interacts with MHC-II (48). In this report, we found that LAG-3 is highly expressed on HSV-specific CD8⁺ T cells from symptomatic (SYMP) individuals, in which HSV-1 reactivation often causes painful recurrent corneal disease (49–52). In contrast, LAG-3 was comparatively low on HSV-specific CD8⁺ T cells from asymptomatic (ASYMP) individuals in which virus reactivation never causes recurrent disease (31, 34, 52, 53). Our results in humans suggest that the magnitude of the HSV-specific CD8⁺ T cell immunity, after ocular HSV-1 reactivation, is subject to control by the LAG-3 pathway.

The high level of LAG-3 expression were detected on HSV- $1 \text{ VP}11/12_{66-74}$ epitope-specific human CD8 $^+$ T cells as well

on CD8⁺ T cells specific to four additional HSV-1 epitopes from VP13/14, gB, UL43, and UL44 proteins (Coulon et al., Manuscript in preparation). However, no upregulation was detected on bulk CD8⁺ T cells, suggesting that the observed T cell exhaustion is restricted to herpes-specific LAG3+CD8+ T cells. The ultimate underlying molecular mechanism by which LAG-3 pathway led to CD8⁺ T cell exhaustion is not defined by the present study. However, as illustrated in Figure S2, the findings are consistent with a potential role of LAG-3 pathway in exhaustion of HSV-specific CD8+ T cells and that mAbs blocking of such pathways reverse such dysfunction associated with protection from recurrent ocular herpes. MHC class II is the main ligand of LAG-3 receptor (54). MHC-II appears to bind with higher affinity to LAG-3 compared to CD4 molecule a, competition that is expected to destabilized the TCR/CD4/MHC-II interaction (55, 56). Doing so, the LAG-3 pathway negatively regulates the function and homeostasis of CD4+ T cells (57, 58). Moreover, LAG-3 pathway also regulates the function and homeostasis of CD8⁺ T cells during chronic viral infection (48). The mechanisms by which LAG-3 pathway regulated CD8⁺ T cells function/dysfunction remain to be fully elucidated. It is also unclear whether LAG-3 competition with MHC class II makes HSV-specific CD4⁺ T cells more exhausted than HSV-specific CD8⁺ T cells, mainly because of lack of CD4⁺ T cell specific tetramers that would help quantify the function HSV-specific CD4⁺ T cells. Nevertheless, we found that regulation of CD8⁺ T cell exhaustion by LAG-3 and PD-1 inhibitory pathways was non-redundant, as blockade of the T cell inhibitory receptors LAG-3 and PD-1 simultaneously and synergistically improved CD8⁺ T cell responses and diminished HSV-1 load and recurrent disease in HLA Tg mice (Roy et al., under review). Thus, antiviral CD8⁺ T cell responses during herpes viral infection appears to be regulated by complex patterns of co-expressed inhibitory receptors.

During HSV-1 neuronal latency in the TG of mice and humans, a small number of latently infected neurons are surrounded by CD8⁺ T cells (9, 59-61). Since CD8⁺ T cells are presumably attracted to these neurons by viral antigens, it is assumed that the neurons surrounded by CD8⁺ T cells are those in which the virus has initiated the early stages of reactivation from latency. In mice, experimental reactivation of HSV-1 from latency is typically accomplished by explanting TG into tissue culture media for up to 14 days and testing for the appearance of infectious (i.e., reactivated) virus (29, 29, 30). In this TG explant induced reactivation model, depleting CD8⁺ T cells with specific mAb leads to the detection of more reactivated virus (9, 62). Conversely, addition of exogenous CD8⁺ T cells reduces detection of reactivated virus (6, 9, 11). Thus, with wild type HSV-1, CD8+ T cells in the TG are apparently able to reduce the detection of infectious reactivated virus. Following T cell activation in vivo, many co-stimulatory and inhibitory receptors are upregulated on T cells. It is possible that inhibitory interactions between the LAG-3 receptor on T cells and its respective ligand on APCs, such infected DCs and MΦ, at the time of priming are attenuating the effector T cell response. In fact, we found that HSV-1 infection of mice lacking LAG-3 expression on hematopoietic cells (i.e., LAG-3^{-/-} deficient mice) generated more HSV-specific IFN- γ -producing cytotoxic CD107⁺CD8⁺ T cells compared to wild type (WT) infected mice. Moreover, we demonstrated that blocking the LAG-3 *in vivo* following administration of anti-LAG-3-specific mAbs at the time of T cell priming significantly enhanced the number of HSV-1 gB₄₉₈—505-specific CD8⁺ T cells in resident tissues. We also demonstrated that blocking the LAG-3 pathway at the time of priming increases the frequency of IFN- γ -secreting HSV-1 gB₄₉₈—505-specific CD8⁺ T cells and improves their cytotoxic potential. It is possible that the inhibitory receptor LAG-3 might be involved in regulating the effector function of HSV specific CD8⁺ T cells.

The recent success of therapies targeting immune checkpoints to treat many cancers has driven a reappearance of interest in therapies targeting immune checkpoints against chronic infections and diseases (63-65). While still in its early stages, basic and clinical data suggest that blockade of CTLA-4 and PD-1 can be beneficial in the treatment of chronic HIV, HBV, and HCV infection, as well as other chronic diseases. Furthermore, novel inhibitory receptors such as TIM-3, LAG-3, and TIGIT are the potential next wave of checkpoints that can be manipulated for the treatment of chronic infections (64). However, caution should be taken when blocking immune checkpoint pathways that help keep the body's immune responses in check. Releasing the "brakes" on the immune system over-activate effector CD8+ T cells that might cause tissue damage. Both PD-1 and LAG-3 play important roles during the normal immune response to prevent autoimmunity. Nevertheless, in the present study we found that mAbs therapies blocking LAG-3 immune checkpoint safely and efficiently led to significant reductions of recurrent corneal herpetic disease following UV-B induced reactivation in B6 mice latently infected with HSV-1. The improved clinical outcome of LAG-3 blockade in mice with established UV-B induced recurrent herpes was directly associated with a multifaceted enhancement of both the numbers of function antiviral CD8+ T cells. Moreover, this report shows for the first time that a combination of a therapeutic blockade of LAG-3 immune checkpoint and a therapeutic vaccination leads to the generation of functional HSV-specific CD8+ T cells in latently infected TG and cornea associated with an even more reduction in virus reactivation and recurrent disease in latently infected mice, following UV-B induced reactivation. No systemic or local side effects were observed following PD-1 and LAG-3 blockade in HSV-1 infected mice pointing to the safety of this treatment. The precise mechanisms by which LAG-3 blockade results in robust numerical and functional enhancement of effector CD8+ T cells remain to be discovered. Our data also demonstrate that the "exhausted" phenotype (i.e., PD-1⁺CD8⁺ T cells and LAG-3⁺CD8⁺ T cells) was predominantly established prior to terminal cell differentiation, at the stage of memory-like T cells. It is likely that compartmentalization of inhibitory receptor expression predicts distinct cellular responses to inhibitory receptor blockade. For example, LAG-3 blockade may preferentially act on the terminally differentiated CD8+ T cells. On the other hand, PD-1 blockade will act on both the memory-like CD8+ T cells and on the terminally differentiated CD8+ T cells. Regardless of the mechanisms, since HSV-1

specific CD8⁺ T cells in SYMP individuals appeared to be functionally exhausted with a significant number of PD-1⁺CD8⁺ and LAG-3⁺CD8⁺ T cells, blockade of the LAG-3 and PD-1 signaling transduction pathways provide new therapeutic options for herpes infected symptomatic patients.

The immune checkpoints are often divided into a first and a second-generation (66-70). The classic examples of the firstgeneration checkpoints are PD-1/PD-L1 and CTLA4 and of the second-generation checkpoints are LAG-3, TIGIT, VISTA, and TIM-3. While blocking of the first-generation molecules is widely employed, a recent shift in focus toward targeting the second-generation molecules is noteworthy, as resistance to first generation therapies are amply reported and a combination of the two show synergistic and non-redundant effects. Some recent reports identify LAG-3, other than the widely studies PD-1, as a powerful inhibitory receptor whose blockade improves T cell immunity and limits diseases (45, 64, 66-68). Blackburn et al. (48) showed that T cell co-expressing multiple inhibitory receptors correlated with a more severe exhaustion and a greater disease load and blockade of LAG-3 and PD-1 show a synergistic effect. LAG-3 is shown to regulate homeostatic proliferation of CD8⁺ T cells and potentiate the suppressor function of regulatory T cells. The KIEELE motif in the cytoplasmic region of LAG-3 has been shown to play a decisive role in its inhibitory effect, although the detailed mechanism is still poorly understood (69, 70).

In this report, we found that the percentage and absolute number of HSV specific IFN- γ^+ CD8+T cells, CD107+CD8+T cells and Ki-67+CD8+T cells were all significantly decreased in TG and cornea of latently infected mice following UV-B induced reactivation compared to latently infected mice with no induced reactivation (*data not shown*). This indicated phenotypic and functional exhaustion of both cytokine expression and cytotoxic activity of these CD8+ T cells. To our knowledge, this is the first report to show significantly more phenotypically and functionally exhausted HSV-specific CD8+ T cells in both the TG and cornea of latently infected mice following UV-B induced reactivation. Thus, our original hypotheses that increasing the number of exhausted CD8+ T cells in the TG and cornea led to HSV-1 escape from the control of CD8+ T cells was correct.

The increased CD8⁺ T cell exhaustion in TG and cornea of mice infected with HSV-1 could be due to increased viral antigens in these tissues. However, during latency in mouse TGs, less than 1 neuron/TG had detectable viral Ag by immunostaining (8, 71, 72). In addition, if spontaneous reactivation occurs in the mice TG, it is minimal (73). Thus, even though CD8⁺ T cells are much more sensitive to Ag than the antibodies used for immunostaining, the very low un-sustained Ag level that appears to be the situation in the mice TGs is unlikely to result in exhaustion of CD8⁺ T cells. Thus, it seems unlikely that the CD8+ T cell exhaustion detected was due to the viral Ag load, unless additional factors contributed to immune stimulation. For example, cornea- and TG-resident HSV-specific CD8+ T cells could have a higher functional avidity (ability to respond to low epitope density) than their counterparts in the periphery (18). Alternatively, CD8⁺ T cell exhaustion may suggest that there is a lot more viral Ag present in the TG and cornea of mice latently infected with HSV-1 than has been previously thought. The HSV-gB₄₉₈₋₅₀₅-epitope and B6 mice were chosen to detect HSV-1 specific CD8⁺ T cells in this study because in this mouse strain the majority (over 60%) of CD8⁺ T cells are directed to this single immunodominant epitope (74–76). The phenotypic and functional exhaustion of CD8⁺ T cells specific to other mouse HSV-1 or human CD8⁺ T cell epitopes in humans still remains to be determined. Using our HLA transgenic mouse model (6, 77), we are currently in the process of assessing the exhaustion of CD8⁺ T cells specific to a set of immunodominant and subdominant human CD8⁺ T cell HSV-1 epitopes that we have recently identified as being recognized by these animals.

Both SYMP and ASYMP individuals shed the virus in tears as a result of sporadic reactivation, but only the SYMP individuals manifest lifelong recurrences of herpetic disease, usually multiple times a year and often require continuous antiviral therapy (i.e., Acyclovir and derivatives). In this study, we applied blockade during a brief span following the UV-B induced reactivation and as our results suggest, an appropriate strategy to limit recurrent keratitis in SYMP humans, would be to monitor the SYMP patients for reactivation episodes and apply the blockade therapy during those brief phases of recurrences. Prior therapeutic immunization is expected to reinforce the effect of the blockade. Ideally, several rounds of treatment are expected to boost the generation of polyfunctional CD8+ T cells in the TG and cornea, improving their versatility. As impaired T cells responses are among the potential causes of symptomatic shedding (3, 78, 79), generation of sturdier polyfunctional T cells in the TG and cornea is expected to restrain or even nullify future harmful reactivation episodes. However, translational hurdles of the study are the safety and timing of the therapy. Another hurdle would be the delivery of mAbs in appropriate amounts to the immunologically recalcitrant sites, TG and cornea. Since our observations indirectly presuppose a significant delivery of mAbs to TG and cornea, it is likely that the timing of delivery is a crucial. In addition, inflammation associated with reactivation episodes increases tissue permittivity. Thus, with optimum dosage through right route of administration at an appropriate time of recurrences will likely make for best delivery of blocking mAbs to the targeted tissues. Such optimal delivery would interfere with virus reactivation from TG and stop or at least reduce recurrent corneal herpetic disease.

In summary, the present study demonstrates, for the first time, that the cornea and TG from HSV-1 infected mice, with UV-B-induced recurrent corneal disease, present more exhausted HSV-specific PD-1⁺CD8⁺ T cells and LAG-3⁺CD8⁺ T cells. Since functional HSV-specific CD8⁺ T cells appear to be important in decreasing reactivation from latency (9), the higher number of functional HSV-specific CD8⁺ T cells was detected following treatment with mAbs that block the LAG-3 pathway associated reduced reactivation and less severe recurrent disease as compared to mock-treated mice. This is also the first study to report that combination of the LAG-3 immune checkpoint blockade together with a therapeutic vaccination leads to generation of functional HSV-specific CD8+ T cells in latently infected TG and cornea associated with even more reduction in virus reactivation and recurrent disease. Blockade of the LAG-3 pathway in combination with vaccination may have great therapeutic promise and open up the possibilities of designing novel combination therapies. This includes therapeutic vaccination and the blockade of T cell exhaustion in confronting HSV-1 reactivation and cure of potentially blinding recurrent ocular herpes.

ETHICS STATEMENT

The manuscript, which has not been submitted elsewhere, does contain both human studies and animal studies, which conform to the Guides for IRB and IACUC published by the US National Institute of Health.

AUTHOR CONTRIBUTIONS

Conceived and designed the experiments: SR, P-GC, RS, LB. Performed the experiments: SR, P-GC, RS, HV, GK, SW, TY, MF, VL. Analyzed the data: SR, P-GC, RS, LB. Contributed reagents, materials, analysis tools: SR, P-GC, RS, LB. Wrote the paper: SR, P-GC, RS, LB.

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SUPPLEMENTARY MATERIAL

The Supplementary Material for this article can be found online at: https://www.frontiersin.org/articles/10.3389/fimmu. 2018.02922/full#supplementary-material

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Herpes Simplex Virus Type 2 Infection-Induced Expression of CXCR3 Ligands Promotes CD4⁺ T Cell Migration and Is Regulated by the Viral Immediate-Early Protein ICP4

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Richard D. Dix, Georgia State University, United States

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*Correspondence:

Qinxue Hu qhu@wh.iov.cn Sitang Gong sitangg@126.com

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¹ The Joint Center of Translational Precision Medicine, Guangzhou Institute of Pediatrics, Guangzhou Women and Children's Medical Center, Wuhan Institute of Virology, Chinese Academy of Science, Wuhan, China, ² State Key Laboratory of Virology, Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan, China, ³ University of Chinese Academy of Sciences, Beijing, China, ⁴ Department of Gastroenterology, Guangzhou Women and Children's Medical Center, Guangzhou Medical University, Guangzhou, China, ⁵ Institute for Infection and Immunity, St George's University of London, London, United Kingdom

HSV-2 infection-induced CXCR3 ligands are important for the recruitment of virus-specific CD8+ T cells, but their impact on CD4+ T cell trafficking remains to be further determined. Given that recruitment of CD4+ T cells to infection areas may be one of the mechanisms that account for HSV-2 infection-mediated enhancement of HIV-1 sexual transmission, here we investigated the functionality of HSV-2 infection-induced CXCR3 ligands CXCL9, CXCL10, and CXCL11 in vivo and in vitro, and determined the viral components responsive for such induction and the underlying mechanisms. We first found that the expression of CXCR3 ligands CXCL9, CXCL10, and CXCL11 was increased in mice following vaginal challenge with HSV-2, while CXCL9 played a predominant role in the recruitment of CD4+ T cells to the vaginal foci of infected mice. HSV-2 infection also induced the production of CXCL9, CXCL10, and CXCL11 in human cervical epithelial cells. Of note, although HSV-2 induced the expression of all the three CXCR3 ligands, the induced CXCL9 appeared to play a predominant role in promoting CD4+ T cell migration, reflecting that the concentrations of CXCL10 and CXCL11 required for CD4⁺ T cell migration are higher than that of CXCL9. We further revealed that, ICP4, an immediate-early protein of HSV-2, is crucial in promoting CXCR3 ligand expression through the activation of p38 MAPK pathway. Mechanistically, ICP4 binds to corresponding promoters of CXCR3 ligands via interacting with the TATA binding protein (TBP), resulting in the transcriptional activation of the corresponding promoters. Taken together, our study highlights HSV-2 ICP4 as a vital viral protein in promoting

CXCR3 ligand expression and CXCL9 as the key induced chemokine in mediating CD4⁺ T cell migration. Findings in this study have shed light on HSV-2 induced leukocyte recruitment which may be important for understanding HSV-2 infection-enhanced HIV-1 sexual transmission and the development of intervention strategies.

Keywords: HSV-2, CXCR3 ligands, CD4⁺ T cells, recruitment, ICP4

INTRODUCTION

Herpes simplex virus type 2 (HSV-2), a large enveloped dsDNA virus, affects $\sim\!500$ million people worldwide and acquires an annual rate of close to 25 million (1), resulting in up to 40% human adults living with HSV-2 latency (2, 3). HSV-2 infections are known to be restricted to mucosal and keratinized epithelia and neuronal ganglia, and cause genital herpes (4) with sexual transmission being the main route (5). Human immunodeficiency virus type 1 (HIV-1) causes destruction of the immune system, leading to acquired immune deficiency syndrome (AIDS) (6). In 2016, there were 1.8 million new HIV-1 infections globally, adding up to a total of 36.7 million people living with HIV-1 (7). The majority of HIV-1 infections are acquired by genital mucosal exposure, with sexual transmission as the leading mode of HIV-1 infection worldwide (8).

Due to the high positive-incidence of HSV-2 and common routes of transmission with HIV-1, mucosal HIV-1/HSV-2 coinfections attract more and more attention. Epidemiological studies show that HSV-2 infection results in an \sim 3-fold increased risk of HIV-1 acquisition (9, 10), but the underlying mechanisms remain to be determined. One of the mechanisms that HSV-2 infection increases the probability of HIV-1 acquisition is the generation of lesions at HSV-2-infection sites, which provides a chance for HIV-1 to contact the target cells in the epidermis and dermis (11). Moreover, the number of CD4⁺ T cells at the infection sites is increased following HSV-2 infection, which may further facilitate HIV-1 to infect these target cells (12–14). However, it is still not fully elucidated concerning the mechanism of CD4⁺ T cell migration induced by HSV-2.

Chemokine CXCL9 is a member of the CXC family and plays an important role in the chemotaxis of CXCR3⁺ immune cells. CXCR3 is a chemokine receptor that is rapidly induced on activated naive cells and sustains highly expression on Th1-type CD4⁺ T cells and effector CD8⁺ T cells (15). CXCR3 could be activated by three interferon-inducible ligands CXCL9 (MIG), CXCL10 (IP-10), and CXCL11 (I-TAC). Although CXCR3 could also be activated by CXCL4 and CXCL4L1, these two chemokines are released by platelets and have been implicated in atherogenesis and acute coronary syndrome (16). It is known that the upregulation of CXCR3 ligands is positively associated

Abbreviations: HSV-2, herpes simplex virus type 2; HIV-1, human immunodeficiency virus type 1; AIDS, acquired immune deficiency syndrome; PBMC, peripheral blood monocyte cell; C/EBP- β , CCAAT/enhancer-binding protein- β ; MIG, monokine induced by gamma-interferon; IP-10, interferon-induced protein-10; I-TAC, interferon-inducible T-cell alpha chemoattractant; TFIIB, transcription factor II B; TBP, TATA binding protein; TFIID, transcription factor II D; Ultraviolet, UV.

with a variety of tumors, inflammatory diseases, and infectious diseases such as AIDS (17). Although the expression of CXCL9 and CXCL10 has been shown to be increased in the cervical tissues of mice infected by HSV-2, the study on mice focused on the roles of recruited CD8⁺ T cells in control of HSV-2 infection (18-20). Our previous study demonstrated that CXCL9 levels in cervical mucus from HSV-2-positive women were significantly increased and that CXCL9 induced by HSV-2 infection in cervical epithelial cells can enhance the migration of CD4+ T cells (14). Although HSV-2-induced expression of CXCL10 and CXCL11 was previously reported (19, 21), the significance of HSV-2-induced CXCR3 ligands in vivo and the molecular mechanisms underlying the HSV-2-induced expression of CXCR3 ligands, in particular CXCL10 and CXCL11, have yet to be addressed. Furthermore, HSV-2 component(s) responsible for the induction and the underlying mechanism remain to be fully investigated.

In the current study, we found that expression of mouse CXCR3 ligands was increased following vaginal challenge with HSV-2 in mice. In addition, HSV-2-induced CXCL9 played a crucial role in promoting CD4+ T cell migration to the vaginal foci of infected mice. In human cervical epithelial cells, HSV-2 infection induced the production of CXCL10 and CXCL11 in addition to CXCL9. Although CXCL10 and CXCL11 were induced following HSV-2 infection, the migration of CD4⁺ T cells was mainly dependent on HSV-2 infection-induced CXCL9, reflecting that the concentrations of CXCL10 and CXCL11 required for CD4⁺ T cell migration are higher than that of CXCL9. Moreover, HSV-2 immediate-early protein ICP4 (also known as RS1) appeared to be the vital viral component to induce the production of CXCR3 ligands. We further explored the molecular mechanisms underlying ICP4-induced CXCR3 ligand expression, revealing that ICP4 binds to corresponding promoters of CXCR3 ligands to activate their transcription by interaction with TBP. Our study together has shed light on the molecular mechanisms underlying HSV-2-induced CD4+ T cell accumulation in mucosal infection sites, which may be crucial for understanding HSV-2 infection-enhanced HIV-1 sexual transmission and the development of intervention strategies.

MATERIALS AND METHODS

Viruses, Cell Lines, Antibodies, and Inhibitors

HSV-2 (G strain) was obtained from LGC standards and propagated in African green monkey kidney cells (Vero). Virus stocks were aliquoted and stored at -80° C before

used for infection. Ultraviolet (UV)-inactivated HSV-2 was obtained by exposure to ultraviolet irradiation for 15 min. HSV-2 titration was determined by plaque assay on confluent Vero monolayers (53). ME180, PM1, and Vero cells were obtained from American Tissue Culture Collection. Human cervical epithelial cell line ME180 and Vero cells were cultured in Dulbecco's modified Eagle medium (DMEM) (Life Technologies, 11965, Australia) supplemented with 10% FBS, 100 units/mL penicillin and 100 units/mL streptomycin at 37°C in a 5% CO2 incubator. Human T cell line PM1 cells were cultured in RPMI-1640 medium (HyClone, SH30809.01B, USA) supplemented with 10% FBS, 100 units/mL penicillin and 100 units/mL streptomycin at 37°C in a 5% CO2 incubator. Abs against p38, phospho-p38, and β-actin, respectively, were purchased from Santa Cruz Biotechnology (sc-7149, sc-101759 and sc-81178, USA). Ab against phospho-C/EBP-β was purchased from Cell Signaling Technology (3084S, USA). Inhibitors specifically against ERK (PD98059), JNK (SP600125), and p38 (SB203580), respectively, were purchased from Merck Millipore (19-143, 420119, and 559389, USA). Abs against HA and Flag tag were purchased from Sigma-Aldrich (H6908 and F1804, USA). Ab against Proliferating Cell Nuclear Antigen (PCNA) and TATA binding protein (TBP) were from Proteintech (10205-2-AP and 22006-1-AP, Wuhan, China). Rabbit normal IgG and Cy3-conjugated goat anti-mouse IgG were purchased from BOSTER (BA1031 and BA1045, Wuhan, China). Abs against mouse CD4, CXCL9, CXCL10, and CXCL11 were purchased from R&D Systems (MAB554, AF-492-NA, AF-466-NA, and AF-572, USA). Abs against ICP4, ICP27, gB, and HSV-2 were from Abcam (ab96431, ab53480, ab6506, and ab21112, England). Ab against gD was from Santa Cruz Biotechnology (sc-69802, USA).

Plasmid Construction

HSV-2 genome was extracted from the cells infected with HSV-2 for 48 h using QIAamp DNA Blood Mini Kit (Qiagen, 51104, Germany). The expression plasmids of US1, RS1, US12, UL54, and RL2, and the reporter of CXCL9 were described previously (14, 22). The open reading frames (ORFs) were amplified by PCR with the primers shown in Table S1. The reporters of CXCL10 and CXCL11 were amplified with forward primers (CXCL10 Luc-F and CXCL11 Luc-F) and reverse primers (CXCL10 Luc-R and CXCL11 Luc-R), respectively. The sequences of primers were showed in Table S1. An N-terminal HA or Flag tag was introduced into ICP4 by the forward primer. N-terminal Flag tag was introduced into UL20, UL46, UL47, UL48, UL56, UL49A, US4, US7, or RL1 by the forward primer. The promoter reporters were cloned into pGL3-basic. Unless otherwise described, other PCR products were cloned into pcDNA3.1(+) (Invitrogen) and the constructed expression plasmids were named UL20, RS1-HA (ICP4-HA), RS1-Flag (ICP4-Flag), UL46, UL47, UL48, UL56, UL49A, US4, US7, RL1, UL20-Flag, UL46-Flag, UL47-Flag, UL48-Flag, UL56-Flag, UL49A-Flag, US4-Flag, US7-Flag, and RL1-Flag, respectively. The constructs were verified by DNA sequencing (Sunny Biotechnology, Shanghai, China).

HSV-2 Challenge and Sampling

Animal experiments were approved by the Institutional Animal Care and Use Committee and performed in accordance with the guidelines of the Hubei Laboratory Animal Science Association. In brief, female BALB/c mice (6-8 wk old) were purchased from Beijing HFK Biotechnology (Beijing, China) and maintained in specific pathogen-free conditions with food and water supplied. Seven days prior to challenge, each mouse was injected with 2 mg progesterone in intraperitoneal, subcutaneous, and intramuscular sites to ensure that each mouse rapidly entered the estrous cycle (23). After the estrous cycle, the mouse vaginal mucosal epithelia became thinner and were more susceptible to HSV-2. One day prior to challenge, the neutralizing Abs against CXCL9 (2 µg, R&D Systems, MAB554, USA), CXCL10 (2 μg, R&D Systems, MAB554, USA), and CXCL11 (2 μg, R&D Systems, MAB554, USA) were delivered to the vagina of mice, respectively, or in combination. Mice were anesthetized with pentobarbital sodium and challenged intravaginally with 10 μ L/mouse HSV-2 at a concentration of 6 \times 10⁷ PFU/mL. Mice challenged with medium alone were set as background controls. The signs of mouse vagina were observed at days 3, 5, and 7 post HSV-2 challenge. Vaginal ulcers arose at day 7 in infected mice but not in the control group. Seven days after challenge, vaginal lavage fluids were collected using a vaginal Transferpettor by washing the vagina three times with sterile PBS plus protease inhibitors (Roche, 11697498001, Germany) in a total volume of 100 µL/mouse. Collected samples were centrifuged (15,000 × g, 10 min at 4°C), and supernatants were aliquoted and stored at -80°C until use. Thereafter, mice were sacrificed by neck dislocation. The cervical-vaginal tissues (Y type, two fallopian tube in the upper and vagina in the lower) were excised according to the characteristics of mouse physiological structure and collected under sterile conditions. The tissues were fixed in 4% formaldehyde followed by immunohistochemistry analysis. The collection of vaginal lavages or tissues was performed by the same people.

CBA for Human CXCL9, CXCL10 and CXCL11, and Mouse CXCL9 and CXCL10

ME180 cells in 6-well plates were transfected with empty vector or plasmid expressing ICP4 for 24 h. In some cases, ME180 cells were infected or mock-infected with HSV-2 for 24 h. Cell supernatants were collected and centrifuged to remove cell debris. Cytometric Bead Assay (CBA) was carried out to quantify secreted human CXCL9, CXCL10, and CXCL11 using the BD Cytometric Bead Array Human Soluble Protein Flexset Kit according to the manufacturer's instructions. Briefly, 50 μL diluted standards or undiluted samples were added into labeled tubes followed by the addition of 50 µL mixed beads. At 1 h postincubation, 50 µL PE conjugated detection antibody was added into all tubes followed by incubation for 2 h at room temperature. All tubes were then washed with 1 mL washing buffer and centrifuged at 1,200 rpm for 5 min. The supernatants were removed and the beads were resuspended with 300 μL washing buffer. The concentration of mouse CXCL9 and CXCL10 in the vaginal lavage fluids was detected using the LEGENDplexTM

Cytometric Bead Array mouse proinflammation Chemokine Mix and Match Subpanel according to the manufacturer's instructions. Briefly, 25 μL assay buffer was added into all tubes, followed by the addition of 25 μL diluted standard or 25 μL undiluted sample to each labeled tube. Thereafter, 25 μL mixed beads and 25 μL detection antibodies were added into all tubes followed by incubation for 2 h at room temperature with shaking. All the tubes were then incubated for 30 min at room temperature after the addition of 25 μL SA-PE solution. Beads were spun down (1,100 rpm, 5 min at room temperature) and washed with $1\times$ washing buffer. The beads were resuspended with 200 μL of $1\times$ washing buffer. All the samples were read on the BD LSRFortessa TM Flow Cytometer.

ELISA for Mouse CXCL11

The concentration of CXCL11 in the vaginal lavage fluids of mice was detected using Mouse CXCL11 ELISA Kit (BOSTER, EK0738, China). The standard of CXCL11 was provided in the Kit. Fifty microliter of undiluted fluids were tested for mouse CXCL11 detection according to the manufacturer's instructions.

Immunohistochemistry

Immunohistochemistry analysis of mouse cervical-vaginal tissues was conducted as described previously (24, 25). Briefly, the specimens obtained from challenged mice were fixed in 4% formaldehyde for 24h at room temperature, embedded in paraffin, and cut into 3-mm sections. For detection of CD4⁺ T cells in cervical-vaginal samples, slides were first dewaxed in xylene and rehydrated in a descendant ethanol scale. Ag retrieval was subsequently performed using Antigen Retrieval Reagent Basic Kit (R&D Systems, CTS013, USA) for 30 min in a water bath according to the manufacturer's instructions, and endogenous peroxidase was blocked by 3% H₂O₂ for 10 min at room temperature. Immunohistochemistry staining was performed using Cell & Tissue Staining Kit (R&D Systems, CTS017, USA) according to the manufacturer's instructions. CD4+ T cells were detected by rabbit anti-mouse CD4 Ab. HSV-2 infection was detected by goat anti-HSV-2 polyclonal Ab. The colorimetric reaction was developed by adding 3, 3'-diaminobenzidine (DAB) at room temperature. For immunofluorescence detection of ICP4 and CXCR3 ligands or HSV-2 in cervical-vaginal samples, slides were first treated as the above instruction. ICP4 was detected with rabbit anti HSV-2 ICP4 Ab. Mouse CXCL9, CXCL10, and CXCL11 were detected by goat anti-mouse CXCL9, CXCL10, and CXCL11 Abs, respectively. HSV-2 was detected by goat anti-HSV-2 polyclonal Ab. FITC-conjugated goat anti-mouse, Cy3 conjugated donkey anti-goat and anti-rabbit (Beyotime, A0568, A0502, and A0516, China) secondary Abs were used in subsequent detection. The images were acquired using the Hungary 3DHISTECH apparatus (Pannoramic MIDI).

Dual Luciferase Report (DLR) Assay

ME180 cells were seeded in 24-well plates overnight and cotransfected with empty vector or plasmid encoding ICP4, Renilla luciferase plasmid phRL-TK and reporter plasmid CXCL9-Luc, CXCL10-Luc or CXCL11-Luc. Transfections were

carried out using X-tremeGENETM HP DNA Transfection Reagent (Roche, 6366236001, Germany) according to the manufacturer's instructions. At 24 h post-transfection, cells were harvested and lysed. The lysates were used for measuring firefly and Renilla luciferase activities using the Dual-Luciferase Reporter Assay System (Promega, E1980, USA) according to the manufacturer's instructions. For some experiments, ME180 cells were co-transfected with reporter plasmid CXCL9-Luc, CXCL10-Luc or CXCL11-Luc, and phRL-TK, followed by infection with HSV-2 or ultraviolet-inactivated HSV-2 at an MOI of 1. At 24 h post-infection, the enzymatic activities of Firefly and Renilla luciferase were measured. Values for the samples were normalized using Renilla luciferase values and expressed as fold increase of the value induced in cells transfected with empty vector or mock-infected with DMEM.

RNA Isolation and Quantitative PCR

Cells were collected and total RNA was extracted using RNA isolation kit (MN, 740955, Germany) according to the manufacturer's instructions. The cDNA was synthesized by Moloney murine leukemia virus transcriptase (Promega, M170B, USA). The newly synthesized cDNA was used as the template for amplifying the genes of CXCR3 ligands and GAPDH. The primer pairs for CXCL9, CXCL10, and CXCL11 were named CXCL9-F/CXCL9-R, CXCL10-F/CXCL10-R, and CXCL11-F/CXCL11-R (Table S1). GAPDH was used as an internal control and amplified with primers GAPDH-F and GAPDH-R (Table S1). Relative real-time quantitative PCR was performed on an ABI StepOne apparatus using a SYBR Green Real-Time PCR Master Mix (Toyobo, QPK-201, Japan) according to the following conditions: 95°C for 1 min, followed by 40 cycles of 95°C for 15 s, 60°C for 15 s, and 72°C for 45 s. The expression difference was calculated on the basis of $2^{-\Delta \Delta Ct}$ values.

Western Blot

Western blot analysis was performed as described previously (22). Briefly, cytoplasmic and nuclear proteins were isolated using the Nucleus and Cytoplasm Protein Extraction Kit (Beyotime, P0028, China). In some cases, cells were lysed with lysis buffer (Life technologies, 87788, USA). Cell extracts were subjected to 10 or 15% SDS-PAGE and transferred onto PVDF membranes (Millipore 0.45 μm or 0.22 μm) followed by blocking with 5% non-fat milk in Tris-buffered saline-Tween (TBST, 50mM Tris-HCl pH 7.5, 200mM NaCl, 0.1% (v/v) Tween-20) at room temperature for 2 h. The membrane was clipped according to the molecular weight of the protein, and then probed with an appropriate primary antibody at room temperature for 2 h. After three washes with TBST, the membrane was incubated with horseradish peroxidase (HRP)-conjugated goat anti-rabbit IgG (BOSTER, BA1054, China), goat antimouse IgG (BOSTER, BA1051, China) or donkey anti-goat IgG (Beyotime, A0181, China) at room temperature for 1 h. Protein bands were visualized by exposure to FluorChem HD2 Imaging System (Alpha Innotech) after the addition of chemiluminescent substrate (Beyotime, P0018, China). Protein molecular weight markers were purchased from Thermo Fisher (26616, USA) and YEASEN (20352, China).

Isolation and Culture of PBMCs and CD4⁺ T Cells

All protocols involving human subjects were reviewed and approved by the local Research Ethics Committee of Wuhan Institute of Virology, Chinese Academy of Sciences. Informed written consents from the human subjects were obtained in this study. Both sexes were used and the donors were free of HSV-1 and HSV-2. PBMCs were isolated from healthy donors by using a Ficoll-Hypaque density gradient. CD4⁺ T cells were separated from PBMCs using CD4⁺ Cell Negative Isolation Kit according to the manufacturer's protocol (Miltenyi Biotec, 130-096-533, Germany). PBMCs and CD4⁺ T cells were activated by stimulating with 1 μ g/mL PHA (Sigma-Aldrich, L4144, USA) and 20 U/mL IL-2 (PeproTech, 200-02, USA). PBMCs and CD4⁺ T cells cultured in complete RPMI 1640 containing 20 U/mL IL-2 were used as controls for flow cytometry. PBMCs and CD4⁺ T cells were harvested at day 7 and used in subsequent assays.

Chemotaxis Assay

Chemotaxis assay was performed using 24-well Transwell plates (Costar, 3415, USA). One milliliter supernatants from ME180 cells which were mock-infected or infected with HSV-2, or mocktransfected or transfected with ICP4 expressing plasmid were added to the lower chamber. To examine the roles of CXCR3 and CXCR3 ligands in mediating cell migration, supernatants or cells were incubated with anti-CXCL9 (10 µg/mL, R&D Systems, MAB392, USA), -CXCL10 (2 µg/mL, R&D Systems, MAB266, USA), -CXCL11 (2 µg/mL, R&D Systems, MAB672, USA) or -CXCR3 (1 µg/mL, R&D Systems, MAB160, USA) neutralizing Abs, respectively, for 1h, according to the manufacturer's instructions. Activated PBMCs and CD4⁺ T cells (5 \times 10⁵) in 100 μL RPMI-1640 medium were added to the upper chamber. The chambers were incubated for 2 h at 37°C in a 5% CO2 incubator. Cell migrated to the lower chambers were collected and counted using an automatic cell counter (Bio-Rad).

Flow Cytometry

PBMCs and CD4+ T cells were collected and resuspended with 3% FBS on ice for 10 min. Hundred microliter cell suspension (1×10^6) was prepared for one test. Two microliter BV421 conjugated mouse anti-human CD25 (BD biosciences, 562443, USA), BB515 conjugated mouse anti-human CD4 (BD biosciences, 564419, USA) and APC conjugated mouse anti-human CD69 (BD biosciences, 560967, USA) Abs or PE conjugated mouse anti-human CXCR3 Ab (BD biosciences, 560928, USA) were added into the corresponding samples, followed by incubation on ice for 15 min. Background staining was assessed by isotype-matched control Abs, including BV421 conjugated mouse IgG1 (BD biosciences, 562438, USA), BB515 conjugated mouse IgG1 (BD biosciences, 564416, USA), APC conjugated mouse IgG1 (BD biosciences, 555751, USA), and PE conjugated mouse IgG1 (BD biosciences, 555749, USA). Cells were washed with 1× PBS for three times. Three hundred microliter cell suspension was filtrated through a 200-mesh membrane and performed on BD LSRFortessaTM Flow Cytometer. Data were analyzed using BD FACSDiva software (BD Biosciences).

Immunofluorescence Assay

ME180 cells were seeded in 35-mm dishes with glass bottom and transfected with HA-tagged plasmid expressing ICP4. At 24 h post-transfection, cells were fixed with 4% formaldehyde and permeabilized with 0.2% Triton X-100. After three washes with 1× PBS, cells were blocked in PBS containing 5% BSA at 4°C overnight. Thereafter, cells were incubated with mouse anti-HA Ab at a dilution of 1:100 at 37°C for 1 h. Following three washes with 1× PBS, cells were then incubated with Cy3-conjugated goat anti-mouse IgG (Beyotime, A0521, China) at a dilution of 1:50 for 1 h at 37°C. Cells were subsequently washed and incubated with DAPI for 10 min at 37°C. After washes, cells were incubated with anti-fluorescence quenching reagent (Beyotime, P0126, China) and observed under a fluorescence microscope (Olympus IX51).

Chromatin Immunoprecipitation (ChIP)

ME180 cells in 6-well plates were transfected with HA-tagged plasmid expressing ICP4 or empty vector. At 24 h post-transfection, ChIP assay was performed as described previously (22) according to the manufacturer's instructions (Millipore, 17-409, Germany). The purified DNA was used as a template for PCR detection of the promoter sequences of CXCR3 ligands with primer pairs CXCL9 pro-F/CXCL9 pro-R, CXCL10 pro-F/CXCL10 pro-R, and CXCL11 pro-F/CXCL11 pro-R, respectively (Table S1).

Co-immunoprecipitation (Co-IP) Assay

ME180 cells in 6-well plates were transfected with HA-tagged ICP4 expression plasmid or empty vector. At 24h posttransfection, cells were harvested and lysed on ice for 10 min in 200 µL of lysis buffer (50 Mm Tris (PH 8.0), 150 mM NaCl, 1% NP40) containing protease inhibitor cocktail (Roche, 11697498001, Germany). To eliminate nonspecific binding of other proteins, the samples were pretreated with dynabeads Protein G (Invitrogen, 10003D, USA) for 2 h at room temperature followed by separation prior to Co-IP assay. Meanwhile, 2 µg rabbit anti-HA Ab or control rabbit Ab was diluted in 200 μL PBS with 1% Tween-20 (PBST) and added to fresh dynabeads protein G. After incubation with rotation for overnight at 4°C, dynabeads-Ab complexes were washed once with 200 µL PBST before mixed with the pretreated samples, followed by overnight incubation with rotation at 4°C to allow the formation of dynabeads-Ab-Ag complexes. The complexes were washed three times with PBST and target antigens were eluted by boiling and subjected to western blot analysis.

Statistical Analysis

All experiments were repeated at least three times and the data are presented as mean \pm S.D. with each condition performed in triplicate or in duplicate unless otherwise specified. Data analyses were performed with GraphPad Prism 5 software (GraphPad). Comparison between two groups was analyzed by two tailed

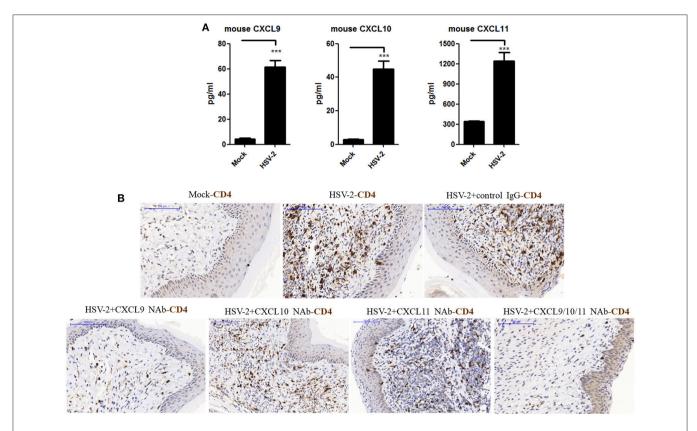


FIGURE 1 | Contribution of HSV-2 infection-induced CXCR3 ligands to CD4⁺ T cell infiltration into mouse vagina. Seven days prior to HSV-2 challenge, BALB/c mice were injected with progesterone in multiple sites. One day prior to HSV-2 challenge, CXCL9, CXCL10, and CXCL11 neutralizing antibodies were delivered to the vagina of mice, alone or in combination, while isotype matched control IgG was used as the control. Mice were then anesthetized with pentobarbital sodium and challenged intravaginally with 10 μ L/ mouse HSV-2 at a concentration of 6 × 10⁷ PFU/ml or mock- challenged. Vaginal lavage fluids and cervical-vaginal tissues were collected at day 7 after challenge. (**A**) HSV-2 infection induces the production of mouse CXCR3 ligands. The protein levels of CXCL9 and CXCL10 ligands in vaginal lavage fluids were measured by CBA, and the protein level of CXCL11 was detected by ELISA. (**B**) CXCL9 mediates the migration of CD4⁺ T cells to the vaginal foci of infected mice. CD4⁺ T cells in infection foci were detected using anti-CD4 Ab by IHC. The scale bar indicates 100 μ m. Data shown are mean \pm S.D. (n = 5 mice/group) of three independent experiments (**A**). ***p < 0.001. One representative out of three independent experiments is shown (**B**).

unpaired Student's t-test, whereas comparisons among more than two groups were analyzed by one-way ANOVA with the Turkey's test. P < 0.05 was considered statistically significant.

RESULTS

Contribution of HSV-2 Infection-induced CXCR3 Ligands to CD4⁺ T Cell Infiltration Into Mouse Vagina

The expression of CXCL9 and CXCL10 has been shown to be increased in the cervical tissues of mice infected by HSV-2 in previous studies (20), which mainly focused on the recruitment of activated CD8⁺ T cells and its contribution to the control of HSV-2 infection. However, the impact of HSV-2 infection on CD4⁺ T cell migration in mice remains to be further addressed. To assess this, mice were challenged with HSV-2 vaginally, and vaginal lavage fluids and cervical-vaginal tissues of the mice were collected for subsequent assessment. We confirmed a productive infection of HSV-2 in mouse

vagina by immunohistochemistry and immunofluorescencehistochemistry assays (Supplementary Material Figures 1A,B), while Cytometric Bead Array (CBA) showed that the production of mouse chemokines CXCL9 and CXCL10 was significantly increased (Figure 1A). ELISA also indicated the enhancement of CXCL11 in mice challenged with HSV-2 (Figure 1A). Meanwhile, immunohistochemistry (IHC) assays showed that the number of CD4+ T cells was significantly increased in the vaginal foci of infected mice (Figure 1B). To identify which chemokine plays a vital role in CD4+ T cell recruitment, mice were vaginally treated with the neutralizing Ab against CXCL9, CXCL10, or/and CXCL11 before HSV-2 challenge. The number of CD4+ T cells was dramatically decreased after the administration of CXCL9 neutralizing antibody to the vagina of mice (Figure 1B). Although the migration of CD4⁺ T cells was almost completely abolished after administration of a combination of neutralizing Abs against CXCL9, CXCL10, and CXCL11 into the vaginal tissue, CD4+ T cells were still significantly recruited to the infection foci after the administration of CXCL10 or CXCL11 neutralizing antibody (**Figure 1B**). These data together indicate that HSV-2 vaginal infection of mice increases the expression of CXCR3 ligands CXCL9, CXCL10 and CXCL11, and the migration of CD4⁺ T cells to the vaginal foci is mainly mediated by CXCL9.

HSV-2 Infection Induces the Production of CXCR3 Ligands in Human Cervical Epithelial Cells

Although HSV-2-induced expression of CXCL10 and CXCL11 was previously reported (19, 21), it remains to be addressed as to how HSV-2 induces the expression CXCR3 ligands in human mucosal epithelial cells. Epithelial cells are the primary HSV-2 target cells during sexual transmission. Having demonstrating the correlation of CXCR3 ligands with CD4⁺ T cell migration in mice, we next addressed the underlying mechanism in cellular models. Our previous study showed that HSV-2 infection of human epithelial cells induces CXCL9 expression (14). To investigate the association between HSV-2 infection and the induction of CXCR3 ligands, human cervical epithelial cell line ME180 was used for assessing CXCR3 ligand expression at promoter, mRNA and protein levels. Our results indicated that HSV-2 infection significantly activated not only the promoter of CXCL9 but also the promoters of CXCL10 and CXCL11 (Figure 2A). We next assessed whether HSV-2 productive infection is necessary for the transcriptional activation of CXCR3 ligands. The results showed that UV-inactivated HSV-2 did not significantly induce the transcriptional activation of CXCL9 and CXCL10. Although CXCL11 appeared to be induced by UVinactivated HSV-2, the level of induction was low (Figure 2A). In agreement, several HSV-2 proteins were undetectable following UV inactivation (Supplementary Material Figure 2). These results together indicated that HSV-2 productive infection is essential for the induced production of CXCR3 ligands. To further confirm the effect of HSV-2 on the induction of CXCL10 and CXCL11, we next investigated the mRNA and protein levels of CXCL10 and CXCL11 following HSV-2 infection. Relative real-time PCR assay and CBA showed that HSV-2 infection significantly promoted the production of CXCL9, CXCL10, and CXCL11 at both mRNA (Figure 2B) and protein levels (Figure 2C).

HSV-2 Infection-induced CXCL9 Plays a Predominant Role in Mediating CD4⁺ T Cell Migration

It is known that CXCR3 is highly expressed on CD4⁺ T cells and CXCL9, CXCL10 or CXCL11 could activate CXCR3⁺ T cells (15). We previously demonstrated the functionality of HSV-2-induced CXCL9 in chemotacting CD4⁺ T cells (14). To assess the functionality of HSV-2-induced CXCL10 and CXCL11 in human cells, chemotaxis assay was performed using activated human peripheral blood mononuclear cells (PBMCs) and CD4⁺ T cells. The percentage of CD4⁺ cells was 95.6 and 33.4% in CD4⁺ T cells and PBMCs, respectively (**Supplementary Material Figure 3**). We also confirmed that CD4⁺ T cells and PBMCs were activated by PHA prior to the onset of chemotaxis assay

(Supplementary Material Figure 4). ME180 cells were infected with HSV-2 for 24 h, and the chemotactic activity of supernatants was determined. In response to supernatants from HSV-2infected cells, the migratory activity of PBMCs (Figure 3B) and CD4⁺ T cells (Figure 3C) was significantly increased. Cell migration was almost abolished upon the addition of anti-CXCL9 neutralizing Ab to supernatants from HSV-2-infected cells (Figures 3B,C), whereas a control Ab, anti-CXCL10 or CXCL11 neutralizing Ab did not have such effect, which is accordance with a previous study (26), indicating the critical role of CXCL9 in inducing CD4⁺ T cell migration. To further confirm the observation, a neutralizing Ab against CXCR3 was mixed well with cells for 1 h and then added into the upper chamber in chemotaxis assay, showing that the migration of CD4⁺ T cells was significantly reduced (Figure 3D). We also demonstrated that HSV-2 infection did not regulate the expression of CXCR3 by flow cytometry assay (Supplementary Material Figure 5A). The concentrations of CXCL9, CXCL10, and CXCL11 in the supernatants of HSV-2-infected ME180 cells used for chemotaxis assays were detected by CBA (Figure 3A), showing that CXCL10 and CXCL11 were produced at levels not less than that of CXCL9. We therefore conducted the chemotaxis assay using recombinant CXCL9, CXCL10, or CXCL11 at the similar concentration as that induced by HSV-2 infection. The results indicated that recombinant CXCL9 induced the migration of CD4+ T cells at a low concentration of 48 pg/ml, whereas CXCL10 and CXCL11 had no significant impact on CD4⁺ T cell migration at the concentrations of 55 pg/mL and 175 pg/mL, respectively (Figure 3E). Nevertheless, CXCL10 or CXCL11, at a much higher concentration than that induced by HSV-2 infection, did promote the migration of CD4⁺ T cells (Figures 3F,G), indicating that the concentrations of CXCL10 and CXCL11 required for CD4+ T cell migration are higher than that of CXCL9. Taken together, our results together indicated that HSV-2 infection-induced CXCL9 likely plays a predominant role in mediating CD4⁺ T cell migration.

HSV-2 ICP4 Promotes the Production of Human CXCR3 Ligands

UV-inactivation attenuated the ability of HSV-2 to induce CXCR3 ligand production, indicating that productive HSV-2 infection is necessary for the induced production of CXCR3 ligands. Given the complexity of HSV-2 genome which contains over 70 genes (27, 28), we next investigated which viral components are responsible for the induction of CXCR3 ligands during HSV-2 infection. ME180 cells were co-transfected with individual HSV-2 protein expression vector and the promoter reporter of CXCL9, CXCL10, or CXCL11. Dual luciferase reporter assay (DLR) indicated that HSV-2 immediate-early protein ICP4 significantly activated the promoters of CXCR3 ligands (Figure 4A). The expression of all tested viral proteins was assessed by Western Blot (Figure 4B). To further confirm the role of ICP4 on transcriptional activation, ME180 cells were transfected with ICP4 expressing plasmid, and cell supernatants were collected for CBA while mRNAs were extracted for reverse transcription PCR. Relative real-time quantitative PCR indicated

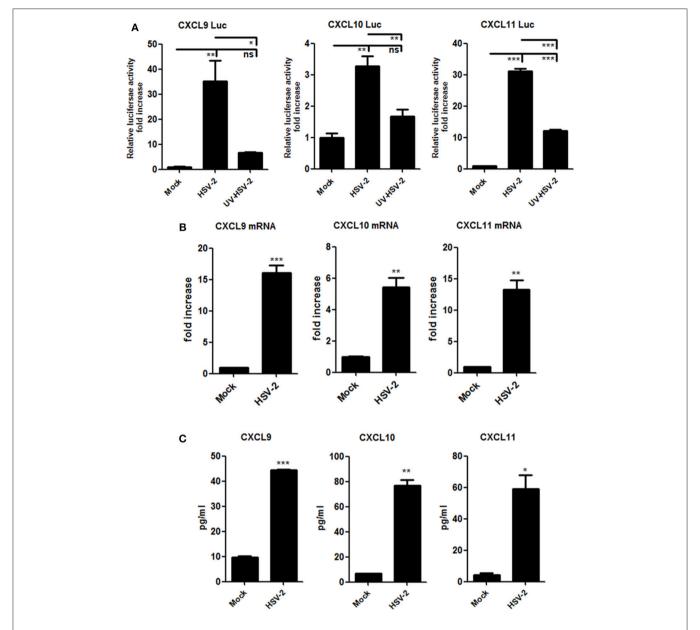


FIGURE 2 | HSV-2 infection induces the production of CXCR3 ligands in human cervical epithelial cells. (A) HSV-2 infection activates the promoters of human CXCR3 ligands. ME180 cells in 24-well plates were co-transfected with 150 ng CXCL9-Luc, CXCL10-Luc or CXCL11-Luc, and 15 ng internal control plasmid phRL-TK. At 4 h post-transfection, cells were infected with HSV-2 or ultraviolet-inactivated HSV-2 (UV-HSV-2) at an MOI of 1 for 24 h. DLR assay was performed. Values for the samples were normalized using Renilla luciferase values and expressed as fold increase of the value induced in mock-infected samples. (B) HSV-2 infection induces the mRNA production of CXCR3 ligands. ME180 cells in 6-well plates were infected with HSV-2 at an MOI of 1 for 24 h. Cells were harvested and total RNA was extracted. The expression of CXCR3 ligands and GAPDH was evaluated by relative real-time quantitative PCR. The Ct values of GAPDH among all groups were equable and not overloaded. mRNA copies of CXCR3 ligands were normalized using GAPDH and expressed as fold increase of the value for the mock-infected control. (C) HSV-2 infection induces the production of CXCR3 ligands. As depicted in (B), cell supernatants were collected, and the protein level of CXCR3 ligands was measured by CBA. Data shown are mean ± S.D. of three independent experiments (A, B, and C). *p < 0.05, **p < 0.01, ***p < 0.001.

that HSV-2 ICP4 enhanced the expression of CXCR3 ligands at mRNA level (**Figure 4C**). CBA showed that HSV-2 ICP4 enhanced the production of CXCR3 ligands at protein level (**Figure 4D**). Subsequent chemotaxis assay was performed to assess the role of ICP4-induced CXCR3 ligands in promoting the migration of activated PBMCs or CD4⁺ T cells. ME180 cells were transfected with ICP4 expressing plasmid, and the

chemotactic activity of supernatants was determined. In response to supernatants from ICP4–transfected cells, the migratory activity of PBMCs (**Figure 4E**) and CD4⁺ T cells (**Figure 4F**) was significantly increased. Cell migration was significantly reduced upon the addition of anti-CXCL9 (**Figures 4E,F**) neutralizing Ab to supernatants from ICP4 expressing plasmid–transfected cells or anti-CXCR3 neutralizing Ab (**Figure 4G**) to cell

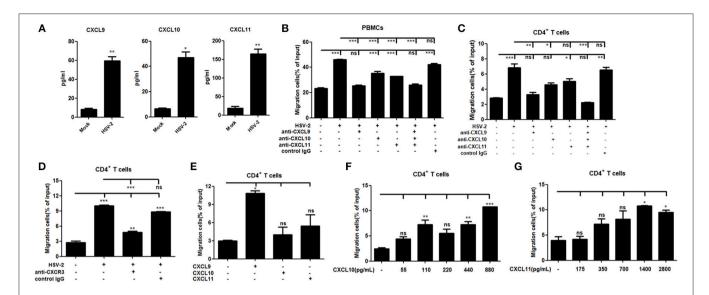


FIGURE 3 | HSV-2 infection-induced CXCL9 plays a predominant role in mediating CD4⁺ T cell migration. (A) The concentrations of CXCR3 ligands in the supernatants of ME180 cells infected with HSV-2 or mock-infected with DMEM were detected by CBA. (B,C) CXCL9 induced by HSV-2 recruits the migration of PBMCs (B) and CD4⁺ T cells (C). ME180 cells in 6-well plates were infected with HSV-2 at an MOI of 1 for 24 h. Cell supernatants were collected and added to the lower chamber of transwell plates in the absence or presence of anti-CXCL9, -CXCL10, or/and -CXCL11 neutralizing Ab or control Ab for 1 h. (D) Neutralization of CXCR3 reduces the migration of CD4⁺ T cells induced by HSV-2 infection. ME180 cells in 6-well plates were infected with HSV-2 at an MOI of 1 for 24 h. Cell supernatants were collected and added to the lower chamber of transwell plates. The activated CD4⁺ T cells were incubated with RPMI 1,640 medium containing anti-CXCR3 neutralizing Ab for 1 h and placed in the upper chamber. (E) Recombinant CXCL9 significantly induces the migration of CD4⁺ T cells. DMEM containing recombinant CXCL9, CXCL10, or CXCL11 (48 pg/mL, 55 pg/mL and 175 pg/mL, respectively; the lowest concentration induced by HSV-2 infection) was added to the lower chamber of transwell plates. (F,G) Recombinant CXCL10 or CXCL11 was added to the lower chamber of transwell plates. CXCL10 or CXCL11 was started from 55 pg/mL and 175 pg/mL, respectively, at a concentration gradient of two times. The activated CD4⁺ T cells were placed in the upper chamber. After 2 h incubation, cells migrated to lower chambers were collected and counted using an automatic cell counter. Cells migration was expressed as percentage of input. Input cells in the upper chamber were 5 x 10⁵. Data shown are mean ± S.D. of three independent experiments (A–G). ns, not significant, *p < 0.05, **p < 0.01, ***p < 0.001.

suspension. In addition, the expression of CXCR3 in ICP4 expressing cells was also detected by flow cytometry assay, showing that ICP4 did not induce the expression of CXCR3 (**Supplementary Material Figure 5B**). These results indicated that the immediate-early protein ICP4 of HSV-2 promotes the production of human CXCR3 ligands, of which CXCL9 plays a predominant role in mediating CD4⁺ T cell migration.

HSV-2 ICP4 Regulates the Expression of CXCR3 Ligands Via the p38 MAPK Signaling Pathway

It is known that HSV-2 could activate MAPK pathway to regulate the expression of downstream genes (29). Our previous study demonstrated that HSV-2-mediated up-regulation of CXCL9 involves the p38 MAPK signaling pathway (14). To investigate whether MAPK pathway is involved in HSV-2-mediated transcriptional activation of CXCL10 and CXCL11 or ICP4-mediated transcriptional activation of CXCL9, CXCL10, and CXCL11, ME180 cells were pretreated with or without PD98059 (ERK inhibitor), SP600125 (JNK inhibitor) or SB203580 (p38 inhibitor), and then transfected with CXCR3 ligand reporter plasmid followed by infection with HSV-2 or co-transfected with CXCR3 ligand reporter plasmid and ICP4 expression plasmid. DLR assay showed that pretreatment

of cells with SB203580, but not with PD98059 or SP600125, significantly decreased HSV-2-mediated activation of CXCL9 (Figure 5A), CXCL10 (Figure 5B), and CXCL11 (Figure 5C) promoters. In accordance, ICP4-mediated activation of CXCL9 (Figure 5D), CXCL10 (Figure 5E), and CXCL11 (Figure 5F) promoters was also decreased after pretreatment with SB203580. In our previous study, we found that HSV-2 infection could induce the phosphorylation of p38 and CCAAT/enhancer-binding protein-β (C/EBP-β). We then determined the impact of ICP4 on the activation of p38 MAPK pathway. ME180 cells were transfected with ICP4 expressing plasmid, and then the total or phosphorylation level of p38 and the phosphorylation level of C/EBP-B were examined by western blot assay. The results showed that, like HSV-2, ICP4 increased the phosphorylation level of p38 (Figure 5G). Taken together, these results suggest that HSV-2 ICP4-induced CXCR3 ligand expression in human cervical epithelial cells is mediated through the activation of p38 MAPK pathway.

HSV-2 ICP4 Binds to the Promoters of CXCR3 Ligands by Interaction With TBP

Although HSV-2 ICP4 induces the expression of CXCR3 ligands via the p38 MAPK signaling pathway, it does not affect the

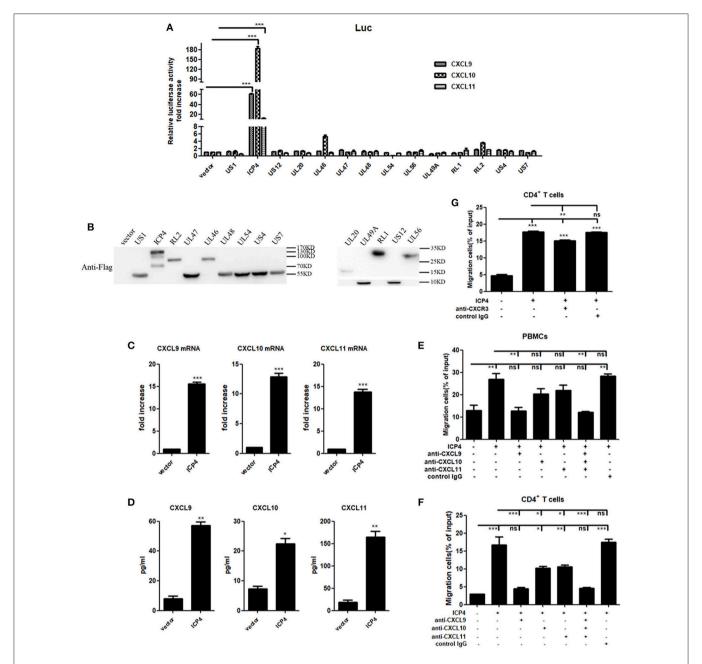


FIGURE 4 | HSV-2 ICP4 promotes the production of human CXCR3 ligands. (A) ICP4 induces the activation of CXCR3 ligand promoters. ME180 cells in 24-well plates were transfected with 300 ng expression plasmid of HSV-2 gene or empty vector together with 150 ng CXCR3 ligand reporter and 15 ng phRL-TK. At 24h post-transfection, DLR assay was performed. Values for the samples were normalized using Renilla luciferase values and expressed as fold increase of the value induced in cells transfected with empty vector. (B) The expression of HSV-2 genes was detected using anti-Flag Ab by Western Blot. ME180 cells were transfected with 3 µg HSV-2 gene expression plasmid for 24 h. The proteins were collected and detected using mouse anti-Flag Ab. (C) ICP4 induces the mRNA production of CXCR3 ligands. ME180 cells in 6-well plates were transfected with 3 µg ICP4 expression plasmid for 24 h. Cells were harvested and total RNA was extracted. The expression of CXCR3 ligands and GAPDH gene was evaluated by relative real-time quantitative PCR. The Ct values of GAPDH among all groups were equable and not overloaded. mRNA copies of CXCR3 ligands were normalized using GAPDH and expressed as fold increase of the value for the empty vector-transfected control. (D) ICP4 induces the production of CXCR3 ligands. As depicted in (C), cell supernatants were collected, and the protein levels of CXCR3 ligands were measured by CBA. (E,F) CXCL9 induced by ICP4 recruits the migration of PBMCs (E) and CD4⁺ T cells (F). ME180 cells in 6-well plates were transfected with 3 µg ICP4 expression plasmid for 24 h. Cell supernatants were collected and added to the lower chamber of transwell plates in the absence or presence of anti-CXCL9, -CXCL10, or/and -CXCL11 neutralizing Ab or control Ab for 1h. (G) Neutralization of CXCR3 reduces the migration of CD4+ T cells induced by ICP4. ME180 cells in 6-well plates were infected with HSV-2 at an MOI of 1 for 24 h. Cell supernatants were collected and added to the lower chamber of transwell plates. The activated CD4+ T cells were incubated with RPMI 1,640 medium containing anti-CXCR3 neutralizing Ab for 1 h and placed in the upper chamber. As depicted in Figure 3, cells migrated to lower chambers were counted. Cells migration was expressed as percentage of input. One representative out of three independent experiments is shown (B). Data shown are mean \pm S.D. of three independent experiments (A,C-G). ns, not significant, *p < 0.05, **p < 0.01, ***p < 0.001.

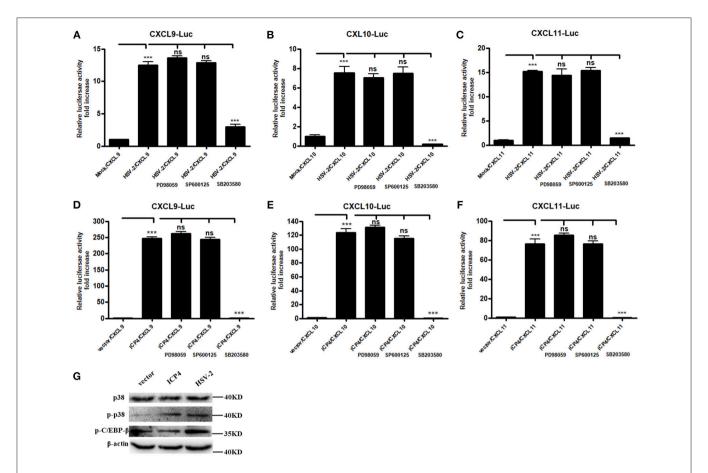


FIGURE 5 | HSV-2 ICP4 regulates the expression of CXCR3 ligands via the p38 MAPK signaling pathway. (A-C) HSV-2 regulates the expression of CXCL9 (A), CXCL10 (B), and CXCL11 (C) via p38/MAPK signaling pathway. ME180 cells in 24-well plates were co-transfected with 150 ng CXCR3 ligand reporter and 15 ng phRL-TK. At 4 h post-transfection, cells were infected with HSV-2 at an MOI of 1 and supplemented with inhibitor PD98059, SP600125, or SB203580. DLR assay was performed at 24 h post-transfection. Values for the samples were normalized using Renilla luciferase values and expressed as fold increase of the value induced in mock-infected samples. (D-F) HSV-2 ICP4 regulates the expression of CXCL9 (D), CXCL10 (E), and CXCL11 (F) via p38/MAPK signaling pathway. ME180 cells in 24-well plates were co-transfected with 300 ng empty vector or ICP4 expression plasmid together with 150 ng CXCR3 ligand reporter and 15 ng phRL-TK. At 4 h post-transfection, cells were cultured in complete DMEM supplemented with inhibitor PD98059, SP600125, or SB203580. DLR assay was performed at 24 h post-transfection. Values for the samples were normalized using Renilla luciferase values and expressed as fold increase of the value induced in cells transfected with empty vector. (G) ICP4 activates p38 MAPK signaling pathway. ME180 cells were transfected with 3 μg ICP4 expression plasmid. The protein level of p38, phospho-p38 (p-p38) or phospho-C/EBP-β (p-C/EBP-β) was detected by Western Blot. Data shown are mean ± S.D. of three independent experiments (A-F). ns, not significant, ****p < 0.001. One representative out of three independent experiments is shown (G).

phosphorylation level of C/EBP-β (**Figure 5G**), suggesting a novel mechanism involved in ICP4-mediated production of CXCR3 ligands. Previous studies have demonstrated that ICP4 is essential for virus growth (30) and functions as a transcriptional activator in some cases (31–34). It is probable that ICP4 binds to the promoters of CXCR3 ligands in the nucleus which results in their transcriptional activation. ICP4 must be located in the nucleus to act as a transcriptional factor. To test this hypothesis, we first analyzed the nucleotide sequence of ICP4, revealing several nuclear localization sequences (NLSs) (**Figure 6A**). ME180 cells were transfected with HA-tagged ICP4, and examined by indirect immunofluorescence (IF) and western blot assay, showing that ICP4 was indeed located in the nucleus (**Figures 6B,C**). In agreement, ICP4 was also located in the nucleus in the context of HSV-2 infection

(Supplementary Material Figure 6). Meanwhile, at 24 h post-transfection with HA-tagged ICP4, ME180 cells were collected for chromatin immunoprecipitation (ChIP) assay. The ChIP assay indicated that ICP4 bound to the promoters of CXCR3 ligands (Figure 6D).

It is known that ICP4 can form a tripartite complex with transcription factor II B (TFIIB) and either TBP or transcription factor II D (TFIID) (35). TBP is required for the initiation of transcription by RNA polymerases I, II, and III, from promoters with or without a TATA box (36–38). TBP associates with a host of factors to form multi-subunit pre-initiation complexes on the core promoter. Through its association with different transcription factors, TBP can initiate transcription from different RNA polymerases (39). Considering that ICP4 induces the phosphorylation of p38 (**Figure 5G**),

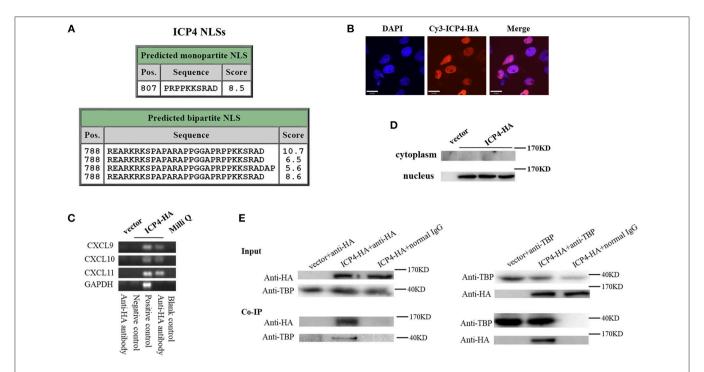


FIGURE 6 | HSV-2 ICP4 binds to the promoters of CXCR3 ligands by interaction with TBP. (A) Schematic representation of the predicted NLSs of ICP4 amino acid (AA) sequence. (B) ICP4 is located in the nucleus. ME180 cells in 35-mm dishes with glass bottom were transfected with 2 μg empty vector or HA-tagged ICP4 expression plasmid for 24 h. Cells were stained with mouse anti-HA mAb, followed by Cy3-conjugated goat anti-mouse (red) as the secondary Ab. Cell nuclei (blue) were stained with DAPI. The images were obtained by fluorescence microscopy using 60× objective. The scale bar indicates 21 μm. (C) The expression of ICP4 was stained using anti-HA mAb. (D) ICP4 binds to the promoters of CXCR3 ligands. ME180 cells were transfected with 3 μg empty vector or HA-tagged ICP4 expression plasmid for 24 h. Cells were lysed and subjected to ChIP assay using mouse anti-HA mAb, mouse anti-RNA polymerase II mAb (positive control) or mouse normal IgG (negative control) for immunoprecipitation. (E) ICP4 interacts with TBP. ME180 cells in 6-well plates were transfected with 3 μg empty vector or HA-tagged ICP4 expression plasmid for 24 h. Cells were lysed and subjected to co-immunoprecipitation (IP) using rabbit anti-HA or anti-TBP Ab. Rabbit normal IgG was used as a negative control. IP products and 5% input samples were examined using rabbit anti-HA and rabbit anti-TBP Abs by western blot. One representative out of three independent experiments is shown (B–E).

and that the transcriptional activation of TBP requires the activation of p38 MAPK signaling pathway (40, 41), ICP4-induced activation of p38 likely contributes to the transcriptional activation of TBP. To verify the interaction of ICP4 with TBP, ME180 cells were transfected with HA-tagged ICP4 for 24 h. Co-immunoprecipitation assays were performed to detect the interaction of ICP4 with TBP. The results indicated that ICP4 interacts with TBP as evidenced by using an anti-HA antibody to pulldown TBP or an anti-TBP antibody to pulldown ICP4 (**Figure 6E**). These data collectively indicated that HSV-2 ICP4 binds to the promoters of CXCR3 ligands by interaction with TBP, leading to the promoter activation of CXCR3 ligands.

DISCUSSION

Recruitment of CD4⁺ T cells, irrespective of their specificity, may significantly increase the chance of HIV-1 transmission (42, 43). Our previous study found that CXCL9 levels in cervical mucus from HSV-2-positive women were significantly increased and that HSV-2 infection induced CXCL9 expression in cervical epithelial cells (14). In addition, the expression of

CXCL9 and CXCL10 was shown to be increased in the cervical tissues of mice infected by HSV-2 in studies to understand the contribution of recruited CD8⁺ T cells in control of HSV-2 infection (20), while CXCL9 induced by HSV-1 infection has been shown to recruit CD4⁺ T cells into the cornea (26). Moreover, circulating memory CD4⁺ T cells could migrate to the genital mucosa in mice challenged with HSV-2 (44). However, how HSV-2 infection affects the migration of CD4⁺ T cells at mucosal sites and the biological consequences remain to be fully determined.

In this study, we observed that, following vaginal challenge with HSV-2, mouse CXCR3 ligands CXCL9, CXCL10, and CXCL11 were all upregulated in the vaginal fluids of infected mice. In addition, CD4⁺ T cells migrated to the vaginal foci of infected mice, while the number of CD4⁺ T cells was significantly decreased after administration of CXCL9 neutralizing antibody to the vagina of mice. These indicate that HSV-2 infection can promote CD4⁺ T cell migration and this is mainly due to the induced CXCL9 expression. Although HSV-2 infection likely induces the expression of many other chemokines, our results showed that the migration of CD4⁺ T cells was significantly reduced after administration of a combination of neutralizing Abs against CXCL9, CXCL10, and CXCL11 into the vaginal

tissue. In human cervical epithelial cells, we demonstrated that HSV-2 infection induced not only the production of CXCL9 but also that of CXCL10 and CXCL11. The common receptor for CXCL9, CXCL10, and CXCL11 is CXCR3, which can be rapidly induced on activated naive cells and sustain high level expression on Th1-type CD4⁺ T cells and effector CD8⁺ T cells (15). The other two ligands of CXCR3, CXCL4, and CXCL4L1, are released by platelets and have been implicated in atherogenesis and acute coronary syndrome (16). Therefore, we mainly focused on how HSV-2 infection enhances the production of CXCR3 ligands CXCL9, CXCL10, and CXCL11.

Early studies on transmitted/founder (T/F) HIV-1 have suggested that CD4+ T cells serve as the main target cells in the establishment of HIV-1 early infection (9, 45). Although CXCR3 ligands induced by HSV-2 can activate and recruit CD8⁺ T cells, these cells are specific for HSV-2 and may have an impact on the control of HSV-2 replication (20, 46, 47). In the current study, we mainly assessed the biological function of CXCR3 ligands induced by HSV-2 on CD4⁺ T recruitment. We found that chemokines induced by HSV-2 can mediate the migration of CD4+ T cells. Following experiments using neutralizing antibodies, the results indicated that the induced CXCL9 plays a crucial role in recruiting CD4⁺ T cells, which was further confirmed by using recombinant CXCL9, CXCL10, or CXCL11 at a concentration similar to that induced by HSV-2. Chemokines CXCL10 and CXCL11 at the concentrations around or higher than 300 pg/mL and 350 pg/mL, respectively, have been shown to have chemotactic activity for CXCR3⁺ cells (48– 50), whereas CXCL9 has the same capability at a much lower concentration (14). We did not see significant reduction of CD4⁺ T cell migration when CXCL10 or CXCL11 was neutralized by the corresponding neutralizing antibody. One reasonable explanation is that the concentrations of CXCL10 and CXCL11 required for CD4⁺ T cell migration are much higher than that of CXCL9. In our study, the concentrations of CXCL10 and CXCL11 induced by ICP4 or HSV-2 were around or lower than 55 pg/mL and 175 pg/mL, respectively, which was unable to have an impact on CD4⁺ T cell migration as evidenced by the chemotaxis assay using recombinant CXCL10 and CXCL11. The recombinant CXCL10 at the concentration of 55 pg/mL had a marginal effect on CD4+ T cell migration, whereas the recombinant CXCL11 at the concentration of 175 pg/mL had no effect on the recruitment of CD4⁺ T cell. Compared to those induced by HSV-2 or ICP4, recombinant CXCL10 and CXCL11 at much higher concentrations chemotracted CD4⁺ T cells in a dose-dependent manner. Although beyond the scope of this current study, it will be important to address the roles of CXCR3 ligands in mediating CD4⁺ T cell migration and HIV-1 mucosal transmission when an animal model become available to study HSV-2 and HIV-1 co-infection.

We found that UV-inactivated HSV-2 did not significantly induce the transcriptional activation of CXCL9 and CXCL10. Although CXCL11 appeared to be induced by UV-inactivated HSV-2, the level of induction was low. These results indicate that productive infection of HSV-2 is essential for the induced production of CXCR3 ligands. HSV-2 genome contains over 70 genes (27, 28). Following screening a range of HSV-2 ORFs,

we identified the immediate-early protein ICP4 as the key viral component in inducing the expression of CXCR3 ligands. ICP4 was barely detectable when cells were treated with UVinactivated HSV-2, further suggesting the importance of ICP4 in inducing CXCR3 ligand expression. In agreement, we observed the co-localization of ICP4 with CXCL9, CXCL10 or CXCL11 in the mouse vaginal epithelial layer by immunofluorescence histochemistry assay (Supplementary Material Figure 8). ICP4induced CXCL9 played a crucial role in the chemotaxis of CD4+ T cells, which is in accordance with that induced by HSV-2. We previously found that HSV-2 infection-induced CXCL9 expression is regulated by the transcriptional factor C/EBP-β (14). In the current study, we found that ICP4 did not affect the phosphorylation of C/EBP-β, although ICP4 induced the production of all the three CXCR3 ligands via p38 MAPK signaling pathway. These together indicate a novel mechanism underlying ICP4-induced CXCR3 ligand production, and that other viral component(s) is likely to be involved in the phosphorylation of C/EBP-β. It is known that ICP4 is a major transcriptional activator and essential for progression beyond the immediate-early phase of infection (28). Indeed, we successfully constructed a ICP4-null HSV-2 bacterial artificial chromosome (BAC) but were unable to rescue the ICP4-null HSV-2 (data not shown), further strengthening the essential role of ICP4 in the regulation of viral gene expression. ICP4 can function as a transcriptional activator in some cases (31-34). It may act as a transcriptional activator to induce the activation of CXCR3 ligand promoter. To function as a transcriptional factor, ICP4 needs to be in the nucleus where it can bind to the promoters of CXCR3 ligands. We found that ICP4 is indeed located in the nucleus and can bind to the promoters of CXCR3 ligands, resulting in the expression of corresponding chemokines. ICP4 was also located in the nucleus in the context of HSV-2 infection. We also observed the interaction of ICP4 with TBP, which could contribute to the binding of ICP4 to the promoters of CXCR3 ligands. Nevertheless, ICP4 seems not to serve as a consensus transcription factor to activate gene expression, as ICP4 did not activate the promoters of other cytokines including TNF, IL-6 (Supplementary Material Figure 7).

In conclusion, we first found that the expression of CXCR3 ligands CXCL9, CXCL10, and CXCL11 was induced following mice vaginally challenged with HSV-2, which was associated with the increased number of CD4+ T cells in the vaginal foci of infected mice as well as CXCL9-mediated cell migration. We further observed that HSV-2 infection induced the production of CXCL10 and CXCL11 in addition to CXCL9 in human cervical epithelial cells. Although CXCL10 and CXCL11 could be induced by HSV-2, HSV-2-induced CXCL9 played a critical role in recruitment of CD4+ T cells. Mechanistically, after identifying HSV-2 ICP4 as a vital viral component in inducing CXCR3 ligands, we demonstrated the contribution of ICP4induced CXCL9 in recruiting CD4+ T cells and a critical role played by p38 MAPK signaling pathway in HSV-2 infection- or ICP4-induced CXCR3 ligand expression. HSV-2 ICP4 binds to the corresponding promoters of CXCR3 ligands by interaction with TBP to activate their transcription. Our study together reveals the molecular mechanism underlying HSV-2-induced CD4⁺ T cell accumulation in mucosal infection sites, which may be crucial for understanding HSV-2 infection-enhanced HIV-1 sexual transmission and the development of intervention strategies.

AUTHOR CONTRIBUTIONS

MZ and QH conceived the study. MZ, XD, XG, BZ, RC, DZ, and MF conducted experiments. MZ conducted experiments in Figures 1–6. XG extracted the cytoplasmic and nuclear proteins in Figure 5. BZ and RC conducted western blot experiment in Figures 5, 6, respectively. XD, DZ, and MF provided help in conducting mouse experiments in Figure 1. LG, KH, ML, and YL offered advices and technical assistance. HH provided help in the construction of Flag-tagged plasmids. MZ, SG, and QH analyzed the data. MZ and QH wrote the manuscript. All authors reviewed the manuscript.

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SUPPLEMENTARY MATERIAL

The Supplementary Material for this article can be found online at: https://www.frontiersin.org/articles/10.3389/fimmu. 2018.02932/full#supplementary-material

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Herpes Simplex Virus Type 2 Immediate Early Protein ICP27 Inhibits IFN-β Production in Mucosal Epithelial Cells by Antagonizing IRF3 Activation

Xinmeng Guan ^{1,2}, Mudan Zhang ^{3*}, Ming Fu ^{1,2}, Sukun Luo ⁴ and Qinxue Hu ^{1,5*}

¹ State Key Laboratory of Virology, Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan, China, ² University of Chinese Academy of Sciences, Beijing, China, ³ The Joint Center of Translational Precision Medicine, Guangzhou Institute of Pediatrics, Guangzhou Women and Children's Medical Center, Wuhan Institute of Virology, Chinese Academy of Science, Wuhan, China, ⁴ Wuhan Children's Hospital (Wuhan Maternal and Child Healthcare Hospital), Tongji Medical College, Huazhong University of Science and Technology, Wuhan, China, ⁵ Institute for Infection and Immunity, St George's University of London, United Kingdom

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*Correspondence:

Mudan Zhang mudan@wh.iov.cn Qinxue Hu ghu@wh.iov.cn

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Guan X, Zhang M, Fu M, Luo S and Hu Q (2019) Herpes Simplex Virus Type 2 Immediate Early Protein ICP27 Inhibits IFN-β Production in Mucosal Epithelial Cells by Antagonizing IRF3 Activation. Front. Immunol. 10:290. doi: 10.3389/fimmu.2019.00290 Herpes simplex virus type 2 (HSV-2) is the main cause of genital herpes and infections are common in the lower genital tract. Although neuronal and immune cells can be infected, epithelial cells, and keratinocytes are the primary HSV-2 target cells. HSV-2 establishes latency by evading the host immune system and its infection can also increase the risk of HIV-1 sexual transmission. Our pervious study found that HSV-2 immediate early protein ICP22, inhibited IFN-\$\beta\$ production by interfering with the IRF3 pathway. However, ICP22-null HSV-2 did not completely lose the capability of suppressing IFN-B induction, suggesting the involvement of other viral components in the process. In this study, by using an ex vivo cervical explant model, we first demonstrated that HSV-2 can indeed inhibit IFN-β induction in human mucosal tissues. We further identified HSV-2 immediate early protein ICP27 as a potent IFN-β antagonist. ICP27 significantly suppresses the Sendai virus or polyinosinic-polycytidylic acid-induced IFN-β production in human mucosal epithelial cells, showing that ICP27 inhibits the IFN-B promoter activation, and IFN-β production at both mRNA and protein levels. Additional studies revealed that ICP27 directly associates with IRF3 and inhibits its phosphorylation and nuclear translocation, resulting in the inhibition of IFN-β induction. Our findings provide insights into the molecular mechanism underlying HSV-2 mucosal immune evasion, and information for the design of HSV-2 mucosal vaccines.

Keywords: HSV-2, ICP27, epithelial cells, IFN-β, IRF3

INTRODUCTION

Herpes simplex virus type 2 (HSV-2) is a large dsDNA virus belonging to the α -Herpesviridae subfamily (1). HSV-2 is mainly transmitted by genital mucosa through sex, causing vesicles, and ulcers after acute infection and can be transported to dorsal root or cranial nerve ganglia to establish life-long latency (2, 3). According to a report by WHO, it is estimated that over 400 million

people were infected with HSV-2 and 19.2 million new infections occurred worldwide in 2012 (4). Due to the greater and more fragile surface of the female reproductive tract, the risk of infection with HSV-2 in females is higher than that in males (5). Epidemiological studies have shown that HSV-2 infection can increase the risk of HIV-1 infection by 3–4 fold (6), with several mechanisms for this increased susceptibility being proposed. For instance, although HSV-2 can infect skin epithelial cells, immune cells and nerve cells, it initially infects mucosal epithelial cells during sexual transmission (7), which may facilitate HIV-1 transmission via perturbation of epithelial integrity. Due to the high positive-incidence of HSV-2 and common routes of transmission with HIV-1, HSV-2 mucosal infection and immune escape has attracted increased attention.

A virus infection initially activates innate immunity through recognition by host pattern recognition receptors (PRRs), including Toll-like receptors (TLRs), RIG-I-like receptors (RLR), and DNA sensors (8-10). These PRRs activate downstream signaling pathways using common components TBK-1 and IKKε, leading to the activation of IRF3 signaling (11). IRF3 is an important transcription factor which regulates the expression of type I interferons (IFNs) and IFN stimulate genes (ISGs). IRF3 exists as an inactive monomer in most cells. Upon activation, IRF3 is phosphorylated and assembled into dimers, and then translocated into the nucleus to initialize the transcription of IFN-β (12). Type I IFNs are normally expressed at low levels, and their expression can be enhanced through the JAK/STAT signaling pathway during viral or bacterial infections, resulting in the transcription activation of ISGs (13). The type I IFN family consists of IFN-α, IFN-β, IFN-ε, IFN-κ, and IFN-ω (14), with IFN-β being the most intensively investigated in antiviral innate immunity (15).

During HSV-2 infection, the induction of type I IFNs is extremely low (16), suggesting that HSV-2 has evolved strategies to antagonize IFN production. However, our current understanding of HSV-2 immune evasion is limited, whereas a large number of studies focusing on HSV-1 indicate the involvement of multiple countermeasures in subverting type I IFN production (17, 18). Given that most of these studies address how HSV-1 proteins interfere with IFN production or/and signaling using various cell lines as models (17), whether and how IFN induction is affected in the context of viral infection, at the tissue level, remain elusive. It is known that HSV-2 and HSV-1 exhibit substantial differences in latency and reactivation patterns (19), implying that they may use distinct mechanisms to counteract the host innate immunity. Previous studies by others indicated that HSV-2 virion host shutoff (vhs) protein UL41 suppresses IFN-β expression in human genital epithelial cells (20), while HSV-2 US2 activates NF-κB by binding to TAK1 (21). Our previous study revealed that HSV-2 immediate early protein

Abbreviations: HSV-2, herpes simplex virus type 2; SeV, Sendai virus; Poly(I:C), polyinosinic-polycytidylic acid; PEI, Polyethylenimine; DLR, dual luciferase report; Co-IP, co-immunoprecipitation; RT-PCR, real-time quantitative PCR; PRR, pattern recognition receptor; TLR, Toll-like receptor; RLR, RIG-I-like receptor; ISG, IFN stimulate gene; FBS, fetal bovine serum; DMEM, Dulbecco's modified Eagle medium; ORF, open reading frame.

(IE), ICP22 (US1), inhibits IFN- β production by antagonizing the association of IRF3 with the IFN- β promoter (22). Nevertheless, we observed that ICP22-null HSV-2 did not completely lose the inhibitory activity on IFN- β induction, while other IE proteins including ICP27 (UL54) also appeared to inhibit the activation of the IFN- β promoter, although the underlying mechanism remains to be fully addressed.

Our current study focused on whether and how HSV-2 and its IE protein ICP27, inhibit IFN- β production in mucosal epithelial cells. We found that HSV-2 can inhibit IFN- β induction in human cervical tissues. We further revealed that HSV-2 ICP27 significantly suppresses the Sendai virus or polyinosinic-polycytidylic acid-induced IFN- β production in human mucosal epithelial cells. Mechanistically, we demonstrated that HSV-2 ICP27 directly associates with IRF3 and inhibits its phosphorylation and nuclear translocation, resulting in the inhibition of IFN- β induction.

MATERIALS AND METHODS

Cell Lines and Viruses

HEK 293T, HeLa, and ME180 cells were cultured in Dulbecco's modified Eagle medium (DMEM) (Hyclone), supplemented with 10% fetal bovine serum (FBS) (Gibico), 100 U/ml penicillin and 100 U/ml streptomycin (Genom). All cells were cultured at 37°C in a 5% CO₂ incubator.

HSV-2 (G strain) was obtained from LGC standards and propagated in Vero cells. The Sendai virus (SeV) was propagated in embryonated eggs. Special pathogen-free embryonated eggs (Beijing Merial Vital Laboratory Animal Technology Corporation) were incubated at $37^{\circ}C$ for 12 days before inoculation with 300 μl 100 HAU ml $^{-1}$ SeV into the allantoic cavity of 12-day-old embryonated eggs and then incubated at $37^{\circ}C$ for 72 h. SeV was collected from allantoic fluids and the titers were measured by hemagglutination (HA) assay using chicken red blood cells.

Isolation of Primary Human Mucosal Epithelial Cells

All protocols involving human subjects were reviewed and approved by the local Research Ethics Committee of Wuhan Institute of Virology, Chinese Academy of Sciences. Informed written consents from the human subjects were obtained in this study, and informed written parental consents were obtained for all participants under the age of 16.

Human cervical or foreskin tissues were obtained from the Wuhan Children's Hospital (Wuhan Maternal and Child Healthcare Hospital), Tongji Medical College, Huazhong University of Science & Technology. Tissues were washed carefully with PBS and then minced into small pieces. Prepared tissue pieces were incubated with 5–10 ml Dispase II Solution (25 U/ml Dispase II in PBS pH 7.4 without Ca/Mg) containing penicillin and streptomycin. 10% FBS was then added to avoid excess damage to cells. Following an incubation at 4°C overnight, peeled off epidermis was rinsed with PBS, and placed into 3–5 ml 0.05% Trypsin with EDTA in a 50 ml conical tube. After an incubation in a 37°C water bath for 15–30 min with agitation

every 5 min, twice the EDTA volume of medium with 10% FBS was added. The epidermal cells were released by inverting the tube several times or by pipetting the suspension. The cell/tissue solution was passed through a sterile sieve followed by centrifugation. Cell pellets were resuspended in EpiLife medium, and the isolated epithelial cells were cultured in 12-well plates at $37^{\circ}\mathrm{C}$ in a 5% CO₂ incubator.

Construction of Plasmids

Primers used for plasmid construction are listed in Supplementary Table 1. The open reading frame (ORF) of HSV-2 ICP27 was amplified from HSV-2 genomic DNA extracted from HSV-2G strain by PCR. For some constructs, an N-terminal Flag or HA was introduced by PCR. PCR products were cloned into pcDNA3.1(+)/(-) (Invitrogen), and the constructed expression plasmids were named ICP27, ICP27-Flag, ICP27-HA, ICP27_(1-138aa), ICP27_(1-152aa), and ICP27_(1-302aa), respectively. All constructs were verified by DNA sequencing (Sunny Biotechnology). The reporter plasmid PRD(III-I)₄-Luc was provided by Dr. Stephan Ludwig (University of Muenster, Muenster, Germany). The reporter plasmid p125-Luc and the internal control plasmid phRL-TK were described previously (23). IRF3 and IRF3-5D expression plasmids pIRES-hrGFP/IRF3-Flag and pIRES-hrGFP/IRF3-5D-Flag (constitutively active mutant of IRF3) were provided by Dr. Yiling Lin (Graduate Institute of Life Sciences, National Defense Medical Center, Taiwan, China). pEF-Flag-RIG-IN (a carboxyterminally truncated, constitutively active RIG-I mutant) expression plasmid was provided by Dr. Takashi Fujita (Kyoto University, Kyoto, Japan). pcDNA3-MAVS-Flag expression plasmid was provided by Dr. Hanzhong Wang (Wuhan Institute of Virology, Wuhan, China). pcDNA3-TBK1-Flag and pcDNA3-IKKE-Flag expression plasmids were provided by Dr. Katherine Fitzgerald (University of Massachusetts Medical School, Worcester, MA). Plasmids encoding influenza virus PR8/NS1 and HSV-2 ICP22, respectively, were described previously (22).

Dual Luciferase Report (DLR) Assay

HEK 293T cells were seeded in 24-well plates overnight and co-transfected with empty vector or plasmid encoding HSV-2 ICP27, truncated HSV-2 ICP27 or influenza virus NS1, reporter plasmid p125-Luc or PRD(III-I)₄-Luc and internal control phRL-TK. Transfections were performed using Lipofectamine 2000 (Life Technology, 11668019) according to the manufacturer's instructions. At 24 h post-transfection, cells were stimulated with or without 100 HAU ml⁻¹ SeV for 16 h. Cells were harvested and lysed, and the lysates were used for measuring firefly and Renilla luciferase activities using a Dual-luciferase Reporter Assay System (Promega, E1980) according to the manufacturer's instructions. For some experiments, HEK 293T cells were co-transfected with empty vector or ICP27 expression plasmid, reporter plasmid p125-Luc and internal control phRL-TK, together with plasmid encoding the IRF3 pathway inducer RIG-IN, MAVS, TBK-1, IKK-ε, or IRF3-5D. At 40 h posttransfection, the enzymatic activities of firefly and Renilla luciferase were measured.

Immunoblot Assay

The proteins extracted from transfected or infected cells were prepared using Pierce IP Lysis Buffer (ThermoFisher Scientific, 87787) supplemented with protein inhibitor (cOmplete Protease Inhibitor Cocktail, 11697498001). The protein samples were resolved by SDS-PAGE and transferred onto PVDF membranes (0.45 μ m, Millipore). Cytoplasmic and nuclear proteins were isolated using the Nuclear-Cytosol Extraction Kit (Applygen, P1200-50).

The antibody (Ab) anti-HSV-1 ICP27+HSV-2 ICP27 was purchased from Abcam (ab31631). Rabbit anti IRF3 Polyclonal Antibody, Rabbit anti PCNA Ab and Mouse mAb anti HAtag were purchased from Proteintech (11312-1-AP, 10205-2-AP, and 66006-1-Ig). Rabbit mAb against phospho-IRF-3 (Ser396) was purchased from Cell Signaling Technology (4947S). Rabbit mAb against HA-tag and Mouse mAb against Flag-tag were purchased from Sigma-Aldrich (H6908 and F1804). Mouse mAb anti β-actin was purchased from Santa Cruz Biotechnology (sc81178). HRP-conjugated goat anti-rabbit IgG (H+L) and HRP-conjugated goat anti-mouse IgG (H+L) were purchased from ThermoFisher Scientific (ZB-2301 and ZB-2305). HRPconjugated mouse anti-rabbit IgG (Light Chain) was purchased from Sangon Biotech (D110059-0100). Mouse IgG and Rabbit IgG were purchased from BOSTER (BA1046 and BA1045). Alexa Fluor 488-labeled Goat Anti-Mouse IgG (H+L), Alexa Fluor 647labeled Goat Anti-Rabbit IgG (H+L) and DAPI Staining Solution were purchased from Beyotime (A0428, A0468, and C1006).

RNA Isolation and Quantitative PCR

The transfected cells were collected and total RNAs were extracted using TRIzol (Invitrogen, 15596-026) according to the manufacturer's instructions. cDNA was synthesized by M-MLV Reverse Transcriptase (Promega, M1705). The newly synthesized cDNA was used as template for the amplification of *IFN-\beta*, *ISG15*, *ISG56*, *CXCL10*, and *GAPDH*. The primer pairs for *IFN-\beta*, *ISG15*, *ISG56*, *CXCL10*, and *GAPDH* were described previously (22, 24). Relative real-time quantitative PCR (RT-PCR) was performed on BioRad StepOne apparatus using a TransStart Tip Green qPCR SuperMix (Transgen, AQ141-02), and GAPDH was used as an internal control with conditions of 95°C for 3 min, followed by 40 cycles of 95°C for 10 s, and 55°C for 30 s. The expression difference was calculated on the basis of $2^{-\Delta \Delta Ct}$ values.

ICP27 Knockdown by siRNA

HSV-2 siRNA sequences were described previously (25), and are listed in the **Supplementary Table 1**. All siRNAs were synthesized by Eurofins Genomics. HeLa or ME180 cells were seeded in 6-well plates overnight. Negative control or siRNAs were transfected into HeLa or ME180 cells using Lipofectamine 2000 (Life Technology, 11668019) according to the manufacturer's instruction. At 4 h post-transfection, HeLa cells were infected with or without HSV-2 at an MOI of 1, or ME180 cells at an MOI of 0.5. At 20 h post-infection, cells were stimulated with or without 100 HAU ml⁻¹ SeV for 16 h, and supernatants were harvested for ELISA or cells were lysed for DLR assay.

Poly(I:C) Stimulation

HeLa or ME180 cells were seeded in 6-well plates overnight and transfected with empty vector, HSV-2 ICP27 expression plasmid, HSV-2 ICP22 expression plasmid or influenza virus NS1 expression plasmid. At 24 h post-transfection, cells were transfected with 2 μ g/well Poly(I:C) (Sigma; P1530-25MG) using Lipofectamine 2000 (Life Technology, 11668019) or mocktransfected. At 16 h post-transfection, cells were lysed for DLR assay or supernatants were harvested for ELISA.

ELISA for IFN-β

HEK 293T cells were seeded in 6-well plates overnight and transfected with empty vector, HSV-2 ICP27 expression plasmid or influenza virus NS1 expression plasmid. At 24h post-transfection, cells were stimulated with or without 100 HAU ml $^{-1}$ SeV for 16h. Cell culture supernatants were collected and centrifuged to remove cell debris. Fifty microliters of supernatants were used for IFN- β detection using a VeriKine TM Human IFN Beta ELISA Kit (PBL Assay Science, 41410) according to the manufacturer's instructions.

Immunofluorescence Assay

HeLa cells were seeded in 35 mm glass-bottom dishes and transfected with an empty vector, HSV-2 ICP27-HA expression plasmid or an influenza virus NS1 expression plasmid. At 24 h post-transfection, HeLa cells were stimulated with or without 100 HAU ml⁻¹ SeV for 16 h. Cells were fixed with 4% paraformaldehyde and permeabilized with 0.2% Triton X-100. After three washes with PBS, cells were blocked with PBS containing 5% BSA for 1h at room temperature, and then incubated with rabbit anti-human IRF3 polyclonal Ab and mouse anti HA-tag mAb at a dilution of 1:100 for 1h at room temperature. After three washes with PBS, cells were incubated with Alexa Fluor 488-labeled Goat Anti-Mouse IgG (H+L) and Alexa Fluor 647-labeled Goat Anti-Rabbit IgG (H+L) at a dilution of 1:50 for 1 h at room temperature. Cells were subsequently washed and incubated with DAPI solution for 10 min at room temperature. Following the addition of 1 ml PBS into the dishes, cells were observed under a Multiphoton Confocal Microscope (Nikon, A1 MP STORM).

Co-immunoprecipitation Assay

HEK 293T cells were seeded in 6-well plates and transfected with ICP27-Flag plasmid or empty vector. At 24 h post-transfection, cells were stimulated with or without 100 HAU ml $^{-1}$ SeV for 16 h. The proteins extracted from transfected cells were prepared using Pierce $^{\text{TM}}$ IP Lysis Buffer (ThermoFisher Scientific, 87787). Three microgram mouse anti-Flag Ab or control mouse IgG was diluted in 200 μl PBS with 0.2% Tween-20 (PBST) and added to fresh Dynabeads protein G (Invitrogen, 10009D). After incubation with rotation at 4°C overnight, Dynabeads-Ab complexes were washed once with 200 μl PBST before mixed with the samples, followed by incubation at 4°C overnight. The complexes were washed three times with PBST, and target Ags were subjected to Western Blot analysis after elution by boiling.

Binding Kinetic Analysis

HEK 293F cells were used for the expression and purification of ICP27-Flag and IRF3-Flag. For every 1 \times 10⁶ cells, 1.5 μg expression plasmid was transfected into HEK 293F cells using Polyethylenimine (PEI) transfection reagent (Polysciences, 23966-1). Cells were cultured in FreeStyle 293 Expression Medium (Gibico, 12338018) at 37°C in a 5% CO2 incubator shaker at 135 rpm. At day 3 post-transfection, cells were harvested and lysed by ultrasonic treatment. The Flag-tagged protein was purified by Anti-DYKDDDDK G1 Affinity Resin (GeneScript, L00432) and eluted with 3 M NaCl. The purified protein was concentrated in PBS using 30 kDa Centrifugal Filter Units (Merck, UFC903008) for binding kinetic study.

The kinetics of binding was performed on a Forte-Bio Octet Red System as described previously (26). This system monitors interference of light reflected from the surface of a sensor to measure the thickness of molecules bound to the sensor surface. IRF3-Flag was conjugated with biotin at a molecular weight ratio of 1:3 at room temperature for 1h followed by washes, and then concentrated in PBS to remove dissociative biotin. 10 microgram/milliliter biotinylated IRF3-Flag was coupled to Biosenors (Fortebio, 18-5019) and immersed in different concentration of ICP27-Flag (50, 200, 500, or 800 nM) for association and disassociation. The response in nm shift was recorded as a function of time.

Statistical Analysis

All experiments were repeated at least three times and the data are presented as mean \pm S.D., unless otherwise specified. Data analyses were performed with GraphPad Prism 7 software (GraphPad). A comparison between the two groups was analyzed using a two tailed unpaired Student's t-test. P < 0.05 was considered statistically significant.

RESULTS

HSV-2 ICP27 Inhibits IFN-β Production in Human Mucosal Epithelial Cells

HSV-2 evades mucosal innate immunity, but the underlying mechanisms remain elusive (16). Our previous study showed that HSV-2 immediate early protein ICP22 strongly inhibited IFN-β production; however, knockout of ICP22 did not fully abolish the inhibitory activity on IFN-β production in the context of HSV-2 infection (22), while other IE proteins including ICP27 (UL54) also appeared to be involved, but the underlying mechanism remains to be fully investigated. In this study, we performed experiments to assess whether HSV-2 ICP27 indeed inhibits IFN-β induction, and if so, what is the underlying mechanism. We first confirmed that IFN-β was expressed at a very low level in HSV-2-infected human cervical tissues (Figure 1A), informing that HSV-2 inhibits IFN-β induction during mucosal infection. To assess the contribution of HSV-2 ICP27 in interfering with IFN-β induction, HEK 293T cells were seeded in 24-well plates overnight and co-transfected with empty vector pcDNA3.1(+), plasmid expressing HSV-2 ICP27 or the positive control influenza virus NS1 together with the reporter plasmid p125-Luc and the internal control phRL-TK. At 24 h

post-transfection, cells were stimulated with or without 100 HAU ml $^{-1}$ SeV for 16 h. As shown in **Figure 1B**, HSV-2 ICP27 strongly inhibited the activation of the IFN- β promoter. We subsequently examined whether HSV-2 ICP27 inhibits the production of IFN- β at mRNA or protein level. HEK 293T cells were seeded in 6-well plates overnight and transfected with pcDNA3.1(+), plasmid expressing HSV-2 ICP27 or the influenza virus NS1. At 24 h post-transfection, cells were stimulated with or without 100 HAU ml $^{-1}$ SeV for 16 h. Total RNAs were extracted and IFN- β mRNA was analyzed by RT-PCR. As shown in **Figure 1C**, HSV-2 ICP27 significantly inhibited the production of IFN- β mRNA. The level of IFN- β proteins in the supernatants was measured by ELISA, showing that HSV-2 ICP27 significantly inhibited the production of INF- β at protein level (**Figure 1D**).

In addition to SeV stimulation, we also conducted experiments under the condition of the IFN-β expression induced by polyinosinic-polycytidylic acid [Poly(I:C)], an artificial dsRNA sequence which can stimulate RIG-I signaling pathway (27). HeLa cells were co-transfected with pcDNA3.1(+), plasmid expressing HSV-2 ICP27, HSV-2 ICP22, or the influenza virus NS1, together with the reporter plasmid p125-Luc and the internal control phRL-TK. At 24 h post-transfection, cells were stimulated with Poly(I:C) for 16h and lysed for DLR assay. The results revealed that HSV-2 ICP27 strongly inhibited Poly(I:C)-induced activation of the IFN-β promoter (**Figure 1E**). In addition, HeLa cells were transfected with pcDNA3.1(+), plasmid expressing HSV-2 ICP27, HSV-2 ICP22, or the influenza virus NS1. At 24h post-transfection, cells were stimulated with Poly(I:C) for 16 h, and supernatants were harvested for ELISA. The results revealed that HSV-2 ICP27 strongly inhibited Poly(I:C)-induced IFN-β induction at protein level (**Figure 1F**). In addition, HSV-2 ICP27 also significantly inhibited Poly(I:C) induced activation of the IFN-β promoter in ME180 cells (Supplementary Figure 1A).

Impaired expression of type I IFNs leads to reduced expression of the downstream interferons stimulated genes (ISGs) (28, 29). To examine the impact of HSV-2 ICP27 on ISG expression, HEK 293T cells were transfected with empty vector pcDNA3.1(+) or plasmid expressing HSV-2 ICP27, followed by stimulation with SeV for 16 h. Total RNAs were extracted, and the mRNAs of ISGs including *ISG56*, *ISG15*, and *CXCL10* were analyzed by RT-PCR. As shown in **Figures 1G–I**, HSV-2 ICP27 strongly inhibited the expression of *ISG56*, *ISG15*, and *CXCL10* at mRNA level.

Having demonstrated the critical role of HSV-2 ICP27 in inhibiting IFN- β induction, we next conducted experiments to examine the impact of HSV-2 ICP27 on IFN- β induction in the context of HSV-2 infection. HeLa cells were co-transfected with the reporter plasmid p125-Luc and the internal control phRL-TK, together with negative control siRNA, ICP27 siRNA-1 or ICP27 siRNA-2, followed by infection with HSV-2. Cells were then stimulated with or without 100 HAU ml⁻¹ SeV for 16h and lysed for DLR assay. As shown in **Figure 2A**, knockdown of HSV-2 ICP27 by ICP27 siRNA-1 reduced the capability of HSV-2 in inhibiting IFN- β production at promoter activation level. To assess the impact of HSV-2 ICP27 on IFN- β production at protein level, HeLa cells were treated with negative control siRNA, ICP27 siRNA-1 or ICP27 siRNA-2, followed by infection

with HSV-2. At 24 h post-infection, supernatants were collected for ELISA and cells were lysed for Western Blot. As shown in **Figure 2B**, knockdown of HSV-2 ICP27 by ICP27 siRNA-1 reduced the capability of HSV-2 in inhibiting IFN- β production at the protein level. Knockdown of HSV-2 ICP27 was detected by a monoclonal antibody against HSV-2 ICP27, while β -actin was used as an internal control (**Figure 2C**). We also found that knockdown of HSV-2 ICP27 reduced the capability of HSV-2 in inhibiting IFN- β promoter activation in ME180 cells (**Supplementary Figure 1B**).

HSV-2 mainly infects epithelial cells and causes genital herpes. In addition to human cervical tissue and cervicovaginal epithelial cell lines, we performed experiments using primary human foreskin epithelial cells. Human foreskin epithelial cells were isolated and transfected with empty vector pcDNA3.1(+), plasmid expressing HSV-2 ICP27 or ICP22, or infected with HSV-2, followed by stimulation with or without 100 HAU ml⁻¹ SeV for 16 h. Total RNAs were extracted for RT-PCR and supernatants were collected for ELISA. In primary human foreskin epithelial cells, HSV-2 ICP27 significantly inhibited SeV-induced IFN-β production at both mRNA (**Figure 3A**) and protein (**Figure 3B**) levels. These results indicated that HSV-2 ICP27 can inhibit IFN-β induction in primary mucosal epithelial cells.

Altogether, the above findings inform that HSV-2 ICP27 plays an essential role in interfering with the induction of IFN- β in human cervical tissues, cervicovaginal epithelial cell lines, and primary human mucosal epithelial cells.

HSV-2 ICP27 Inhibits IFN-β Production Through IRF3 Signaling Pathway

HSV-1 ICP27 has recently been reported to inhibit type I IFNs by interacting with STING-TBK1 complex in macrophages (30), whereas our previous study found that HSV-2 can interrupts RIG-I mediated IFN-β signaling pathway in human epithelial cells (22). Given that DNA viruses produce dsRNAs during viral replication, which can be recognized by RNA sensors like RIG-I (31, 32), our current study focused on how HSV-2 ICP27 interferes with dsRNA-mediated induction of type I IFNs. We first determined whether HSV-2 ICP27 affects the IRF3-mediated signaling pathway. HEK 293T cells were seeded in 24-well plates overnight and co-transfected with empty vector pcDNA3.1(+), plasmid expressing HSV-2 ICP27 or the influenza virus NS1, together with PRD(III-I)₄-Luc which contains four repeats of IRF3 responsive domain of the IFN-β promoter and the internal control phRL-TK. At 24 h post-transfection, cells were stimulated with or without 100 HAU ml⁻¹ SeV for 16 h and lysed for DLR assay. As shown in Figure 4A, HSV-2 ICP27 blocks the activation of the IRF3 responsive promoter induced by SeV.

We next carried out experiments to address whether HSV-2 ICP27 directly affects the IRF3 signaling pathway. HEK 293T cells were seeded in 24-well plates overnight and co-transfected with a plasmid expressing IRF3 signaling pathway component RIG-IN, MAVS, TBK1, IKK- ϵ , or IRF3-5D and HSV-2 ICP27 expressing plasmid or empty vector pcDNA3.1(+), together with the reporter plasmid p125-Luc and the internal control phRL-TK.

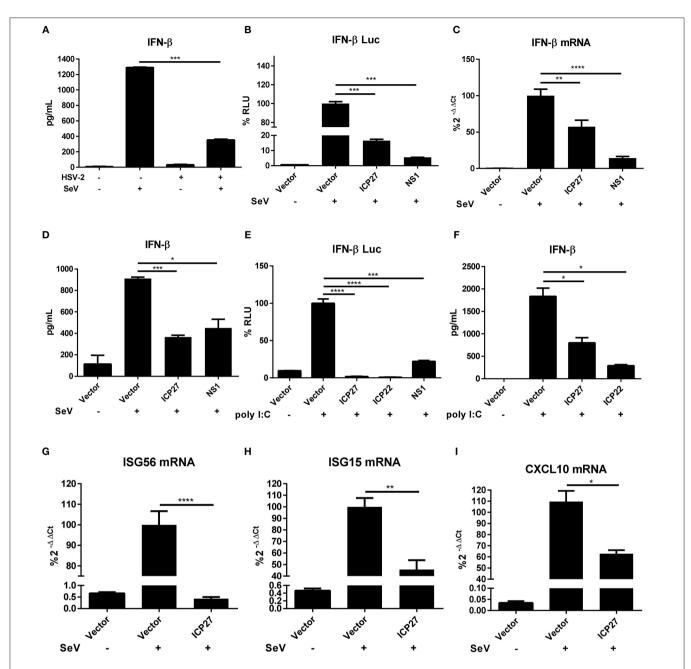


FIGURE 1 | HSV-2 ICP27 inhibits IFN-β production in human mucosal epithelial cells. (A) HSV-2 inhibits IFN-β production in human cervical tissues. Human cervical tissues were prepared and infected with or without HSV-2. At 4 h.p.i, the tissues were stimulated with or without 100 HAU ml⁻¹ SeV for 16 h, and the supernatants were harvested for ELISA. (B) HSV-2 ICP27 inhibits the activation of the IFN-β promoter. HEK 293T cells were seeded in 24-well plates and co-transfected with empty vector pcDNA3.1(+), HSV-2 ICP27 or influenza virus NS1 expressing plasmid, together with the reporter plasmid p125-Luc and the internal control phRL-TK. At 24h post-transfection, cells were stimulated with or without 100 HAU ml⁻¹ SeV for 16 h and lysed for DLR assay. (C,D) HSV-2 ICP27 inhibits IFN-β production at both mRNA and protein levels. HEK 293T cells were seeded in 6-well plates and transfected with empty vector pcDNA3.1(+), plasmid expressing HSV-2 ICP27 or influenza virus NS1. At 24 h post-transfection, cells were stimulated with or without 100 HAU ml⁻¹ SeV for 16 h and total RNAs were extracted for RT-PCR (C), while the supernatants were harvested for ELISA (D). (E) HSV-2 inhibits the Poly(I:C)-induced activation of the IFN-β promoter. HeLa cells were seeded in 6-well plates and co-transfected with empty vector pcDNA3.1(+), plasmid expressing HSV-2 ICP27, ICP22 or the influenza virus NS1, together with the reporter plasmid p125-Luc and the internal control phRL-TK. At 24 h post-transfection, cells were transfected with 2 µg/well Poly(I:C) or mock-transfected for 16 h and lysed for DLR assay. (F) HSV-2 ICP27 inhibits Poly(I:C)-induced IFN-β production at protein level. HeLa cells were seeded in 6-well plates and transfected with empty vector pcDNA3.1(+), plasmid expressing HSV-2 ICP27 or ICP22. At 24 h post-transfection, cells were transfected with 2 µg/well Poly(I:C) or mock-transfected for 16 h, and the supernatants were harvested for ELISA. (G-I) HSV-2 ICP27 inhibits the production of ISGs. HEK 293T cells were seeded in 6-well plates and transfected with empty vector pcDNA3.1(+) or HSV-2 ICP27 expressing plasmid. At 24 h post-transfection, cells were stimulated with or without 100 HAU ml-1 SeV for 16 h and lysed for RT-PCR to measure the expression of ISG56 (D), ISG15 (E), and CXCL10 (F) at the mRNA level. The data shown are representative of three independent experiments, with each condition performed in triplicate (mean \pm SD) (A-I). *P < 0.05; **P < 0.01; ***P < 0.001; ***P < 0.001; ***P < 0.0001.

HSV-2 ICP2 Inhibits IFN-6 Production

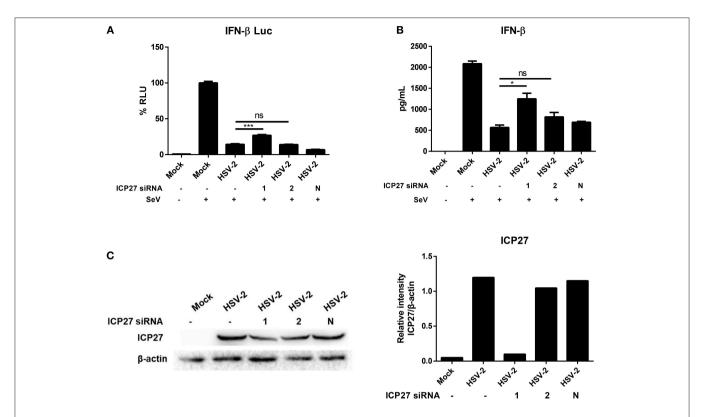


FIGURE 2 | HSV-2 ICP27 inhibits IFN-β production in the context of virus infection. (A) Knockdown of ICP27 reduces the capability of HSV-2 in inhibiting the IFN-β promoter activation. HeLa cells were seeded in 6-well plates and co-transfected with HSV-2 ICP27 siRNA-1, siRNA-2, or negative control siRNA (N), together with the reporter plasmid p125-Luc and the internal control phRL-TK. At 4 h post-transfection, cells were infected with HSV-2 at an MOI of 1 or mock-infected. At 20 h.p.i, cells were stimulated with or without 100 HAU ml⁻¹ SeV for 16 h and lysed for DLR assay. (B) Knockdown of ICP27 reduces the capability of HSV-2 in inhibiting the IFN-β production at the protein level. HeLa cells were seeded in 6-well plates and transfected with HSV-2 ICP27 siRNA-1, siRNA-2, or negative control siRNA (N). At 4 h post-transfection, cells were simulated with or without 100 HAU ml⁻¹ SeV for 16 h, and the supernatants were harvested for ELISA. (C) Knockdown efficiency of HSV-2 ICP27 siRNA. HeLa cells were seeded in 6-well plates and transfected with HSV-2 at an MOI of 1 or mock-infected. At 20 h.p.i, cells were simulated with or without 100 HAU ml⁻¹ SeV for 16 h and lysed for Western Blot. Gray scale scanning was performed by Image J software (version 1.52a). The data shown are representative of three independent experiments, with each condition performed in triplicate (mean ± SD) (A,B). *P < 0.05; ***P < 0.001. One representative experiment out of three is shown (C).

As shown in **Figures 4B–F**, HSV-2 ICP27 blocks the activation of the IFN- β promoter induced by all the tested IRF3 signaling pathway components in a dose-dependent manner.

Altogether, the above results indicate that, unlike HSV-1 ICP27, HSV-2 ICP27 inhibits IFN- β induction through an IRF3 dependent pathway.

HSV-2 ICP27 Blocks IRF3 Activation by Physically Interacting With IRF3

There are two main steps involved in IRF3 activation, phosphorylation and nuclear translocation (12). We first investigated whether HSV-2 ICP27 interferes with IRF3 nuclear translocation. Hela cells were seeded in 35 mm glass-bottom dishes overnight and transfected with plasmid expressing HSV-2 ICP27-HA or influenza virus NS1, or empty vector pcDNA3.1(+). At 24 h post-transfection, cells were stimulated with or without 100 HAU ml⁻¹ SeV for 16 h. Indirect immunofluorescence assay was performed to assess IRF3 localization in the presence or absence of HSV-2 ICP27. As

shown in **Figure 5A**, IRF3 translocation from the cytoplasm to the nucleus was partially blocked in the presence of HSV-2 ICP27.

Subsequent experiments were conducted to examine whether HSV-2 ICP27 blocks the phosphorylation of IRF3. HEK 293T cells were seeded in 6-well plates overnight and transfected with plasmid expressing HSV-2 ICP27 or influenza virus NS1, or empty vector. At 24 h post-transfection, cells were stimulated with or without 100 HAU ml⁻¹ SeV for 16 h. The phosphorylation of IRF3 was detected by an anti-p-IRF3 Ab, showing that HSV-2 ICP27 significantly inhibited IRF3 phosphorylation in cells (**Supplementary Figure 2**), and particularly in the nucleus (**Figure 5B**).

We next asked whether there is an interaction between HSV-2 ICP27 and IRF3. Co-immunoprecipitation (Co-IP) was therefore carried out. HEK 293T cells were seeded in 6-well plates overnight and transfected with plasmid expressing HSV-2 ICP27-Flag or empty vector pcDNA3.1(+). At 24 h post-transfection, cells were stimulated with or without 100 HAU ml⁻¹ SeV for 16 h, followed by Co-IP with a control IgG or an anti-Flag Ab. The

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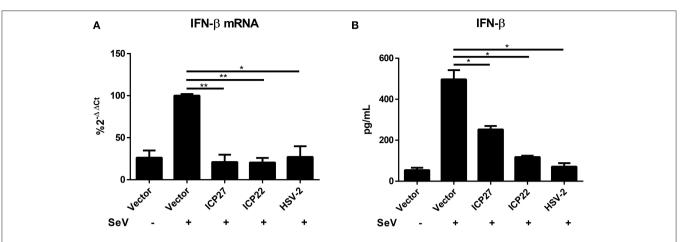


FIGURE 3 | HSV-2 ICP27 inhibits IFN-β production in primary mucosal epithelial cells. (**A,B**) HSV-2 ICP27 inhibits IFN-β production in human foreskin epithelial cells. Primary epithelial cells were isolated from human foreskin tissues and transfected with empty vector pcDNA3.1(+), plasmid expressing HSV-2 ICP27 or ICP22 or infected with HSV-2. At 24 h post-transfection, cells were stimulated with or without 100 HAU ml⁻¹ SeV for 16 h, and total RNAs were extracted for RT-PCR (**A**), while the supernatants were harvested for ELISA (**B**). The data shown are representative of three independent experiments, with each condition performed in triplicate (mean \pm SD) (**A,B**). * $^{*}P$ < 0.05; * $^{*}P$ < 0.01.

precipitates were analyzed by Western Blot using an anti-IRF3 Ab against endogenous IRF3. As shown in **Figure 5C**, HSV-2 ICP27 was able to specifically precipitate the endogenous IRF3, indicating a physical interaction between HSV-2 ICP27 and IRF3. To further confirm the interaction between IRF3 and ICP27, we purified ICP27 and IRF3 proteins, and carried out binding kinetic analyses. A biotinylated IRF3-Flag was coupled to Biosenors and immersed in different concentrations of the ICP27-Flag for association and disassociation. As shown in **Figure 5D**, there was a strong association between IRF3 and ICP27, and a higher concentration of ICP27 resulted in a stronger association.

Altogether these results indicate that HSV-2 ICP27 antagonizes the IRF3 signaling pathway by interacting with IRF3.

The 1-138aa Domain of HSV-2 ICP27 Is Mainly Responsible for the Inhibition of IFN-β Induction

To map the functional region of HSV-2 ICP27 involved in the inhibition of IFN-β production, we constructed several HSV-2 ICP27 truncation mutants according to its structure (https:// www.uniprot.org/uniprot/P28276) (Figure 6A). HEK 293T cells were co-transfected with empty vector pcDNA3.1(+), truncated or full-length HSV-2 ICP27 expressing plasmid, with the reporter plasmid p125-Luc and the internal control phRL-TK. At 24 h post-transfection, cells were stimulated with or without 100 HAU ml⁻¹ SeV for 16 h and lysed for DLR assay. To measure IFN-β at protein level, HEK 293T cells were transfected with empty vector pcDNA3.1(+), truncated or full-length HSV-2 ICP27 expressing plasmid, followed by stimulation with or without 100 HAU ml⁻¹ SeV for 16 h, and supernatants were harvested for ELISA. As shown in Figures 6B,C, the 1-138aa domain of HSV-2 ICP27 significantly inhibited IFN-β induction at both promoter activation and protein levels, and the capability was comparable to that of the full-length HSV-2 ICP27. The expression of ICP27 mutants was confirmed by Western Blot (**Supplementary Figure 3**). In contrast to that of HSV-1 ICP27 (30), we did not observe a direct contribution of the RGG box, which is located in the 138-152aa domain of HSV-2 ICP27, to the inhibited IFN- β induction. Our findings indicate that the 1-138aa domain, rather than the RGG box of HSV-2 ICP27 is mainly responsible for the inhibition of IFN- β induction.

DISCUSSION

HSV-2 is a large enveloped dsDNA virus, and its infections are known to be restricted to mucosal and keratinized epithelia and neuronal ganglia. HSV-2 infection causes genital herpes with sexual transmission being the main route. It is known that HSV-2 can evade the host mucosal innate immunity, but the underlying mechanisms remain to be defined (16). Our current study has demonstrated that HSV-2 immediate early protein, ICP27, interferes with RIG-I-MAVS-IRF3-mediated IFN- β induction in mucosal epithelial cells and HEK 293T cells. Mechanistically, ICP27 directly associates with IRF3 and inhibits its phosphorylation and nuclear translocation, resulting in the inhibition of IFN- β induction. Findings in this study reveal an unconventional strategy exploited by a dsDNA virus to interrupt the type I IFN signaling pathway.

It is generally accepted that DNA viruses are recognized by DNA sensors such as TLR9 and cGAS (33), while RNA viruses are sensed by RNA sensors including TLR3, TLR7/8, RIG-I and MDA5 (34, 35). Indeed, a number of studies on HSV-1 reported that the virus can interfere with the cGAS-STING pathway to inhibit type I IFN induction (30, 36–38). Of interest, we previously found that HSV-2 can also interrupt RIG-I-MAVS-IFN-β pathway in human mucosal epithelial cells (22). One explanation is that, DNA viruses produce dsRNAs during their replication cycles, which can be recognized by RNA sensors like RIG-I (31, 32). In addition, STING has also been reported

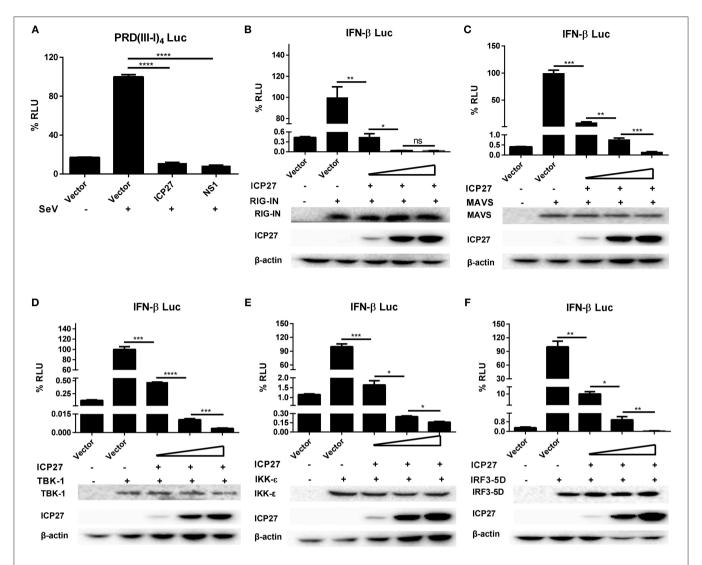


FIGURE 4 | HSV-2 ICP27 inhibits IFN-β production through IRF3 signaling pathway. (A) HSV-2 ICP27 inhibits the IRF3 promoter element PRD(III-I)₄. HEK 293T cells were seeded in 24-well plates and co-transfected with empty vector pcDNA3.1(+), plasmid expressing HSV-2 ICP27 or influenza virus NS1, together with PRD(III-I)₄-Luc and the internal control phRL-TK. At 24 h post-transfection, cells were stimulated with or without 100 HAU ml⁻¹ SeV for 16 h and lysed for DLR assay. (B-F) HSV-2 ICP27 inhibits RIG-I, MAVS, TBK1, IKK-ε, or IRF3-5D induced IFN-β promoter activation in a dose-dependent manner. HEK 293T cells were seeded in 24-well plates and co-transfected with empty vector pcDNA3.1(+) or HSV-2 ICP27 expressing plasmid, and plasmid expressing IRF3 signaling pathway component RIG-IN, MAVS, TBK1, IKK-ε, or IRF3-5D, together with the reporter plasmid p125-Luc and the internal control phRL-TK. At 40 h post-transfection, cells were lysed for DLR assay. At the same time, cells were lysed for Western Blot. RIG-I, MAVS, TBK1, IKK-ε, and IRF3-5D were detected by Anti-FLAG Ab while actin was detected by Anti-actin Ab. The data shown are representative of three independent experiments, with each condition performed in triplicate (mean ± SD) (A-F). *P < 0.05; **P < 0.01; ***P < 0.001; ****P < 0.0001. For Western Blot, one representative experiment out of three is shown (B-F).

to be involved in RNA virus recognition (39). In the case of HSV-2, its RNAs are rapidly generated during the life cycle of its primary infection (40), which may represent an important alternative source of pathogen-associated molecular patterns to trigger innate immune responses.

HSV-2 and HSV-1 have different initial infection and transmission sites, with HSV-2 mainly resulting in genital infections and HSV-1 normally causing orofacial infections (41). In addition, HSV-2 has a high positive-incidence of infections and common mucosal transmission routes with HIV-1 (42). For instance, HSV-2 predominantly infects mucosal epithelial cells which forms the primary mucosal barriers against HIV-1

infection, and interruption of these barriers may facilitate HIV-1 transmission (5). In the current study, we found that HSV-2 can significantly inhibit IFN- β induction in human cervical tissues. Moreover, by using mucosal epithelial cell lines and primary mucosal epithelial cells as models, we demonstrated that HSV-2 ICP27 contributes to such inhibited IFN- β induction. The significance of HSV-2 ICP27 in inhibiting IFN- β induction was further confirmed in the context of virus infection by the specific siRNA knockdown of HSV-2 ICP27, although knockdown of HSV-2 ICP27 did not fully abolish HSV-2-mediated inhibition of IFN- β induction. Given the complexity of the HSV-2 genome encoding at least 74 proteins, it is highly likely

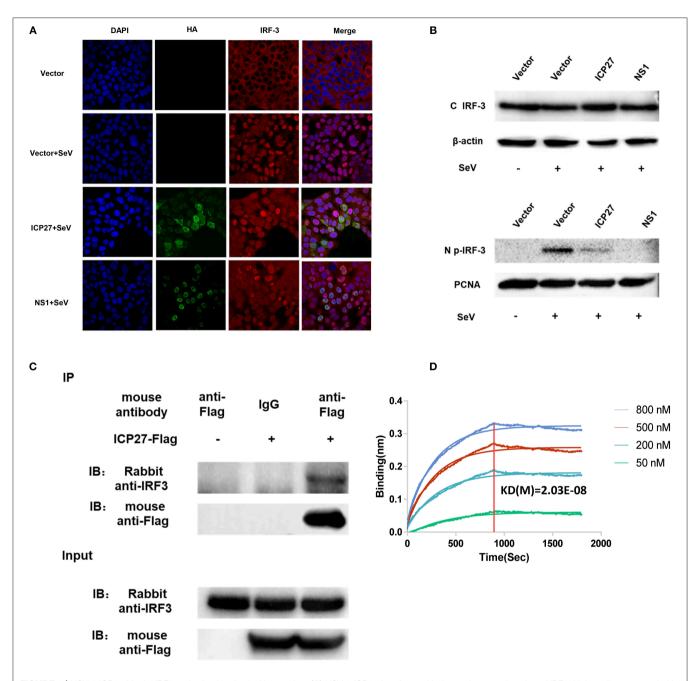


FIGURE 5 | HSV-2 ICP27 blocks IRF3 activation by physical interaction. (A) HSV-2 ICP27 interferes with the nuclear translocation of IRF3. HeLa cells were seeded in 35 mm glass-bottom dishes and transfected with empty vector pcDNA3.1(+), plasmid expressing HSV-2 ICP27-HA or influenza virus NS1-HA. At 24 h post-transfection, cells were stimulated with or without 100 HAU ml⁻¹ SeV for 16 h and prepared for immunofluorescence assay. IRF3 was detected under 647 nm wavelength, ICP27-HA or NS1-HA under 488 nm wavelength, and nuclei under 405 nm wavelength. (B) HSV-2 ICP27 inhibits IRF3 phosphorylation. HEK 293T cells were seeded in 6-well plates and transfected with pcDNA3.1(+), plasmid expressing HSV-2 ICP27 or influenza virus NS1. At 24 h post-transfection, cells were stimulated with or without 100 HAU ml⁻¹ SeV for 16 h. Nuclear and cytoplasmic proteins were isolated, and phosphorylated IRF3 was detected with a p-IRF3 mAb. (C) HSV-2 ICP27 interacts with endogenous IRF3. HEK 293T cells were seeded in 6-well plates and transfected with pcDNA3.1(+) or HSV-2 ICP27-Flag. At 24 h post-transfection, cells were stimulated with or without 100 HAU ml⁻¹ SeV for 16 h and lysed for immunoprecipitation assay. One representative experiment out of three is shown (A-C). (D) Kinetics of ICP27-IRF3 binding. The kinetics of binding was performed on a Forte-Bio Octet Red System. Purified IRF3 was conjugated with biotin at a molecular weight ratio of 1:3. Ten microgram/milliliter biotinylated IRF3-Flag was coupled to Biosenors and immersed in different concentration of ICP27-Flag (50, 200, 500, or 800 nM) for association and disassociation. The response in nm shift was recorded as a function of time. KD (M) = 2.03E-08.

that other unidentified HSV-2 proteins may also contribute to the suppression of IFN- β production. Because of the importance of IFN- β in inhibiting SHIV mucosal transmission (43), future

studies are warranted to investigate whether HSV-2 infection-mediated IFN- $\!\beta$ reduction plays a role in enhancing HIV-1 genital transmission.

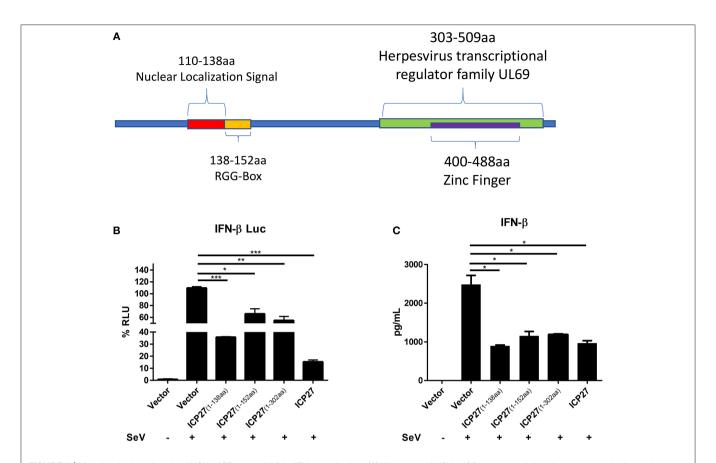


FIGURE 6 | Mapping the key domain of HSV-2 ICP27 that inhibits IFN-β production. (A) Illustration of HSV-2 ICP27 structural domain. 110-138aa is the nuclear localization signal of ICP27; 138-152aa is the RGG-box domain; 303-509aa is the Herpesvirus transcriptional regulator family UL69; 400-488aa is the zinc ring finger domain. (B) The 1-138aa domain of ICP27 inhibits the IFN-β promoter activation. HEK 293T cells were seeded in 24-well plates and co-transfected with empty vector pcDNA3.1(+), plasmid expressing HSV-2 ICP27 or its truncation mutant, together with the reporter plasmid p125-Luc and the internal control phRL-TK. At 24 h post-transfection, cells were stimulated with or without 100 HAU ml⁻¹ SeV for 16 h and lysed for DLR assay. (C) The 1-138aa domain of ICP27 inhibits IFN-β induction at protein level. HEK 293T cells were seeded in 24-well plates and transfected with empty vector pcDNA3.1(+), plasmid expressing HSV-2 ICP27 or its truncation mutant. At 24 h post-transfection, cells were stimulated with or without 100 HAU ml⁻¹ SeV for 16 h, and supernatants were harvested for ELISA. The data shown are representative of three independent experiments, with each condition performed in triplicate (mean ± SD) (A,B). *P < 0.05; **P < 0.01; ***P < 0.001.

We revealed in the current study that HSV-2 ICP27 can inhibit IFN-β production via the RIG-I-MAVS pathway. HSV-1/2 ICP27 is an essential multifunctional immediate early protein which regulates viral gene expression (44, 45). To date, most of the studies on ICP27 have focused on HSV-1 (44-46). For instance, HSV-1 ICP27 was shown to inhibit the phosphorylation and accumulation of STAT-1 in the nucleus, resulting the interruption of type I IFN signaling (47). In agreement, HSV-1 ICP27 knockout enhanced the activation of IRF3 and NF-κB in macrophages and DCs (48). More recently, HSV-1 ICP27 has been reported to inhibit type I IFN induction by interfering with the cGAS-STING-TBK1 signaling pathway in human macrophages (30). However, HSV-1 ICP27 appeared not to interfere with TBK1 phosphorylation, and the association of HSV-1 ICP27 with TBK1 required STING (30). In agreement, we found that, HSV-2 ICP27 strongly inhibited the production of IFN-β in HEK 293T cell line (22), which does not express STING (49), further strengthening that HSV-2 ICP27 can inhibit IFN production through a cGAS-STING-TBK1 independent pathway.

IRF3 plays a crucial role in type I IFN-mediated antiviral immune response (50). Activation of IRF3 during IFN-β production has several key steps: phosphorylation, dimerization, and cytoplasm-to-nucleus translocation. We previously found that, HSV-2 ICP22 inhibits IFN-β induction by antagonizing the association of IRF3 with the IFN-β promoter without suppressing the phosphorylation and nuclear translocation of IRF3 (22). Unlike the mechanism used by HSV-2 ICP22, we demonstrated in the current study that HSV-2 ICP27 interacts with IRF3 and interferes with IRF3 activation by blocking IRF3 phosphorylation and nuclear translocation, thereby inhibiting the production of IFN-β and ISGs. Given the complexity of HSV-2 genome containing over 70 genes, it is probable that multiple HSV-2 components likely contribute to the suppression of type I IFN induction by HSV-2. Indeed, although our current understanding of HSV-2 immune evasion is limited, work on HSV-1 has revealed multiple countermeasures in subverting type I IFN production (17, 18). By designing and analyzing HSV-2 ICP27 truncation mutants, we found that the 1-138aa region of HSV-2 ICP27 is the key functional domain responsible for HSV-2

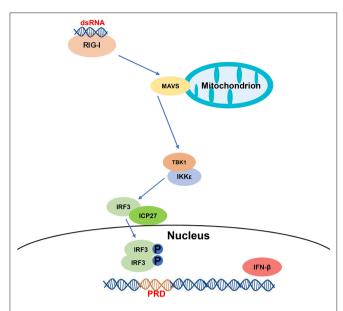


FIGURE 7 A schematic model of the mechanism by which HSV-2 ICP27 inhibits IFN- β production. HSV-2 dsRNA is detected by RIG-I, which recruits MAVS and downstream TBK1 and IKK- ϵ complex. HSV-2 ICP27 interacts with IRF3 and interferes with IRF3 activation by blocking IRF3 phosphorylation and nuclear translocation, thereby inhibiting the production of IFN- β and ISGs.

ICP27-mediated IFN-β reduction. In contrast, a study on HSV-1 ICP27 has shown that its RGG box, which is located in the region of 139-152aa, is the main determinant antagonizing the cytosolic DNA-stimulated IFN-β production, by targeting TBK1 and STING (30). Although HSV-2 ICP27 shares 79% of amino acid sequence with HSV-1 ICP27, the key function domain, the N-terminus is only 65% identical, which may explain the differences in biological functions. For instance, compared with HSV-1 ICP27, HSV-2 ICP27 is less efficient in promoting the cytoplasmic localization of ICP4, another important immediate early protein of HSV 1/2 (44). In addition, the capability of HSV-2 ICP27 in inhibiting IFN-β production appeared to be much stronger than that of HSV-1 ICP27 when the ICP27 of HSV-1 was replaced with HSV-2 ICP27 (30), indicating the distinction of HSV-2 ICP27 in inhibiting IFN-β production.

In conclusion, we have demonstrated that HSV-2 ICP27 inhibits IFN- β induction in human cervical tissues, cervicovaginal epithelial cell lines, and primary human mucosal

epithelial cells. We further addressed the underlying mechanism and proposed one model based on the RIG-I-MAVS-IRF3 pathway (Figure 7). During HSV-2 infection of mucosal epithelial cells, a number of by-products, such as viral dsRNA, are yielded and can be recognized by the RIG-I receptor. RIG-I binds to dsRNA through the helicase domain and signals through caspase activation and recruitment domains to the adaptor MAVS. Engagement of RIG-I initiates signaling through two downstream protein kinase complexes, ΤΒΚ-1/ΙΚΚ-ε, leading to the phosphorylation and dimerization of IRF3. IRF3 dimers translocate from the cytoplasm into the nucleus to bind to the IFN- β promoter, and promote IFN- β transcription (51). On the other hand, HSV-2 immediate early protein ICP27 interacts with IRF3, and interferes with IRF3 phosphorylation and nuclear translocation, thereby inhibiting the production of IFN-β and ISGs. Our findings provide important information for understanding how HSV-2 evades mucosal innate immunity and a potential viral target for intervention.

AUTHOR CONTRIBUTIONS

QH conceived the study. XG, MZ, and MF conducted the experiments. SL provided tissues samples. XG, MZ, and QH analyzed the data. XG and QH wrote the manuscript. All authors reviewed the manuscript.

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SUPPLEMENTARY MATERIAL

The Supplementary Material for this article can be found online at: https://www.frontiersin.org/articles/10.3389/fimmu. 2019.00290/full#supplementary-material

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Mechanisms of Immune Control of Mucosal HSV Infection: A Guide to Rational Vaccine Design

Naomi R. Truong 1,2†, Jacinta B. Smith 1†, Kerrie J. Sandgren 1,2 and Anthony L. Cunningham 1,2*

¹ Centre for Virus Research, The Westmead Institute for Medical Research, Sydney, NSW, Australia, ² Sydney Medical School, The University of Sydney, Sydney, NSW, Australia

Herpes Simplex Virus (HSV) is a highly prevalent sexually transmitted infection that aside from causing cold sores and genital lesions, causes complications in the immunocompromised and has facilitated a large proportion of HIV acquisition globally. Despite decades of research, there is no prophylactic HSV vaccine ready for use in humans, leaving many questioning whether a prophylactic vaccine is an achievable goal. A previous HSV vaccine trial did have partial success in decreasing acquisition of HSV2-promising evidence that vaccines can prevent acquisition. However, there is still an incomplete understanding of the immune response pathways elicited by HSV after initial mucosal infection and how best to replicate these responses with a vaccine, such that acquisition and colonization of the dorsal root ganglia could be prevented. Another factor to consider in the rational design of an HSV vaccine is adjuvant choice. Understanding the immune responses elicited by different adjuvants and whether lasting humoral and cell-mediated responses are induced is important, especially when studies of past trial vaccines found that a sufficiently protective cell-mediated response was lacking. In this review, we discuss what is known of the immune control involved in initial herpes lesions and reactivation, including the importance of CD4 and CD8 T cells, and the interplay between innate and adaptive immunity in response to primary infection, specifically focusing on the viral relay involved. Additionally, a summary of previous and current vaccine trials, including the components used, immune responses elicited and

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*Correspondence:

Anthony L. Cunningham tony.cunningham@sydney.edu.au

[†]Co-first authors

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the feasibility of prophylactic vaccines looking forward, will also be discussed.

1. INTRODUCTION

1.1. The Need for a Herpes Simplex Virus Vaccine

A prophylactic vaccine for herpes simplex virus types 1 and 2 (HSV1 and 2) is a global public health priority for development, as stated by WHO (1, 2) for several reasons: (1) genital herpes caused by HSV1 or 2 is now the commonest sexually transmitted infection; (2) it causes severe disease in neonates; (3) HSV1 is the leading cause of infectious blindness in western countries; (4) prior HSV2 infection leads to a three to six fold increased risk of HIV infection globally (3–5). Up to 50% of HIV transmissions in sub-Saharan Africa are estimated to occur in a setting of HSV2 infection (6, 7) and are more likely to occur soon after HSV2 acquisition (8). Antiviral

therapy for recurrent genital herpes markedly reduces clinical episodes but does not completely suppress viral shedding and does not reduce HIV acquisition (9), probably because of inadequate pharmacokinetics of acyclovir/valaciclovir (10). In contrast a prophylactic HSV vaccine would be likely to reduce HIV spread (11).

1.2. The History of Herpesvirus and HSV Vaccine Development

The development of vaccines for herpesviruses has met with variable success. The only major human successes have been with the vaccines for chicken pox and herpes zoster (shingles), both caused by varicella zoster virus (VZV). Progress with vaccines for herpes simplex virus has been very slow and partial so far.

Both VZV and HSV are alphaherpesviruses and their pathogenesis is similar as both infect skin and nerves and develop latent infection in trigeminal and dorsal root ganglia (TG and DRG), from where they reactivate, but much more frequently for HSV. The live attenuated varicella virus Oka strain (Varivax) was shown to prevent chicken pox in Japan in the 1990s and has been successfully deployed worldwide. Then in 2005, "Zostavax," consisting of a 14-fold more concentrated preparation of the Oka strain, was shown to prevent herpes zoster in 51% of immunized subjects and prolonged pain or postherpetic neuralgia (PHN) in 65% of them. However, vaccine efficacy against the incidence of zoster, although not PHN, is diminished in subjects >70 years of age and markedly declines over 8 years (12, 13).

Unlike live attenuated vaccines, recombinant protein vaccines require combination with an adjuvant to stimulate the immune system. Adjuvants enhance the immune response to an antigen and direct the immune system toward particular arms of the immune response, for example, toward T cell or antibody responses or both. This is usually mediated through antigen presenting cells, particularly dendritic cells (DCs). Recently, a recombinant protein vaccine for herpes zoster (RZV) was shown to be highly effective with >90% efficacy, even in subjects>80 years of age. There was no significant decline in protection over 4 years, with immunogenicity retained for 9 years (14). The vaccine contains a single varicella glycoprotein and the adjuvant system, AS01B, which consists of deacylated monophosphoryl lipid A (dMPL) and QS21, formulated in liposomes. dMPL, a toll-like receptor 4 agonist, is extracted from the cell wall of the bacterium Salmonella Minnesota and the saponin QS21 is derived from the bark of the soap bark tree (Quillaja saponaria). This adjuvant system stimulates VZV glycoprotein-specific CD4 T cells (and low level CD8 memory T cells) and humoral responses, although primary or naïve CD8 T cells are not stimulated (15).

Thus, very high levels of protection can be induced against herpes zoster by a single recombinant viral protein combined

Abbreviations: HSV1/2, Herpes Simplex Virus 1/2; HIV, Human Immunodeficiency Virus; VZV, Varicella Zoster Virus; DC, Dendritic Cell; dMPL, deacylated Monophosphoryl Lipid A; MHC, Major Histocompatibility Complex; IFN, Interferon; pDC, Plasmacytoid Dendritic Cell; NK, Natural Killer Cell; AS DC, Axl+ Siglec6+ Dendritic Cell; ILC, Innate Lymphoid Cell; DRG, Dorsal Root Ganglia; T_{RM} , Tissue Resident Memory T cell; Tregs, Regulatory T Cells; LCs, Langerhans cells; MNPs, Mononuclear Phagocytes; PBMCs, Peripheral Blood Mononuclear Cells

with an adjuvant that induces the appropriate adaptive (T and B cell) immune response by targeting antigen presenting cells. This is a strong improvement over the response induced by the live attenuated vaccine (16).

During 60 years of mostly unsuccessful attempts at development of an HSV vaccine, live attenuated candidates have been avoided because of concerns about potential carcinogenicity (initially as HSV2 was thought to cause cervical cancer) and recombination with clinical strains to produce new, highly virulent strains. However, new live attenuated candidates have been specifically mutated to achieve attenuation, e.g., via deletions of two key proteins, rather than simple point mutations to reduce the likelihood of reversion to virulence, and are currently in clinical trials, such as HSV529 (17). Other vaccine candidates have included DNA vaccines, hybrid recombinant viruses, and recombinant viral proteins.

In the 1990s two recombinant viral protein vaccine candidates were trialled. The Chiron vaccine candidate consisted of HSV2 entry glycoproteins B and D combined with oil in water emulsion adjuvant, MF59. When administered to subjects with recurrent genital herpes it induced high levels of neutralizing antibody but had no persistent or significant effect on frequency of recurrences (18). The GSK vaccine candidate, Simplirix, consisted of just the HSV2 entry glycoprotein D (gD), and the adjuvant system AS04. HSV2 gD is widely recognized by human populations, inducing both neutralizing antibody and CD4 T cells (19). AS04 consists of alum and dMPL. Simplirix showed 74% efficacy but only in HSV1/2 seronegative women with long-term HSV2infected partners (20). However, the subsequent Herpevac trial of Simplirix in randomly selected HSV1 and 2 seronegative women surprisingly showed significant efficacy against genital herpes caused by HSV1 (58%) but not HSV2 (only 20% and insignificant efficacy) (21). Thus, cross-protection against HSV1 was achieved with recombinant HSV2 gD, which is highly conserved between the two serotypes (22). This protection correlated with HSV1 neutralizing antibody titers whereas HSV2 neutralizing antibody titers were low. The better efficacy of the first trial could be explained by subclinical genital exposure to HSV2 shed by the infected partner, priming a later successful vaccine response. The efficacy of the novel adjuvant dMPL was attributed to induction of CD4 Th1 T cells as well as neutralizing antibody. However, no specific CD8 T cells were induced (23).

1.3. What Can be Learned From Comparison of the Efficacy and Immunogenicity of the Recent Herpes Zoster and Herpes Simplex Vaccines?

Why is there such a marked difference between the remarkable efficacy of the RZV vaccine and the partial success of the Simplirix vaccine given that they are similarly formulated and how can this inform development of a better HSV vaccine? The answer probably lies in understanding the mechanisms of immune control of natural herpes zoster and initial genital herpes. These include (1) "immunotherapy" vs. prophylaxis—the vaccine for herpes zoster seeks to control a reactivation disease, whereas the HSV vaccine seeks to control primary infection and

disease (2) possible differences in the immune responses required for control, (3) differences in the mechanism of action of the adjuvants and (4) immune evasion strategies of each virus. The latter is reviewed in Abendroth et al. (24) and Su et al. (25).

The distinction between an immunotherapeutic vaccine and prophylactic vaccine is critical. Prophylactic vaccines (such as Simplirix) aim at preventing acquisition of a pathogen and need to stimulate broad and durable immunity at the site of the entry of the pathogen. The Simplirix vaccine stimulated both antibody titers and CD4 T cell responses but antibody correlated best with vaccine efficacy in the Herpevac trial (23). Examination of the immune responses to HSV in nerve ganglia and skin suggest both are important, as well as CD8 T cells. Correlation of immune effectors with vaccine efficacy in trials of candidate immunotherapeutic vaccines from Agenus and Genocea as discussed below, also suggest all three are importantand perhaps are also important for prophylactic HSV vaccines. For a prophylactic vaccine to successfully stimulate the desired antibody, CD4 and CD8 T cell responses, it will need to stimulate dendritic cells (DCs), which are the only immune cell that can stimulate naïve responses.

In contrast, therapeutic vaccines aim to minimize disease severity and duration or reduce recurrences. Herpes zoster is caused by VZV reactivation in the neuronal ganglia so the RZV vaccine is effectively an immunotherapeutic vaccine. It is not intended as and may never be used as a primary prophylactic vaccine although it may effectively protect those previously immunized with Varivax from HZ when this cohort begins to reach the age of 50. This is suggested by the fact that CD4 T cell immunity generated by RZV was unaffected by previous Zostavax administration (26). RZV was demonstrated to activate blood memory T cells into a long-lasting polyfunctional state (27) which may partly explain its increased efficacy compared to Simplirix, although the presence of such T cells in critical tissues–neuronal ganglia or skin/mucosa, is unknown.

From the above discussion it is clear that definition of the innate immune response, in particular the role of critical subsets of DCs, which leads to the required effector response for prevention of infection or disease should make a major contribution to improving vaccine design. To do this it is important to know (1) the type of effector immune responses required (e.g., CD4 and/or CD8 T cells; which cytokines) and especially which pathogen proteins are most immunogenic in this setting; (2) which DCs need to be targeted to stimulate this response and their location; (3) how to target and activate those DCs with adjuvants and (4) how and where these adjuvants work; (5) any "off-target" effects of adjuvants likely to lead to unacceptable toxicity.

2. IMMUNE CONTROL OF HSV

2.1. Innate Immunity

2.1.1. Keratinocytes

Keratinocytes are the first line of defense against HSV infection in the skin and form a formidable barrier to pathogen entry. Keratinocytes also play a key role in innate immunity against pathogens (28). They express many pattern recognition receptors

including Toll-like receptors (TLRs), Nod-like receptors (NLRs) and RIG-I-like receptors (RLRs) for the detection of bacterial, fungal, and viral components (29). Keratinocytes produce a vast array of antimicrobial peptides such as LL-37, β defensins, RNases, and S100 family members (29). Additionally, keratinocytes produce chemokines and cytokines in response to pathogenic stimuli, including the chemokines CCL3, 4, and 5 in response to HSV infection. CCL3 was highly chemotactic for activated CD8 T cells, CCL4 for activated CD4 T cells, and CCL5 for resting and activated CD4 or CD8 T cells (30). Keratinocytes produce pro-inflammatory cytokines such as TNF, IL-1 α , IL-1 β , IL-6, IL-10, IL-18, and IL-33, which direct the immune response toward a Th1 responses, Th2/Treg responses or have direct antiviral effects (30-32). In addition, keratinocytes have also been shown to be an accessory or "non-professional" antigen presenting cell that upregulate MHC class II in response to IFN- γ produced by T cells (33, 34). In an in vitro model of a recurrent herpes simplex lesion, IFN-γ stimulated, HLA-DR expressing human keratinocytes were capable of both presenting HSV antigen to T cells and acting as targets for HSV-specific T cell cytotoxicity (33).

2.1.2. Type I Interferon, Plasmacytoid DCs, and AXL+SIGLEC6+ DCs

Type I Interferons (IFNs) are a key component of innate antiviral immunity. They are produced by antigen presenting cells following detection of a pathogen and activation of pattern recognition receptor signaling, such as the TLR signaling pathway. The Type I IFNs expressed in humans include IFN- α (of which multiple subtypes have been identified), IFN- β , IFN- ε , IFN- ω , and IFN- κ , although the functions of IFN- α and - β have been best characterized (35, 36). Type I IFNs induce the expression of antiviral genes known as IFN stimulated genes (ISGs), which play a role in inhibiting viral replication and promoting degradation of viral mRNA (36). Type I IFNs also activate multiple immune cell types in response to HSV infection, including neutrophils, macrophages, natural killer cells, and DCs (35).

Plasmacytoid dendritic cells (pDC) are extremely potent producers of IFN- α , and thus play an important role in antiviral defense. pDCs can also produce other cytokines and chemokines such as TNF, IL-6, CXCL10, and CCL3, for the recruitment and activation of other immune cells (37). Additionally, pDCs are thought to contribute to adaptive immunity through the activation of T cells. Viral stimulation not only triggers IFN- α , but can also differentiate pDCs into antigen presenting cells, via the upregulation of HLA-DR, CD80, and CD86, that are capable of T cell stimulation and cytokine production (38). In particular, studies of both mouse and human pDCs have demonstrated cross-presentation of exogenous antigens, resulting in the activation of naïve or memory CD8 T cells (39, 40).

In a study of human recurrent genital herpes lesions, pDCs infiltrated at both early (day 4) and late (day 10) phases. They were often found at the dermo-epidermal junction and were closely associated with CD69⁺ T cells as well as NK cells (41). Despite expressing the HSV entry receptors nectin1, nectin2, and HVEM, pDCs were resistant to HSV infection *in vitro*, but were

able to stimulate virus-specific autologous T cell proliferation, particularly in CD8 T cells, indicating their capacity to cross-present antigens. This study demonstrated specifically in the context of HSV that pDCs are both strong producers of IFN- α and stimulated T cell proliferation in response to the virus. However, more recent studies challenge the notion that T cells proliferation is stimulated by pDCs.

Recently, a new DC sub population with characteristics of both conventional (c)DC and pDC has been described. AS DCs, named for their expression of AXL and SIGLEC6, express markers in common with both pDCs and cDCs (42). Upon cell sorting to obtain pure populations, it was found that pDCs were the producers of Type I IFN with weak ability to stimulate T cell proliferation, while AS DCs had the inverse functional responses. This study also provides evidence that traditional pDC gating is contaminated with AS DCs, suggesting that previous work investigating the role of pDCs in HSV infection would also contain contaminating AS DCs, and that AS DCs may be the true stimulators of T cell proliferation.

No work has as yet been conducted on AS DCs in relation to HSV infection, and it has not been assessed whether they are recruited to the skin during inflammation, as has been shown for pDCs. Therefore, studies investigating the presence of AS DCs in the HSV inflammatory infiltrate need to be conducted. By establishing what role AS DCs play in response HSV infection, it may bifurcate functional roles previously thought to be carried out by pDCs, i.e., Type I IFN and T cell stimulation.

2.1.3. Natural Killer and Innate Lymphoid Cells

Several studies point to an important role for natural killer (NK) cells in response to HSV infection, particularly in controlling the severity of infection. In mouse studies, mice that lack NK cells or are depleted of NK cells have increased susceptibility to HSV2 infection and increased viral titers in the vaginal mucosa, spinal cord, and brain stem (43, 44). Similarly, a more recent study examining the severity of cutaneous HSV infection in mice with atopic dermatitis (AD) compared to normal mice found that AD mice had defective NK cell activity, which correlated with increased severity of skin infection. Furthermore, normal mice that were depleted of NK cells prior to HSV infection also had increased skin inflammation and viral titers compared to those with NK cells present (45). In humans, case studies examining patients with a specific lack of NK cells have correlated this with increased susceptibility to severe HSV infections (46, 47), suggesting an important role for NK cells in control of HSV. Furthermore, enrichment of NK cells has been observed in recurrent herpes lesions (48), interacting with pDCs (41), and CD4 T cells (49). In in vitro studies, TLR2-stimulated NK cells could directly activate HSV gD-specific CD4 T cells (49), and their high frequency of contact with CD4 T cells in herpetic lesions suggests they play a role in stimulating CD4 T cells in this setting. These studies indicate that NK cells play a role in controlling HSV infection by restricting viral replication and spread through the early production of IFNy, and may also be important stimulators of adaptive immunity. However, studies in both mice and humans have not identified a correlation between NK cell activity and viral clearance, which appears to be the role of T lymphocytes (48, 50–52).

In recent years knowledge of the network of innate lymphocytes has become more complex. NK cells are part of a network of innate lymphoid cells (ILCs), whose functions are analogous to T cell subsets (53). NK cells can be considered the innate counterpart of CD8 T cells, while ILC1, ILC2, and ILC3 represent the innate counterparts of CD4 T helper 1 (Th1), Th2 and Th17 cells, identified by the same transcription factors and cytokines: NK/CD8 express Eomes, granzymes and IFN-γ, ILC1/Th1 express Tbet and IFN-γ, ILC2/Th2 express Gata-3 and IL-4, IL-5, and IL-13, and ILC3/Th17 express RORyt or AHR, IL-17, and IL-22 (53). ILCs preferentially localize into barrier tissues such as the skin, lungs and gut (54). Recently, a study examined the in situ ILC subset quantities and distribution in human skin (55) and found that there were differences in the proportions of different ILC subsets in normal, AD and psoriasis skin. Additionally there were increased numbers of ILCs in both AD and psoriasis compared to normal skin. However, the location of the ILC subsets was consistent: located in the upper dermis, close to the epidermis, not associated with blood vessels and in close proximity to T cells. Since ILCs were shown to infiltrate into inflamed skin, they are therefore likely to also be present in the inflammatory infiltrate during HSV infection. However, to date, no studies have investigated the presence and role of ILCs in HSV infection.

2.2. Adaptive Immunity

2.2.1. The Role of B Cells and Neutralizing Antibodies in HSV Infection

B cells are the key immune cells of the humoral immune response, producing antibodies, such as IgG and IgA, that protect against many infectious pathogens. Levels of IgG and mucosal IgA are increased in vaginal secretions of mice, guinea pigs, and nonhuman primates intravaginally vaccinated with HSV2 (56-58), as well as in cervical secretions of women with primary HSV2 infection (56). Antibody responses vary, with IgG present as early as a few days while IgA presents up to 2 weeks post infection, however both persist for weeks after infection. Both antibodies react to various HSV glycoproteins, including gD, gB, and gC (56). However, the role of antibody-mediated protection against HSV2 pathogenesis is unclear (36) and data from vaccine trials is contradictory. In a human in vitro model of fetal dorsal root ganglia (DRG) innervating autologous epidermal skin explants, neutralizing antibodies reduced transmission of virus from axons to epidermis by 90% by binding to the virus in the intercellular gaps between axon termini and epidermal cells. It was suggested that antibodies might also be effective in preventing epidermisto-neuron transmission during primary HSV infection (59). Some murine studies have demonstrated the importance of the antibody response to HSV. One study demonstrated that adoptive transfer of IgG from HSV2 vaccinated mice reduced viral load and pathological signs of disease in the vaginal lumen of naïve mice (60). Later studies showed that antibodies played a role in controlling viral titers and protection with the use of B cell-deficient mice (61, 62). Further studies in mice and guinea pigs have correlated pan-HSV2 antibodies with protection

from vaginal challenge (63). However, other murine studies have shown that humoral immunity alone was unable to control HSV infection and failed to protect against infection. Two studies that compared T cell and B cell depletion found that T cells, rather than B cells, were critical for protection against lethal challenge of HSV2 (64, 65). Additionally, passive transfer of immune serum or anti-HSV antibodies did not protect against vaginal infection (66, 67).

However, most recently, the importance of neutralizing antibodies has once again been demonstrated in studies of a trivalent vaccine containing HSV2 gC, gD, and gE with CpG and alum in rhesus macaques. When the vaccine was administered before virus challenge it induced plasma and mucosae neutralizing antibodies that blocked gD and gE immune evasion activities and stimulated CD4 T cell responses. In guinea pigs, the trivalent group had genital lesions on <1% of days and shedding of virus on 0.2% of days (68). When the vaccine was administered to guinea pigs previously infected with HSV2, the vaccine significantly boosted ELISA and neutralizing antibody titers, reduced the frequency of recurrent lesions and vaginal shedding of HSV2 DNA by approximately 50% and almost completely prevented viral shedding (69). Therefore, neutralizing antibodies were protective against vaginal challenge and contributed significantly to reductions in genital lesions and viral shedding in animal models.

2.2.2. Maternal Immunization: Clues for Protection

Studies of neonatal herpes and the protective effects of maternal immunization also provide some strong evidence for the importance of neutralizing antibodies in protection against HSV infection. Neonatal HSV infections are rare, but cause considerable morbidity and mortality in infants, with an estimated fatality rate of 60% worldwide (70). Globally, there are an estimated 14 000 cases annually, with the highest prevalences in Africa and the Americas (70). The risk of neonatal herpes infection is highest in mothers who have first-episode primary infection at the time of delivery, with transmission rates up to 60%, whereas babies born to mothers with recurrent HSV are only 1–2% likely to develop neonatal herpes (71–73). This is consistent with the hypothesis that maternal immunity provides protection to the neonate.

During pregnancy, antibodies (mostly IgG) are transferred from mother to child across the placenta (74), to ensure the temporary health and survival of the young infant. Low neutralizing antibody titre and avidity have been identified as risk factors for transmission to neonates (71, 72). However, not all pregnant women have protective concentrations of antibodies against pathogens (75), and thus maternal immunization may be an avenue for protection. Maternal immunization has already been shown to provide protection to neonates against tetanus and seasonal influenza (75) and could also be an avenue to protect against neonatal herpes.

Limited studies have investigated the effects of maternal immunization against neonatal herpes in humans, with most work conducted in mice. Murine studies have produced some promising but also conflicting results. In one study that utilized vaccination with a replication defective HSV2 mutant, HSV

specific IgG antibodies passively transferred from mother to pup and reduced dissemination of virulent HSV but replication of virus or spread of virus to the CNS in pups was not prevented (76). More recently another study that utilized vaccination with a Δ gD-2 HSV2 showed that maternal immunization did lead to protection from neuronal involvement of HSV and latency in the pups. Increased antibody levels were also found in the serum of these pups (77). Differences in these findings could be due to the viruses the female mice were immunized with, as the more recent study used a virus that was known to protect adult mice from HSV infection upon re-challenge.

Another recent study found that both mice and humans had HSV specific antibodies in the trigeminal ganglion (TG) during HSV1 latency. Furthermore, in a murine model they demonstrated that maternal IgG accessed and persisted in neonatal TG and was protective not only against disseminated infection but also against neurological disease following neonatal HSV challenge (78). These recent studies provide evidence that maternal immunization could provide protection against neonatal herpes, and that neutralizing antibodies play a critical role in mediating this protection.

Overall, evidence suggests that humoral immunity is likely to play an early beneficial role in primary HSV infection, and may be particularly beneficial in preventing vertical transmission from mother to neonate, but ultimately cell-mediated immunity is necessary for HSV clearance and protection (36).

2.2.3. The Role of T Cells in HSV Infection

CD4 and CD8 T cells are the key components of the cell-mediated immune response. CD4 T cells are critical for the activation of B cells and antibody class-switching, as well as for "licensing" DCs to activate CD8 T cells (79, 80). CD4 T cells also secrete the Type II IFN, IFN- γ , which performs a number of antiviral roles including limiting HSV viral replication and spread (81) through the induction of antiviral genes such as protein kinase RNA-activated (PKR), which inhibits translation within infected cells (82). CD8 T cells have the important role of killing virally infected cells via their cytotoxic components perforin and granzymes, mediated through the engagement of MHC class I molecules on target cells (82). HSV T cell immunity operates at two sitesneuronal ganglia and the mucosa.

In mice, CD4 and CD8 T cells surround the neurons and adherent satellite cells of trigeminal ganglia (TG) and control latency and (some) reactivation. CD8 T cells secrete granzymes which degrade intracellular ICP4 and contribute to this control (83, 84). In the human TG or DRG, there are abundant HSV infected neurons (3% of 27000 neurons per DRG). Effector memory CD4 and CD8 T cells expressing IFN- γ , TNF and CCL5 are found in HSV DNA⁺ ganglia and occasional clusters of these CD4 and CD8 T cells are found around neurons and are HSV specific and activated (CD69⁺). The satellite cells surrounding neurons express MHC class II, IL1 and TGF- β which can support (resident) memory T cells. Whether these T cells are truly tissue resident memory (T_{RM}) cells has not been confirmed (85, 86).

From early studies of human recurrent herpes lesions in genital skin and mucosa, we know CD4 T cells infiltrate early and are the predominant T cell subset in the first 12–48 h

post onset (52). CD4 T cells produce IFN-y, which has been shown to restore HSV-induced MHC class I downregulation and upregulate MHC class II in infected keratinocytes (87). CD4 T cell depletion studies in mice provide evidence of the critical role of CD4 T cells in the immune response to HSV. For example, CD4 deficient or depleted mice fail to recruit CD8 T cells to the vaginal epithelium. CD4 T cell IFN- γ stimulates epithelial cells to secrete CXCL9 and CXCL10, which recruits CD8 T cells to the site of infection (88). In human studies, CD4 T cells have been observed persisting in genital skin at the site of HSV2 reactivation for at least 6 months post-healing (89) and continue to produce IFN-γ early after HSV antigen exposure and lesion healing (90). Similarly, in human recurrent herpetic lesions, CD8 T cells infiltrate later than CD4 T cells (52), and their recruitment into genital lesions is strongly correlated with viral clearance, confirmed by the selective depletion of CD4 T cells (48).

Upon lesion healing, HSV specific CD8 T cells persist at the dermo-epidermal junction adjacent to peripheral nerve endings in small, enriched clusters, and function as sentinels for reactivation in the female genital tract (91, 92). Resident HSV-specific CD8 T cells encounter HSV quite frequently, and as such express genes for antiviral function, chemotaxis, and recruitment (93), as well as a lack of chemokine receptor expression for egress and recirculation, and the ability to produce cytolytic granules during clinical quiescence (94). These findings demonstrate that these cells remain active in immunosurveillance after episode clearance. HSV-specific CD8 T_{RM} located in genital skin and mucosa have also been identified as CD8 $\alpha\alpha$ + T cells that express two CD8 α chains, instead of an α and β chain. This homodimer expression has been associated with high affinity antiviral effector T cells (94).

Recently, studies of CD8 T cells and HSV have focused on investigating the spatial distribution of CD8 T_{RM} cells. Despite CD8 T_{RM} cells remaining in the genital tract as sentinels to protect against recurrences, shedding continues to occur and at variable rates between individuals. Schiffer and colleagues developed a mathematical model that spatially models the effects of variability of CD8 T_{RM} cells in HSV lesions, as well as HSV replication and spread. The model found that high levels of overall CD8 T cell density did not equate with total control of HSV and that high shedding drove frequent mucosal T cell turnover. HSV was also found to capitalize on the spatial heterogeneity of local immunity, exploiting the gaps and allowing reactivation to occur (95).

Schiffer and colleagues, using a mathematical model, found that HSV infection did not induce sufficient T_{RM} cells in the human genital tract to eliminate reactivation, and that strict spatial distribution is maintained during infection, as was found in murine models. The strict distribution and heterogeneity of T_{RM} cells provide areas for HSV replication to occur upon reactivation. The spatial distribution and heterogeneity of T_{RM} cells calculated from the mathematical model was also confirmed in histological genital biopsies. Understanding how genital tract T_{RM} cells are spaced in the tissue provides insight as to how reactivation continues to occur, even in their presence (96).

Therefore, CD8 T cells have been found to play important roles in HSV infection. They initially clear active lesions, then

become T_{RM} cells, immune sentinels, that ensure reactivation is a rare occurrence. These studies on CD8 T cells suggest important insights into why previous vaccines, which have not been able to stimulate CD8 T cell activation, were unsuccessful. New vaccine designs should incorporate a focus on the stimulation of CD8 T cells and induction of a T_{RM} population that remain in the tissue as sentinels, ready for an encounter with HSV. Such vaccines would need to induce high T_{RM} cell numbers in the genital tract to overcome heterogeneous spatial distribution and provide higher killing efficiency and IFN- γ production (96).

Regulatory T cells (Tregs) are a population of CD4 T cells that suppress T cell effector functions. They are characterized by the expression of CD4, CD25, and the transcription factor Foxp3 (97). Tregs are an inherent component of any immunological response as they silence and suppress effector and cytotoxic immune responses to ensure harm does not come to the body. The role Tregs play in HSV lesions is controversial. Some murine studies have found that Tregs are beneficial either in facilitating an effective immune response or suppressing immunopathology. Tregs are essential for promoting the accumulation of HSV specific CD4 T cells in infected tissue and ensuring DCs traffic to the appropriate draining lymph node from the vaginal mucosa, resulting in effective CD4 T cell priming (98). However, other murine studies found that Tregs suppressed T cell effector responses to HSV. Depletion of Tregs before HSV infection significantly enhances HSV-specific CD8 T cell cytotoxicity in neonatal mice, and significantly enhances the IFN- γ responses of CD4 and CD8 T cells in both adult and neonatal mice (97). Furthermore, depletion of Tregs prior to HSV infection significantly decreases skin lesion severity and granulocyte cell numbers at the site of ganglionic spread from flank HSV2 (99). In human genital biopsies from HSV2 recurrent lesions, the density of Tregs directly correlated with HSV2 titers (100) Thus, it may be the balance between effector T cells and Tregs that determines whether Tregs are beneficial or detrimental during HSV infection.

A significant limitation of murine HSV infection models is that HSV does not cause recurrent lesions in mice, and so the role of Tregs in reactivation cannot be assessed. Therefore, it is important to assess the role of human Tregs in response to HSV infection. One study conducted on the peripheral blood of HSV+ patients found that CD4+CD25+ memory Tregs suppressed the proliferation of HSV specific CD4 T cells at times of clinical quiescence (101). It is known that high numbers of Tregs infiltrate the site of viral reactivation in genital skin biopsies and persist in proximity to T cells, specifically during reactivation. There is also a correlation between high Treg numbers and increased viral replication, indicating that Tregs may be suppressing immune effectors and allowing virus to proliferate. This correlates with the observation that Tregs were found to localize with CD4 T cells in the upper dermis (100). Shedding biopsies also had significantly higher ratios of Tregs to other T cells, and this affected the clinical presentation of disease; for example, an increase in Tregs could result in insufficient effector function (100). In the context of human HSV infection, the evidence suggests Tregs could be more detrimental than beneficial, particularly during virus reactivation. Therefore,

an additional consideration for new vaccine designs could be the addition of adjuvants that suppress the activation of Treg responses, particularly in immunotherapeutic vaccines that aim to reduce virus reactivation.

Gamma-delta ($\gamma \delta$) T cells are non-conventional T cells that are uniquely defined by the expression of a $\gamma\delta$ TCR, unlike conventional CD4 and CD8 T cells which express an $\alpha\beta$ TCR. $\gamma \delta$ T cells are enriched in epithelial tissues such as skin, where they maintain epidermal integrity (102). Studies in mice have investigated the role of $\gamma\delta$ T cells in HSV infection. One study found that $\gamma \delta$ T cells were protective, limiting the severity of HSV1 induced epithelial lesions and preventing the development of lethal viral encephalitis (103). They provided evidence that $\gamma \delta$ T cells decrease viral replication and restrict viral progression into the brain. Another murine study found that epidermal $\gamma \delta$ T cells were the first immune effector to encounter HSV and were directly infected, prior to the infection of Langerhans cells (104). However, human $\gamma \delta$ T cells are different to their murine counterparts. Murine $\gamma \delta$ T cells reside in both the epidermis and dermis, whereas human $\gamma \delta$ T cells mainly reside in the dermis and near the dermo-epidermal junction (105). Some reports investigating human blood $\gamma \delta$ T cells suggest that they could play a protective role in antiviral immunity, particularly to HSV (106, 107). However, the role of skin $\gamma\delta$ T cells during HSV infection has not been investigated in human skin or genital mucosa and such studies could reveal important differences between the role of murine and human $\gamma\delta$ T cells in HSV infection and whether they are important targets for vaccine design.

2.2.4. The Role of Dendritic Cells in Stimulating HSV Immunity

Dendritic cells (DCs) are the most important bridge between the innate and adaptive immune system. They patrol blood and tissue compartments to detect pathogens and take up antigens, after which they mature and migrate to lymph nodes where they present the antigens to naïve T cells, thereby activating the adaptive immune response (108). Several subsets of DCs have been identified in various tissue compartments (e.g., blood, skin, liver, brain etc.).

Due to limitations in obtaining tissue-derived human DCs, earlier studies of the role and response of human DCs to HSV infection made use of model DCs generated from monocyte-derived DCs (MDDCs). These studies provided evidence that immature DCs could be productively infected by HSV, HSV induced apoptosis in human MDDCs (a process that HSV normally inhibits) and that uninfected DCs pulsed with apoptotic HSV-infected DCs could cross-present and stimulate HSV specific CD8 T cells (109, 110). These models still must be confirmed in tissue-derived human DCs; a complex process.

2.2.5. The Complexity of the DC/Macrophage Network in Human Skin

It has been known for a long time that Langerhans cells (LCs) are the major DC subtype located in the epidermis. Whether LCs were important in HSV infection was first shown in the 1980s, where mice whose skin was abraded, leading to the fleeing of LCs, and inoculated with HSV1, had an increase in viral pathogenicity

due to the absence of LCs. When LCs were present, interactions between LCs and HSV1 were observed as early as 2 h.p.i, and LCs became HSV1 gD positive, indicative of virus uptake (111).

A more recent study of LCs in mice following HSV infection showed that LCs became infected with HSV, however uninfected or bystander LCs were the main emigrant DC subset at 24 h.p.i. Additionally, most infected LCs failed to downregulate Ecadherin (preventing their emigration) and became apoptotic (104). When investigating the role of LCs in humans, one major difference is seen. LCs still become productively infected, mature and become apoptotic, however all infected LCs migrate into the dermis (112). Therefore, unlike murine LCs, where HSV infection seemed to inhibit migration of at least a significant proportion, in human LCs HSV infection induced migration to the dermis. Such differences highlight the importance of examining the immune response to HSV in human skin and in particular the role of subsets of human DCs.

In recent years, the development of technologies such as single cell RNA-sequencing have facilitated the classification of DC subsets. In human dermis, the two main DC subsets are conventional DC type 1 and 2 (cDC1 and cDC2) (113). cDC1s are a minor subset proportionally, but are highly efficient at cross-presentation of exogenous antigen to CD8 T cells (114). They are characterized by the expression of CD141, XCR1, the C-type lectin receptor CLEC9A and TLRs 1, 2, 3, 6, 7, and 8, and are recognized as the equivalent of murine CD103+/CD8 α + cross-presenting DCs (115-117). The major dermal DC subset are cDC2s, which have conventional antigen-presenting capacity to stimulate CD4 T cells, but also have some ability to crosspresent to CD8 T cells (117, 118). They express CD1a, CD1c, CD11b, CD11c, and some express langerin (108) and may be the equivalent of murine submucosal CD11c+ and CD11b+ DCs. Single cell analysis has also complicated the definition of what is considered a DC or a macrophage. Dermal CD14+ mononuclear phagocytes (MNPs) were originally classified as DCs due to their ability migrate out of tissue explants, their expression of MHC class II and CD1c, and ability to influence T cells; all properties that dermal DCs have (119, 120). However, there is no known murine equivalent to human CD14+ DCs, yet mice and humans tend to have homologous cells (117, 121). Furthermore, a study found that CD14+ MNPs (which also express DC-SIGN) were transcriptionally and functionally similar to tissue resident monocyte derived macrophages (MDMs). For example their ability to stimulate memory T cells like macrophages but not stimulate naïve T cells, an ability unique to DCs. However, these cells also have DC properties in their ability to migrate out of tissue, making them a MDM with DC-like ability (122).

It has been known for some time that the process by which skin DCs take up HSV and present antigen to CD4 and CD8 T cells leading to the development of memory T cells is complex. Several studies have tried to unravel this complexity and define the process in murine models. It has been shown in mice that LCs take up HSV in the epidermis (111), but they do not present HSV antigen to T cells in lymph nodes. Neither LCs nor lymph node resident DCs present HSV2 antigens to CD4 T cells, but submucosal CD11c+ and CD11b+ DCs (cDC2s) do (123). Furthermore, naive CD8 T cells are primed by CD8 α + DCs and

CD103+ dermal DCs (cDC1s) (124, 125) and the latter are the predominant cells transporting HSV antigens out of murine skin explants (104).

In our recent human study, we investigated the interaction of HSV-infected LCs with dermal cDC1s in human inner foreskin explants and in biopsies of initial herpes simplex virus lesions. HSV1 infected LCs became apoptotic and migrated to the dermis to interact with cDC1s in clusters. LC fragments were detected within some cDC1s, and cDC1s emigrated from HSV1 infected explants, similar to CD103+ dermal DCs in murine models. Additionally, DC-SIGN+ MNPs were also observed in clusters interacting with HSV-infected LCs in the dermis (112). Therefore, this study demonstrated that epidermal LCs take up HSV, become infected and transfer the virus or viral antigens to subsets of dermal DCs/MNPs, facilitating viral relay. This has filled an important gap in knowledge of the immunological processes facilitating HSV antigen presentation to T cells. However, important questions remain: What role do human cDC2s play in interactions with HSV infected LCs? Are there differences in the interactions of different dermal DC/MNP subsets with the LCs that could determine their specific contributions to the activation of CD4 and CD8 T cells? By understanding the roles of specific human DC subsets in response to HSV infection, it should drive vaccine design toward stimulating pathways that induce the same immune responses as natural infection and, in particular, CD8 T cell responses that were not induced by previous vaccine candidates. A summary of the HSV viral relay and localization of immune cell subsets in human skin is shown in Figure 1.

3. BUILDING ON KNOWLEDGE OF NATURAL IMMUNITY TO DESIGN A VACCINE

3.1. Challenges of Designing a Protective Vaccine

Prophylactic and immunotherapeutic vaccines have different goals and as such there are challenges to overcome in the development of a successful prophylactic vaccine that are not critical for an immunotherapeutic vaccine. Since prophylactic vaccines aim to prevent acquisition of a pathogen, they need to stimulate effective primary immune responses at the site of pathogen entry. To generate primary immune responses, naïve T cells require two signals to differentiate into effector cells: an antigen-specific signal and a second costimulatory signal (such as CD80/86 ligation of CD27). DCs are the critical cell type for stimulating naïve T and B cells as they provide the second costimulatory signal to T cells that other "secondary" or "non-professional" antigen presenting cells cannot provide. Therefore, a successful prophylactic vaccine needs to stimulate the appropriate DCs. In contrast, immunotherapeutic vaccines aim to reduce morbidity by reducing clinical episodes, and reduce transmission by reducing viral shedding. This may be an easier immunological task than prophylaxis, as it relies on restimulating already existing memory T cell responses. Compared to stimulating naïve T cell responses, memory T cells are more abundant and do not require a costimulatory signal for activation. Therefore, a much wider range of immune cells than DCs can act as antigen presenting cells (including keratinocytes and monocytes). This also means memory T cell stimulation is more likely to occur in the periphery (91, 94). It is undetermined yet whether naïve HSV-specific T cell priming occurs in mucosal tissues or only in lymph nodes.

There is now compelling evidence that the presence of T_{RM} cells and neutralizing antibodies in the mucosa are critical for protection against release of virus from the DRG and also likely to prevent virus entry into the DRG during initial infection. T_{RM} cells may also be important in restricting reactivation in the DRG (86). It is therefore important to consider how to design a prophylactic vaccine that will induce the development of local T_{RM} cells and mucosal antibody to prevent infection with HSV as recruitment of B and T cells from the blood may be too slow to prevent viral seeding of the nerves.

3.2. Targeting Key Antigens and Epitopes

HSV1 and 2 consist of double-stranded DNA contained in a capsid, surrounded by a tegument layer and an envelope containing glycoproteins including gB, gC, gD, and gH/gL (126). HSV replication involves the production of rounds of viral proteins for the assembly of the virus, beginning with immediate-early (IE), followed by early (E) then late (L) structural proteins (127). The immune response is capable of targeting many of these viral components and it is important that a vaccine stimulates responses to antigenic epitopes that have been identified as key targets for neutralizing antibodies, CD4 and CD8 T cells.

The late structural proteins gD and gB are dominant targets for HSV neutralizing antibodies, of which multiple epitopes are recognized (128, 129), along with gC and gH/L, specifically seen in human sera directed against HSV1 (19, 128-131). Other glycoproteins, such as gK, have only been investigated in murine models (132). Therefore, gD and gB were used as immunogens in the Chiron trial and gD combined with dMPL (AS04) used in the Simplirix and Herpevac trials. In the Herpevac trial, HSV2 gD was seen to confer protection for genital infection caused by HSV1 (but not HSV2), which correlated with high gD antibody titers, supporting the importance of antibodies in mediating this protection. When investigating the antibody response elicited from this vaccine in guinea pigs, the protection provided against genital disease was due mostly to neutralizing antibodies directed against gD, with various epitopes recognized, such as ID3, DL6, and MC14. The more epitopes the animals recognized, the better protected they were against genital disease. Upon investigating the epitope-specific antibody responses in women from the Herpevac trial, it was found that significantly fewer crucial gD epitopes were recognized compared to the guinea pigs (133). The recently developed trivalent vaccine candidate containing gC, gD and gE provided sterilizing immunity in 98% of guinea pigs due, to the high levels of plasma and mucosal neutralizing antibodies induced (69). Anti-gE is aimed at preventing cell to cell spread. Human antibody responses to this vaccine have not yet been assessed. Perhaps assessment of the efficacy of this vaccine and any future vaccines should evaluate epitope-specific antibody responses, such as to the gD2 epitopes ID3, DL6, and MC14.

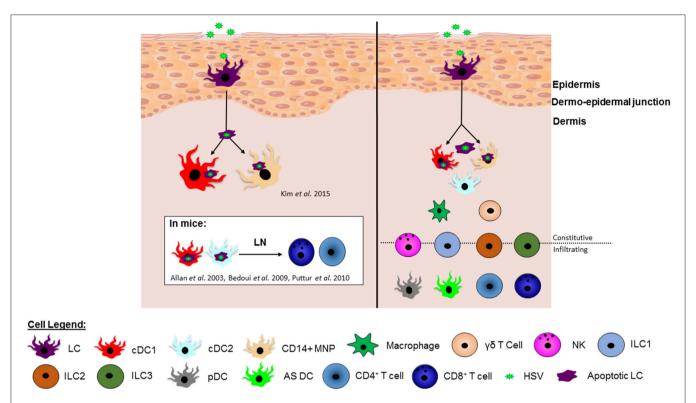


FIGURE 1 | The HSV viral relay and localization of immune cell subsets in human skin. **(Left)** In humans, HSV infects Langerhans cells (LCs) causing them to mature and migrate to the dermis and undergo apoptosis. Once in the dermis, HSV infected apoptotic LCs have been observed in clusters with and taken up by dermal cDC1s and CD14+ MNPs (112), potentially for antigen presentation to T cells. In mice it is known that murine dermal cDC1s and cDC2s present HSV antigen to CD8+ and CD4+ T cells in the lymph node, however this has not yet been shown in human studies. **(Right)** Whilst we have pieced together multiple cellular players in this viral relay, there are an abundance of other innate and adaptive immune cells residing in the dermis, including additional DC subsets, macrophages and $\gamma \delta$ T cells, as well as infiltrating immune cells, such as pDCs and T cells. NK cells and ILCs are found both constitutively in skin in low numbers and also infiltrate into the skin during infection or inflammation. There is increasing evidence that at least some of these additional cell types influence the developing immune response to HSV infection in the skin and further illuminating this complex picture would inform vaccine design.

Interestingly, a live attenuated viral vaccine, with a gD deletion, elicited mucosal antibodies with low neutralization activity but high antibody-dependent cellular cytotoxicity (ADCC) activity, provided sterilizing immunity in murine models and passively transferred immunity against vaginal infection with multiple clinical isolates (134-136). It is noteworthy that they authors did not include complement in their neutralization assays, which should be considered as an alternative mechanism to ADCC. The authors propose that the removal of the immunodominant gD protein may unmask alternative epitopes important in a protective immune response or remove a possible immunosuppressive effect of gD. Furthermore, another live, attenuated vaccine candidate HSV529 (deleted for UL5 and UL29) was shown to induce significant HSV2-specific antibody dependent ADCC, as well as neutralizing antibodies, in humans. (137). ADCC activity may warrant further attention in vaccine evaluations.

Although the above studies provide evidence for the importance of vaccines eliciting strong neutralizing antibody responses, many of the previous human clinical trial vaccines did induce neutralizing antibodies and yet were unsuccessful (138, 139). Although it has been suggested that this may be

partially explained by a lack of epitope-specific responses, also neutralizing antibodies may not be sufficient by themselves to provide protection against HSV infection. CD4 and CD8 T cells are also likely to be required. Therefore, the ability to stimulate them in a vaccine needs to be improved from the previous vaccine candidates.

CD4 and CD8 T cells respond to various viral proteins, some of which overlap with those that neutralizing antibodies recognize. CD4 T cells predominately respond to late HSV glycoproteins, such as gD, gB, gC, and gH and the tegument protein VP16 (19, 87, 140). Several immunodominant HSV2 gD epitopes are recognized by CD4 T cells from both HSV1 and HSV2 seropositive patients (141), and such cross-reactive epitopes for HSV1 and HSV2 would be advantageous to use in a vaccine to target both viruses at the same time. CD4 T cells can also recognize the tegument protein UL49 and capsid protein VP5 (140). CD8 T cells recognize a variety of HSV proteins, especially IE and E viral proteins such as ICP27, ICP4, and ICP0 (87, 142), as well as several tegument and capsid proteins (143). Recent studies have found a conserved epitope between VZV, HSV, and EBV that is recognized by CD8 T cells, that has now extended to 13 conserved epitopes between VZV and HSV that

are recognized by both CD4 and CD8 T cells (144, 145). Finally, a study has found that gD is selectively taken up by cDC1s, which can then cross-present to CD8 T cells, meaning that gD may be an important target for both CD4 and CD8 T cells (146), as well as B cells. The identification and use of conserved and cross-reactive epitopes in new vaccine designs may lead to the possibility of targeting multiple immune cells against multiple herpesviruses in the one vaccine.

Many studies that have identified HSV-specific T cell epitopes in humans have investigated the responses of T cells derived from PBMC. However, recent evidence indicates that there may be compartmentalization of T-cell receptor (TCR) repertoires and expansion of particular T cell clones at distinct anatomical sites. This may have important implications for how T cell responses to potential vaccine candidates should be assessed. One study compared the frequency of cervical and PBMC-derived HSV2reactive CD4 T cells in HSV2 infected women and found there was a 25-fold enrichment of cervical HSV2 reactive CD4 T cells compared to PBMC, demonstrating that there are differences in frequency of HSV-specific CD4 T cells at different anatomical sites in natural HSV2 infection (92). Furthermore, recent data from the same lab presented at the International Herpesvirus Workshop investigated the overlap of TCR sequences between genital skin and PBMCs in HSV2 infected patients and also in response to an immunotherapeutic vaccine. The data suggest there is very little overlap in the TCR repertoires of tissue resident T cells in genital skin and those found in PBMCs. Therefore, it will be important to evaluate tissue-based immune responses in response to vaccines (147, 148).

3.3. Vaccine Delivery

As HSV infects the genital mucosa, vaccine strategies need to be effective at developing protective immunity at mucosal surfaces. One such strategy is direct immunization of the genital tract, a strategy that has been successful in animal models. A group investigating a live attenuated, replication defective HSV2 vaccine candidate (HSV2-gD27) has shown that intravaginal delivery gave the best protection against HSV2 intravaginal challenge compared to intranasal, subcutaneous, or intramuscular delivery (149). However, intravaginal vaccination may be a difficult or impractical strategy to use in human trials. As an alternative approach, Shin and Iwasaki developed the "prime and pull"strategy where systemic T cells were primed by parenteral vaccination then pulled to the genital mucosa by the topical application of CXCL9 and CXCL10 (150). Long term CD8 T_{RM} cells were established in mice, which conferred protection against HSV2 challenge via IFN- γ production (151).

Experimental vaccines using nanoemulsion-based adjuvants are also being investigated for their efficacy in generating mucosal immunity. Intranasally administered nanoemulsiion vaccines have demonstrated the induction of high antibody titers, robust Th1-skewed T cell responses and potent Th17 responses in RSV and TB vaccines (152, 153). A nanoemulsion vaccine for HSV2 is also being developed by BlueWillow Biologics (formerly known as NanoBio Corporation). Preliminary evidence indicates that the intranasal vaccine can protect naïve animals from acute genital HSV2 infection and the establishment of latency,

and also significantly reduces lesion recurrence in already infected animals (154). It would be worthwhile to further investigate whether intranasally administered nanoemulsion vaccines generate protective systemic and mucosal HSV immunity without directly immunizing the genital tract. Other experimental vaccines being investigated include the use of peptides as the epitope, either lipopeptides or synthetically designed peptides, or the use of nanoparticle adjuvants. None of these experimental vaccines are currently in Phase I clinical trials but they do hold some promise. Peptide based vaccines are the most developed and promising with these vaccines able to stimulate high titers of polyfunctional cytotoxic CD8 T cells that are found both locally in the genital mucosa and draining lymph nodes, as well as systemically. These CD8 T cells also induced high levels of IFN-γ, IL2, IL12, and TNF, and protected against lethal rechallenge of HSV (155, 156). Work on nanoparticle adjuvants is limited but work on a calcium phosphate based nanoparticle and HSV2 epitope was shown to lead to enhance mucosal and systemic protection. This vaccine was shown to protect against lethal rechallenge with live virus, as well as induce specific IgG and IgA responses. However, no adaptive response was induced by this vaccine (157).

3.4. Vaccine Adjuvants

In contrast to live attenuated vaccines, recombinant protein vaccines are often formulated with an adjuvant to act as antigen carriers (Eg. alum, emulsions such as MF59, liposomes) and as immune stimulants (namely TLR agonists), often combined as "adjuvant systems." Adjuvants can modulate the immune response by activating DCs (replacing endogenous pathogen stimuli), and stimulate the appropriate immune pathway via different patterns of cytokine production. With an expanding pool of chemically well-defined and functionally characterized adjuvants available, there is an opportunity to tune the immune response to the desired outcome.

A protective recombinant protein vaccine will need to induce a combination of robust neutralizing antibody, CD4 and CD8 T cell responses and facilitate the establishment of T_{RM} cells. A number of adjuvants have been shown to induce neutralizing antibody responses including the traditionally used alum, MF59 which was used in the Chiron subunit vaccine (18), dMPL which was used in the Simplirix vaccine (20, 21), and more recently the combination of CpG and alum was used in the recent trivalent vaccine containing HSV2 gC, gD and gE. Notably, although this vaccine was administered intramuscularly in animal models, it elicited mucosal neutralizing antibodies that were protective upon intravaginal challenge (69).

However, for the activation and polarization of T cell responses, there are striking differences in the type of responses stimulated by different adjuvants. Alum adjuvanted vaccines do not elicit strong T cell responses (158, 159). Adjuvants such as MF59 and ISCOMs, as well as TLR2 and TLR5 ligands, enhance T cell responses without altering their Th1/Th2 balance of responses. In contrast, more polarized Th1 cell responses are elicited by adjuvants that incorporate agonists of TLR3, TLR4, TLR7-TLR8, and TLR9. Complete Freund's adjuvant (CFA) and CAF01 induce mixed Th1 and Th17 cell responses. Thus,

selection of an appropriate adjuvant is influenced by the type of CD4+ T cell response required for protection.

Simplirix was the first partially successful HSV vaccine and this was attributable to the Th1 pattern of cytokines (IFN- γ) induced by the adjuvant dMPL, however no CD8 T cell responses were detected. One of the main hurdles in the advancement of vaccine development has been finding adjuvants that enhances cross-presentation, which is necessary for the induction of CD8 T cell responses to soluble antigen. Saponin-based adjuvants have been shown to induce strong T cell responses and in particular memory CD8 T cell responses, and their use in recently trialled immunotherapeutic vaccines has shown some success. The highly successful RZV vaccine for herpes zoster contains dMPL formulated together with QS21, a saponin, in liposomes. RZV induced VZV-specific CD4 T cells as well as memory CD8 T cells, although not naive CD8 T cells (15). Similarly, the Agenus HerpV vaccine contains a patented QS21 stimulon adjuvant and the Genocea vaccine contains a saponin Matrix M2 adjuvant. Both the immunotherapeutic Agenus and Genocea vaccines induced a combination of neutralizing antibody, CD4 and CD8 T cell responses in animal models. In the human clinical trial of the Genocea vaccine, equivalent CD8 T cell responses were induced to both HSV gD and ICP4, confirming that gD contains CD8 T cell epitopes, and that saponin-based adjuvants are able to induce memory CD8 T cell responses through cross presentation (160, 161).

In order to achieve the breadth of immune responses required (antibody, CD4 and CD8 T cells) in a vaccine for HSV, it may also be important to consider targeting adjuvants to additional immune cells that may assist in enhancing the overall responses. For example in our previous study of the LC-dermal DC viral relay, we suggested that for the targeting of dermal DC subsets by subunit vaccines, adjuvants may need to simulate the immune effects of HSV infected apoptotic LCs (112). Additionally, cell types that have traditionally been overlooked in the design of

vaccine candidates, such as NK cells, should also be considered as targets for vaccine adjuvants, especially since NK cells are known to mature DCs and augment CD4 T cell responses (49). NK cells may perhaps also augment CD8 T cell responses as it appears NK cells can stimulate cross-presenting DCs (162, 163).

It is also important to consider whether adjuvants can be used to suppress certain aspects of the immune response that may not be beneficial for an effective response to HSV, such as Tregs. As Tregs are a component of any immune response, they are likely to be recruited in the context of vaccination. A recent study focusing on T cell vaccines for influenza, found that primary and repeated vaccination with viral peptides alone induced antigen specific FoxP3+ Tregs, but that the addition of certain adjuvants, such as CpG, suppressed this phenomenon. This study also found that in the context of influenza, depletion of vaccine induced antigen specific Tregs promoted viral clearance, indicating that Tregs have an inhibitory role in vivo (164). Most studies investigating Tregs in the context of HSV vaccination have used mouse models, where Tregs were found to be beneficial (98, 165), however the trend is not carried over into humans. Although not specifically studied in vaccines, Tregs have been shown to decrease effector T cell function in HSV infection as discussed previously (100, 101). Therefore, it is possible that adjuvant suppression of Tregs could be beneficial for a HSV vaccine, and that this is not an influenza specific phenomenon. However, it is also possible that Treg suppression could cause increased inflammation in response to the vaccine and in response to HSV infection. Therefore, the suppression of Tregs would need to be tested to determine whether it is ultimately beneficial or harmful in the context of HSV vaccination.

It is important to note that there are some concerns about potential safety issues in manipulating the immune response with adjuvants e.g., the possibility of inducing or reactivating autoimmune disease. So far, in tens of thousands of subjects immunized with RZV this has not been observed.

TABLE 1 | The developmental status of HSV vaccine candidates.

Vaccine candidate	Company	Vaccine constitution	Developmental stage	References
SUBUNIT/S + ADJUVANTS				
Simplirix/ Herpevac	GlaxoSmithKline	gD2 and AS04 (dMPL)	Ceased after Phase III trials	(21, 166)
GEN-003	Genocea	gD2 and Matrix M2	Ceased after Phase II trials	(167-169)
HerpV	Agenus	Peptide vaccine + QS-21 Stimulon	No development since Phase II trials	(170, 171)
VCL-HB01	Vical	gD2 +/- UL46 and Vaxfectin DNA vaccine	Ceased after Phase II trials	(172, 173)
COR-1	Admedus	gD2 codon optimized DNA vaccine	Phase IIb planned	(174-176)
NE-HSV2	BlueWillow Biologics	Nanoemulsion with gB2 and gD2 antigens	Pre-clinical, clinical trial planned	(154, 177)
HSV2 trivalent vaccine	University of Pennsylvania	gC2, gD2, gE2	Pre-clinical	(68, 178)
G103	Immune Design	HSV2 gD, UL19 and UL25	Pre-clinical	(179)
LIVE-ATTENUATED				
HSV529	Sanofi Pasteur	Replication defective HSV2, UL5, UL29 deletion	Phase I trial ongoing	(17, 180)
RVX201	Rational Vaccines	HSV2 ICP0 deletion mutant	Phase Ib/IIa planned	(181)
VC2	Louisiana State University	HSV1 with mutations in gK and UL20	Pre-clinical	(132, 165, 182)
R2	Thyreos LLC	HSV1 with UL37 R2 region mutation	Pre-clinical	(183)
HSV2 ∆gD2	Albert Einstein College of Medicine	HSV2 with US6 (gD) deletion	Pre-clinical	(134, 136)

However, extensive post-marketing surveillance will be required. Furthermore, the RZV adjuvant QS21 has been shown to elicit a high degree of systemic and local (infection site) reactogenicity as well as efficacy. Efficacy does not necessarily correlate with reactogenicity for individual subjects. However, whether the toxic and immunogenic aspects of such adjuvants can be dissociated, leading to chemical modifications, depends on a detailed understanding of the immunologic mechanisms of each. A summary of the developmental status of current HSV vaccine candidates is provided in **Table 1**.

4. CONCLUDING REMARKS

A new generation of vaccines aim to specifically manipulate the immune response or alternatively attenuate live vaccine candidates through specific mutations. Surprisingly, RZV has a higher degree of efficacy (and also more reactogenicity) than the live attenuated HZ vaccine, Zostavax. RZV is also more immunogenic (26, 27). Whether such higher adjuvant induced efficacy can be extended to vaccines against initial genital herpes infection remains to be proven. More antigens may be needed. These studies demonstrate that the need for a much more detailed understanding of initial protective immune responses and also the need to further analyse partially successful vaccines for immunologic correlates of efficacy (in protected vs unprotected patients) e.g., Genocea, Herpevac.

There remains much to be explored including the role of the microbiome in interacting with mucosal immunity. In sub-Saharan Africa, many women have a "diverse" vaginal microbiome without Lactobacilli which increases the likelihood of HIV and possibly HSV acquisition (86, 184–187). How

mucosal immunity is altered and how this might be improved by immunization for HSV are topics for future investigation.

Thus, a successful prophylactic vaccine against initial genital herpes will need to prevent seeding of the neuronal ganglia by both HSV1 and HSV2. In addition to inducing high levels of neutralizing antibodies which are known to penetrate the epidermis, the vaccine would probably need to induce resident immune cells that can quickly migrate into the stratified squamous epidermis or produce rapidly diffusing protective cytokines upon infection and contain/destroy the virus before it enters nerve terminals in the skin. We now know that even if viruses such as HIV obtain a "toehold" in mucosal epidermal cells they can be contained by these mechanisms. More needs to be known about the interaction of key innate and adaptive immune responses. It is becoming clear that multiple innate immune cells such as multiple DC subsets, NK cells, monocytes/macrophages and $\gamma \delta$ T cells are interacting in the mucosae during initial HSV infection and together with antibody and T cells may all have a role in successful control or protection of initial infection.

AUTHOR CONTRIBUTIONS

NT and JS are equal first authors. AC is the corresponding author. NT, JS, KS, and AC all contributed to writing and editing the manuscript.

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The Role of T Cells in Herpes Stromal Keratitis

Naveen K. Rajasagi and Barry T. Rouse*

Biomedical and Diagnostic Sciences, College of Veterinary Medicine, The University of Tennessee, Knoxville, TN, United States

The blinding inflammatory lesion stromal keratitis (SK), which occurs in some patients in response to ocular herpes simplex virus (HSV) infection, represents mainly an immune cell mediated inflammatory response to the virus infection. The principal orchestrators of the immunopathological lesions are T cells although additional events participate that include the extent of recruitment of non-lymphoid cells, the extent of neoangiogenesis, and the extent of damage to nerve function. This review focuses on evidence that the balance of the functional subsets of T cells has a major impact on lesion severity and duration. Accordingly, if proinflammatory Th1 and Th17 CD4T cells, and perhaps in some cases CD8T cells, predominate lesions occur earlier and are more severe. Lesions are diminished when cells with regulatory function predominate. Moreover, when regulatory cells acquire the property to produce Amphiregulin this may facilitate lesion resolution. An objective to controlling lesions is to learn how to manipulate the balance of T cells to favor the representation and function of regulatory T cells and their products over proinflammatory cells. In this review we emphasize how exploiting the differential metabolic requirements of immune cells could be a valuable approach to control SK.

Keywords: herpes stromal keratitis, CD4T cells, metabolism, regulatory T cells, plasticity

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*Correspondence:

Barry T. Rouse btr@utk.edu

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BACKGROUND

Herpes simplex virus (HSV) type 1 is a major human pathogen worldwide. It is estimated that around 67% of people worldwide (under age 50) are infected with HSV-1 (1). HSV-1 establishes a lifelong, latent infection for which no effective vaccine is currently available (2). Primary infection with HSV-1 is usually mild or subclinical and most individuals remain asymptomatic (3). However, HSV-1 infection can cause several complications in humans. Among these, corneal infection can lead to blinding immunopathological lesions in the eye referred to as herpes stromal keratitis (SK) (4, 5). Epidemiology studies outside of the United States have estimated incidence rates of HSV eye disease range from \sim 4 to 13 new cases per 100,000 per year. A previous study from Rochester, Minnesota, estimated an incidence of 8.4 new cases per 100,000 and 20.7 total episodes per 100,000 people per year. Extrapolating these data to the US population census in 2000, the study predicted an estimated incidence of \sim 24,000 new cases and 58,000 total episodes per year (6). Moreover, a study published in 2014, estimated an incidence of 6.8 new cases/100,000 in Northern California (7). Thus, herpes keratitis represents a clinically relevant syndrome and the SK form is a frequent cause of vision damage.

Primary ocular infection most likely occurs by the direct infection of the eye with HSV-1. Upon infection, the virus replicates in the corneal epithelial cells and can causes epithelial lesions. These primary lesions can last up to 2 weeks and usually resolve with minimal damage and the virus is efficiently cleared by the immune system (8). However, one of the consequences of HSV ocular infection is the establishment of latency in the trigeminal ganglia (TG) (9). Some of the HSV virions can enter the sensory nerve endings which innervate the infected cells and traffic via retrograde transport mechanisms to the sensory ganglia where the virus can persist in a latent stage (10). Sometimes the latent virus reactivates by disturbances caused by environmental or physiological stress and the reactivated HSV replicates in the TG. The virus can then travel by anterograde axonal transport to the peripheral tissues and cause recurrent lesions either in the corneal or orofacial tissues often resulting in clinical consequences (11). In humans, recurrent virus infections of the cornea are usually confined to the epithelial layer, but in some individuals such frequent recurrent infections could affect the deeper corneal stroma leading to an immunopathological disease referred to as herpes stromal keratitis (SK). This chronic inflammatory response in the corneal stroma is mediated by both innate and adaptive immune cells in response to virus infection and can lead to progressive corneal scarring and vision loss. The local corneal epithelial lesions and virus infections are usually treated using antivirals such as acyclovir, but SK lesions are often treated with a combination of an antiviral and a corticosteroid (12).

Most of our current understanding of the pathogenesis of SK in humans comes from studies done animal models (5, 13). HSV-1 corneal infection in mice is the most widely used animal model to study SK as it offers several advantages and the inflammatory lesions in the corneal stroma mimic SK lesions observed in humans (14). However, one limitation of the mice model is that it is mainly a primary infection model, but not a reactivation model of disease as mostly occurs in humans. The immune response to HSV-1 ocular infection occurs in a bi-phasic manner and involves both innate and adaptive components of the immune system (8). During the pre-clinical or acute phase, the first wave of immune cells mainly consisting of neutrophils, natural killer cells, and macrophages enter into the corneal stroma and help to clear the replicating virus (5). In the later clinical or chronic phase of the disease, CD4 T cells start to appear in the cornea around day 6–7 post-infection, a stage when virus is usually already cleared from the cornea (8). The CD4 T cells are considered to be the primary orchestrators of SK lesions as they facilitate the influx of the second wave of neutrophils (15). The massive cellular infiltration especially neutrophils coupled with the inflammatory mediators secreted by the immune cells are primarily responsible for the swelling and destruction of the cornea (16, 17).

ROLE OF Th1, Th17, AND CD8T CELLS IN SK LESIONS

Stromal keratitis (SK) is an immunopathological disease orchestrated by T cells (14). This view is supported by findings which show that mice depleted of T cells are less susceptible to

HSV-1 induced corneal stromal disease. In both humans and mice, there is a predominance of CD4 T cells in the ocular tissues during SK and their functional activities are often associated with the tissue damage in the corneal stroma. In mice, CD4T cells appear in the corneas around day 6 post-ocular infection with HSV-1 and their numbers continue to increase during the latter stage of SK development. Among the CD4T cell population, there is a preferential accumulation of CD4 T helper (Th1) subset in the eye (18). Th1 cells express the transcription factor, Tbet, and produce various immune-modulatory mediators which play a role in SK lesion expression. The Th1 cells secrete the cytokines IFN-γ and IL-2 which are capable of inducing corneal inflammation and neovascularization (19, 20). In addition, these cytokines also modulate chemokine factors, and in doing so could facilitate the massive influx of neutrophils and macrophages into the cornea during the latter phase of SK development (21, 22). Another CD4 subset which gained recent prominence in inflammation and autoimmunity are the Th17 cells (23). These cells express the transcription factor ROR-yt and produce cytokines such as IL-17, IL-21, and IL-22. They preferentially produce IL-17 which is a potent inducer of additional proinflammatory cytokines, chemokines, and metalloproteinases (24, 25). Th17 cells accumulate in the HSV infected cornea during the later stages of SK pathogenesis and help sustain and expand the disease (26, 27). Moreover, HSV-1 ocular infection of IL-17R knock-out mice or neutralization of IL-17 using monoclonal antibodies delayed disease progression and reduced the severity of HSK (26). Importantly, IL-17 was expressed in corneas of patients with SK (28). In addition, the human corneal fibroblasts constitutively express the IL-17R. The data from these studies suggest that IL-17 strongly induces the production of key inflammatory mediators such as IL-6, IL-8, and matrix mettalloproteinase-1 in the human corneal fibroblast cultures (28). Thus, Th17 cells through the production of IL-17 modulate the levels of chemotactic factors such as CXCL-1 and IL-8 and influence the migration of neutrophils into the inflamed corneal tissues (26).

Although, CD4T cells are considered to be the chief perpetuators of SK, the data presented in some experimental models implicate CD8T cells in the pathogenesis of SK. The outcome depends to a large extent on the virus strain used for the studies. Some studies found that ocular infection of mice with the HSV-1 RE strain mainly induces SK mediated by CD4 T cells, whereas infection of the same stain of mice with HSV-1 KOS show SK which is dependent on CD8T cells (29). In mice infected with a recombinant stain of HSV-1 (HSV-gK), the corneal scaring and the corneal disease were mainly mediated by CD8 T cells (30, 31). Results from these studies suggest that gK strongly induces CD8 T cell responses leading to exacerbation of SK lesions. Of note, the recombinant HSV-gK strain used in these studies contains three copies of glycoprotein K (gk) (a protein essential for virus replication) compared to one copy in the wild type HSV-1 McKrae strain (30). The HSV-1 mutant strains which lack gK were found to be defective in infectivity and failed to establish latency in the neurons in mouse models which suggests that gK expression is crucial for virus replication (32). Thus, the respective roles of different CD4 and CD8 subsets in SK is not clear and remains an unresolved issue. Additionally, some evidence shows that CD8 T cells mainly play more of a protective role (33). Observations in both mice and humans show that HSV-1 specific CD8 T cells are selectively retained in the TG and might help control HSV reactivation (34–36). These tissue resident CD8 T cells appear to use IFN- γ and non-cytolytic mechanisms to block virus reactivation in the TG (37, 38).

ROLE OF REGULATORY T CELLS (TREG) IN SK PATHOGENESIS

A beneficial subset of CD4T cells in SK are regulatory T cells (Treg) (39, 40). Treg express the master transcription factor, Foxp3 which controls their development, and function (41). Treg are either produced as a functionally mature T cell sub population in the thymus (natural Treg) or are induced in the periphery from naive CD4T cells (induced Treg). Treg mainly function to maintain tolerance to self-antigens and prevent autoimmune diseases (42). They also constrain excessive immune responses to non-self-antigens or infectious agents and help to maintain peripheral tolerance and immune homeostasis (41). Treg use several mechanisms to suppress aberrant immune responses and these include immunomodulatory cytokines (IL-10, TGF-β, IL-35) or contact dependent suppression (granzyme/perforin) (41, 43, 44). In addition, Tregs also exert their function on effector T cells through inhibitory molecules such as CTLA-4. Treg also condition dendritic cells to secrete indoleamine 2,3-dioxygenase, a molecule which suppresses the activation of effector T cells (44).

During microbial infections, a major function of Treg is to control the excessive inflammatory responses to prevent collateral tissue damage and limit injury to the host. In HSV-1 ocular infection, Treg were shown to be crucial to control HSV induced corneal immunopathology. SK lesions were more severe if mice were depleted of Treg before infection using monoclonal antibody treatment, whereas adoptive transfer of in vitro converted Treg suppressed HSK severity (45, 46). Furthermore, findings using the depletion of regulatory T cells (DEREG) transgenic mice showed that lesions became more severe even when depletion was begun in the later phases (clinical/chronic phase) of the disease (47). The DEREG mice carry the diphtheria toxin receptor-enhanced green fluorescent protein (DTR-eGFP) transgene under the control of an additional Foxp3 promoter, which facilitates specific depletion of Treg by application of diphtheria toxin at any chosen point of time (48). Thus, measures to expand the representation of Treg by the administration of various reagents have been useful in reducing the severity of SK lesions in the mouse model. One such approach used was galectin-9 which induces apoptosis of pathogenic CD4 Th1 cells and increases the representation of the anti-inflammatory Treg population (49). In addition, a combination treatment using a tumor necrosis factor receptor superfamily member 25 (TNFRSF25) agonist antibody which expands Treg numbers along with galectin-9 was particularly effective in diminishing HSV-1 induced corneal immunopathology (50). Other approaches that were successful in expanding Treg population and reducing SK lesions included the use of IL-2/anti-IL-2 mAb complexes and the fungal metabolite drug, fingolimod hydrochloride (FTY720) (51, 52). In addition, phosphorylated FTY720 also targets sphingosine-1-phosphate receptor and perhaps diminishes inflammation by modulating lymphocyte trafficking (53).

Although increasing the representation of Treg in lesions is a valuable approach to minimize lesion severity, it has become evident that the Treg population is functionally heterogeneous. Accordingly, some functions are more valuable to achieve control than others. For example, our group recently observed that a function of Treg valuable for resolving SK lesions is their ability to produce amphiregulin (AMP) (54). This molecule acts to facilitate tissue repair by binding to the epidermal growth factor receptor expressed mainly on epithelial cells and stem cells and its binding can result in the activation of downstream signaling kinases resulting in growth, proliferation, and migration of cells (55). Treg that produce AMP are relatively infrequent in the early stages of SK, but their representation is most evident in later stages. The change of Treg function to become AMP producers appears to be driven by the cytokines IL-12 and IL-18. In fact, exposure of AMP negative Treg cells in vitro to these cytokines can induce them to become AMP producers. In addition, if animals were treated in vivo with a plasmid which expresses IL-18, this led to the reduced expression of SK lesions, an effect that correlated with a higher frequency of Treg that were AMP producers (54). Finding practical approaches to induce cells in SK to become AMP producers could represent a useful approach to therapy, an issue that merits further investigation.

PLASTICITY OF REGULATORY T CELL POPULATIONS

Some recent observations suggest that Treg might become unstable in certain highly inflammatory environments and lose their regulatory activity (56). Under such conditions, Treg that downregulate Foxp3 expression might even take up an effector phenotype and start producing pro-inflammatory cytokines such as IFN-y and IL-17 Treg, a phenomenon commonly referred to as plasticity (57-59). In recent times, plasticity in T cells has been a matter of debate as it has biological implications especially in therapeutic regimens which use Treg (60, 61). Factors which influence Treg stability are as yet not clear and remains an active area of research. Although multiple mechanism might be involved in the stability and plasticity of Treg, most evidence indicates that Treg stability and Foxp3 expression is controlled by epigenetic mechanisms, namely DNA methylation in the non-coding region (CNS2) of the Foxp3 gene locus, also known as Treg-specific demethylation region (TSDR) (62). Any changes or modifications in the DNA methylation status in the TSDR region tend to have an effect on Foxp3 expression and stability of Treg populations (63). Most Treg populations are generally resistant to destabilization and reprogramming and maintain their transcriptional expression of regulatory genes and functional phenotype (61). Some of the Tregs generated in vitro or in vivo which have incomplete demethylation status in the cytosine-phospho-guanine (CpG) sites in the TSDR region are more prone to instability when exposed to cytokine milieu containing IL-6, IL-12, IL-21, or IL-23 (57, 64). The Bluestone group, using Foxp3-Cre reporter mice in an Experimental autoimmune encephalomyelitis (EAE) model observed that some of the Treg cells downregulated Foxp3 expression and these were referred to as exFoxp3 cells (59). Such exFoxp3 cells isolated from the CNS at the peak of the response produced IFN- y when stimulated with cognate antigen (59). Our group using fate mapping mice showed that Treg plasticity can occur in HSV-1-induced inflammatory environment and such Treg may contribute to SK lesion severity by secreting the proinflammatory cytokine IFN-y (65). In particular, Treg cells showing low expression of the IL-2R (CD25) could exhibit instability, in part due to the exposure to the pro-inflammatory cytokine IL-12 in the cornea (65). In such circumstances, drugs such as azacytidine, retinoic acid, and vitamin C which maintain demethylation of the TSDR region of Foxp3, can be helpful in promoting the stability and improving the functionality of Treg especially under chronic inflammatory conditions (65). In fact, in a recent study, Treg generated in vitro in the presence of Azacytidine expressed a fully demethylated TSDR and these cells displayed enhanced suppressive activity (66). Moreover, administration of 5-Azacytidine reduced the incidence of SK lesions in mice infected ocularly with HSV-1 (66).

MANIPULATING METABOLISM TO CONSTRAIN SK LESIONS

In the previous section, we have argued that the clinical expression of SK is affected by the representation of different participants in lesions. When the T cell participants were dominated by Treg, lesions will be less severe and may even resolve. Hence, a potentially valuable approach to therapy is to use maneuvers that can shift the balance of events away from dominance by proinflammatory components. This therapeutic challenge is also faced by those working with other in other chronic inflammatory diseases, especially autoimmune diseases (AID). In the AID field, some are considering using approaches such as adoptive cell transfer to enrich the population of Treg (67). However, such an approach, which is most effective when the Treg are antigen specific, would likely fail to adequately gain access to the eye. Other approaches include administering reagents that expand the Treg population as we discussed previously. A potentially more useful therapeutic option would be to exploit the accumulating knowledge that cells involved in immune function may differ in the major metabolic pathways they use to provide them with energy and other events that maintain of their various functions (68, 69). For example, proinflammatory and Treg cells use different pathways to provide energy with the former mainly use extracellular glucose and Treg rely on fatty acid oxidation (68). Rathmell's group reported that effector T cells (both CD4 and CD8) express high levels of the glucose transporter Glut1 and utilize the mammalian target of rapamycin (mTOR) pathway to increase glycolysis to support their function (70). In contrast, Treg primarily use AMP-activated protein kinase and rely upon lipid oxidation for their energy. The activated AMPK pathway in Treg acts to inhibit mTOR by suppressing mTOR signaling and promotes mitochondrial oxidative metabolism rather than glycolysis and is considered to be anti-inflammatory (70). In our own studies, we have begun to exploit the differences by which proinflammatory and Treg cells derive their energy needs. We have shown that if glucose utilization is inhibited, as can be achieved by the use of 2 deoxy glucose administration from the initial time of lesion development, that lesions are significantly reduced (71). The outcome occurred because the activity of proinflammatory cells such as Th1 and Th17 cells were inhibited, but Treg were unaffected. Thus, the representation of the two populations changed with Treg becoming enriched (71). Findings from another group demonstrated the importance of hypoxia associated glycolytic molecules in SK pathogenesis (72). Besides glycolytic metabolism, T effectors, and Treg also show differences in amino acid metabolism. Amino acids, particularly glutamine, plays a key role in fueling effector T cell differentiation, whereas Treg are less dependent on amino acids for their energy (68). In addition, microbial metabolites such as short chain fatty acids or diets rich in vitamin A promote Treg differentiation and function in the gut (73, 74). Additional metabolic differences are also under investigation such as the differential use of lipid oxidation and synthesis pathways. Thus, manipulating metabolic pathways to influence inflammatory lesions is in the early stages of investigation but the approach has great potential and could be more affordable than many of the alternatives. However, the strategy will need considerable scrutiny especially if used for long term therapy. Indeed, our own studies have already documented some untoward consequences when glucose metabolism is compromised during the time when virus is actively replicating.

CONTRIBUTION OF CORNEAL NERVE DAMAGE TO SK PATHOLOGY

Following corneal infection, HSV-1 replicates in the epithelial cells and gains access to the sensory nerve endings which drain the corneal tissues and can travel up (retrograde) to the TG where the virus establishes latency. The virus travels back (anterograde) from the TG to the cornea through the sensory nerves after reactivation. HSV-1 corneal infection can result in destruction of corneal nerve endings resulting in loss of corneal sensitivity (75). Such loss of corneal sensation and nerve function is one of the hall marks of SK in humans and is commonly referred to as neurotrophic keratopathy (76). Evidence from recent studies in mice have shown that sympathetic nerves innervate the cornea and replace the sensory nerve endings lost after HSV-1 corneal infection (75). These sympathetic nerves enhance the infiltration of immune cells resulting in severe corneal inflammation and pathology. A surgical procedure called superior cervical ganglionectomy (SCGx) that removes sympathetic nerves from the cornea helped to alleviate SK severity. Of note, after the SCGx procedure, the sensory nerves reinnervated the cornea resulting in the restoration of corneal sensitivity (75). The exact mechanisms involved in sympathetic corneal innervation are not known and this aspect requires further examination. It is likely that immune cells such as CD4 T cells could play a key role, as their depletion resulted in reversing nerve damage (77). Findings from another study suggest that the molecule involved in cell migration, semaphorin 7A might play a role in the corneal nerves degeneration and regeneration process in HSV-1 infected mice (78). The cytokine IL-6 produced during the inflammatory response to HSV-1 infection in the cornea might also be responsible for causing corneal sensory nerve damage (79).

CONCLUDING REMARKS

Stromal keratitis (SK) caused by HSV-1 corneal infection is a debilitating disease and one of the major causes of vision loss due to an infectious agent. As T cells are the primary orchestrators of SK, steps to improve the host environment which favors Treg over pathogenic Th1/Th17 cells is likely to help ease the severity of SK lesions. In addition, it is becoming increasingly clear from recent developments that metabolism plays a key role in immune function. Thus, as discussed in this review, understanding the

events involved in pathogenesis along with key molecules and metabolic pathways involved in inflammation and applying this knowledge to develop better therapies might help control SK in the future.

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All authors listed have made a substantial, direct and intellectual contribution to the work, and approved it for publication.

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An Intra-Vaginal Zinc Oxide Tetrapod Nanoparticles (ZOTEN) and Genital Herpesvirus Cocktail Can Provide a Novel Platform for Live Virus Vaccine

Alex Agelidis ^{1,2†}, Lulia Koujah ^{1,2†}, Rahul Suryawanshi ¹, Tejabhiram Yadavalli ¹, Yogendra Kumar Mishra ³, Rainer Adelung ³ and Deepak Shukla ^{1,2*}

¹ Department of Ophthalmology and Visual Sciences, University of Illinois, Chicago, IL, United States, ² Department of Microbiology and Immunology, University of Illinois, Chicago, IL, United States, ³ Institute for Materials Science, Kiel University, Kiel, Germany

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*Correspondence:

Deepak Shukla dshukla@uic.edu

[†]These authors have contributed equally to this work

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Herpes simplex virus type-2 (HSV-2) is a common cause of genital infections throughout the world. Currently no prophylactic vaccine or therapeutic cure exists against the virus that establishes a latent infection for the life of the host. Intravaginal microbivac is a developing out-of-the-box strategy that combines instant microbicidal effects with future vaccine-like benefits. We have recently shown that our uniquely designed zinc oxide tetrapod nanoparticles (ZOTEN) show strong microbivac efficacy against HSV-2 infection in a murine model of genital infection. In our attempts to further understand the antiviral and immune bolstering effects of ZOTEN microbivac and to develop ZOTEN as a platform for future live virus vaccines, we tested a ZOTEN/HSV-2 cocktail and found that prior incubation of HSV-2 with ZOTEN inhibits the ability of the virus to infect vaginal tissue in female Balb/c mice and blocks virus shedding as judged by plaque assays. Quite interestingly, the ZOTEN-neutralized virions elicit a local immune response that is highly comparable with the HSV-2 infection alone with reduced inflammation and clinical manifestations of disease. Information provided by our study will pave the way for the further development of ZOTEN as a microbivac and a future platform for live virus vaccines.

Keywords: herpes simplex virus, genital herpes, immunotherapy, live virus vaccine, viral infection

INTRODUCTION

Herpes simplex virus-2 (HSV-2) is a neurotropic double stranded DNA virus capable of lytic infection in multiple host cell types as well as latent infection in neuronal cells (1). The viral DNA genome is encased in an icosadeltahedral protein capsid which is surrounded by tegument proteins (2). The capsid and tegument are enveloped in a lipid bilayer composed of multiple viral proteins and glycoproteins on the surface of the virus particle (3). HSV-2 entry into the host cell primarily involves the interaction of the viral entry glycoproteins with various cell surface receptors that facilitate virion envelope fusion with the plasma membrane of the host cell causing capsid penetration into the cytoplasm (4). Once the genome reaches the nucleus, viral protein production occurs in a sequential manner beginning with immediate early gene products that promote immune evasion and neurovirulence (5). Early proteins are then synthesized which are required for viral

DNA replication. This is followed by production of late proteins, providing structural components of the capsid that are necessary for viral egress. HSV spreads rapidly to neighboring cells as well as the dorsal root ganglia where it establishes latency (6).

Primary infection of HSV-2 results in a variety of prolonged clinical manifestations, ranging from genital ulcerations to more severe cases like meningitis (7). While HSV-2 infection most commonly occurs in the genitalia, it may also result in oral, ocular and neurologic infections (8). In addition, genital ulcerations caused by HSV-2 and viral shedding have been definitively linked to an increased risk for acquisition of human immunodeficiency virus (HIV) infection (9, 10). HSV-2 infects over 400 million people worldwide and is one of the most common sexually transmitted infections (11). Despite its high prevalence, no cure or vaccination has been developed. Acyclovir, a nucleoside analog, is widely used to treat primary HSV-2 infection and has shown to be an efficacious therapeutic in most cases. However, acyclovir resistant strains have also evolved and treatment options are limited in those cases (12–14).

A traditional antiviral may not be the best choice since diverse response from infected patients has been observed with variations in episodes of viral shedding due to the varying degrees of localized immune response among individuals. Roughly 80% of HSV-2 seroprevalent persons are asymptomatic and report no genital lesions even with detection of viral genomes at the site of infection (15). Upon infection in immunocompetent individuals, the virus is rapidly contained by a prompt innate immune response and further suppressed by resident memory HSV-specific T cells (16-18). For the large majority of HSV-2 infected individuals, cell-mediated immune responses are able to control and protect against clinical recurrences and genital lesion development (19). While the majority of currently prescribed antivirals target the virus itself, the development of an antiviral or immunotherapeutic that inhibits infection and at the same time, facilitates a protective immune response can better guard the host against the deleterious effects of primary HSV-2 infection as well as recurrences (20-22). Alternatively, since subunit vaccines have failed to show real promise in clinical trials, a safe live virus vaccine may provide a better solution (23).

Previously, our group discovered a novel microbicidal and vaccine-like (or microbivac) platform against primary and secondary female genital herpes infections (24). The dual microbivac platform was demonstrated through the ability of uniquely designed zinc oxide tetrapod nanoparticles (ZOTEN) with engineered oxygen vacancies to strongly trap HSV-2 virion, neutralize the virus and prevent cell entry in the vaginal epithelium (25, 26). ZOTEN showed to be an effective suppressor of HSV-2 genital infection in female BALB/c mice with apparent reduction of clinical signs of vaginal infection and decreased animal mortality. ZOTEN therapy ultimately was found to create a platform for viral antigen presentation and therefore was presented as a novel microbivac with the potential to prevent primary infection and viral shedding (27). Interestingly, treatment of ZOTEN was found to have adjuvant-like properties, enhancing immunity against the virus in mice (24). The proposed mechanism for this is that ZOTEN acts to capture the virus, allowing for detection by immune cells which in turn results in enhanced T cell-mediated and antibody-mediated responses to infection and thereby suppressing a reinfection. ZOTEN's ability to target the virus particle and manipulate the host immune system demonstrates its novel and multifunctional antiviral properties with promising prophylactic and therapeutic effects (28).

In this article, we aim to better understand the vaginal immune responses and antiviral benefits of a short-term acute infection in female BALB/c mice using a ZOTEN/HSV-2 cocktail. Such a cocktail could provide more information on the microbivac benefits of ZOTEN while demonstrating its promise as a unique platform for live virus vaccine development. Our tissue specific analyses show that the cocktail inhibits infection but generates a local immune response that is highly comparable to the infection with the virus alone. It also shows the promise that ZOTEN can be given alongside to reduce the possibility of infection via any live virus vaccine.

MATERIALS AND METHODS

Mouse Model of Genital Herpes Infection

Animal care and procedures were performed in accordance with institutional and NIH guidelines and approved by the Animal Care Committee at the University of Illinois at Chicago. Six to Eight-weeks-old female BALB/c mice obtained from Charles River Laboratories were injected with 0.1 mL medroxyprogesterone acetate (Depo-Provera) (Greenstone) to synchronize estrous cycles. Seven days after injection, mice were inoculated with HSV-2, or mock infected, with or without ZOTEN. HSV-2 strain 333 was used for all experiments. Synthesis and use of ZOTEN in antiviral assays have been described previously (24, 26, 29). ZOTEN cocktail treatment consisted of preincubating HSV-2 (or mock) in PBS for 30 min at room temperature with or without 0.1 mg/mL ZOTEN and then inoculating female mice genitals with respective solution. Each infected mouse received a viral inoculum of 5×10^5 pfu in a 10 μL volume. Untreated mice received virus that was similarly incubated at room temperature.

Synthesis of ZOTEN (Tetrapod-Form ZnO Micro-Nanoparticles)

Nanoparticles were synthesized and characterized according to our previously published studies (24). Spherical zinc microparticles, polyvinyl butyral (PVB) powder, and ethanol were obtained commercially. A mixture using these materials is prepared and burned together in the furnace at 900°C. Zn microparticles (in the form of Zn atoms, Zn dimers, Zn trimers, etc.) are generated in the flame that results from the burning of polymer PVB. In the presence of oxygen from the surrounding environment, the unstable atomic variants of Zn microparticles participate in nucleation and growth processes. Initially, Zn and O combine to form a primary cluster and once the stable nucleus has been formed, further available Zn and O atoms contribute to conventional 1D spike growth which results in growth of tetrapod-type structures. The process continues as PVB decomposes completely into CO2 and O2, resulting in an actual yield of 99.9% of ZOTEN. The formation of uniform ZnO tetrapods (ZOTEN) has been confirmed by electron microscopy; as well as the size and shape by scanning electron microscopy (30). Identical ZOTENs were used for all experiments demonstrated in this article.

Mouse Vaginal Swabs and Detection of Virus Shedding

At days 2 and 4 post infection, mouse vaginal canal was sampled using calcium alginate swabs (Puritan, 25–800) previously dipped in OptiMEM for approximately 2 min. Swabs were performed by gently streaking vaginal canal in a circular motion 5 times and then dipping the swab into 500 μL OptiMEM. This process was performed twice for each mouse. Collected washes were briefly vortexed and centrifuged then plated on confluent monolayers of Vero cells in a plaque assay.

Plaque Assay

Monolayers of Vero cells grown in DMEM + 10% FBS + 1% penicillin/streptomycin were washed once with PBS, then overlaid with vaginal swab washes freshly collected from mice. After incubation for 2 h, inocula were aspirated, and Vero cells were overlaid with DMEM containing 5% methylcellulose. 72 h later, cells were fixed with methanol for 10 min, media was removed, and cells were then incubated with crystal violet staining solution for 30 min to visualize plaques.

Flow Cytometry

Mouse vaginal tissue was dissected and dissociated by incubating in 100 μL of 2 mg/mL collagenase in PBS for 4h at 37°C. The resulting mixture was triturated with a pipet tip, suspended in an additional 1 mL of FACS buffer (5% FBS in PBS) and passed through a 70 µm filter. Cells were aliquoted into 96-well round bottom plates for staining. F_c receptors were blocked using TruStain FcX (101319, Biolegend) according to the manufacturer's protocol, and cells were then stained with the following antibodies from BioLegend: APC anti-mouse Gr-1 (108411), FITC anti-mouse CD45 (103107) APC anti-mouse CD3e (100311), FITC anti-mouse CD49b (103503) APC antimouse CD11c (117309) and PE anti-mouse F4/80 (123109). Cells were incubated with fluor conjugated primary antibodies for 1 h on ice, washed twice with FACS buffer, and analyzed with a BD Accuri C6 Plus flow cytometer. 10,000 singlet non-debris events were collected for each sample, and FlowJo X was used to process and analyze the data.

Quantitative Polymerase Chain Reaction

Mouse vaginal tissue was dissected and dissociated by incubating in 100 μL of 2 mg/mL collagenase in PBS for 4 h at 37°C. The resulting mixture was triturated with a pipet tip, suspended in 1 mL of Trizol, and frozen at $-80^{\circ} C$ until processing. RNA extraction was performed according to Trizol manufacturer's guidelines. 2 μg of total RNA was reverse transcribed to cDNA using High Capacity cDNA Reverse Transcription kit (Thermo Fisher). Real time qPCR was performed with Fast SYBR Green Master Mix (Thermo Fisher) with the QuantStudio 7 Flex system (Life Technologies). The following mouse specific primers were used in this study:

β-actin fwd 5'-GACGGCCAGGTCATCACTATTG-3' β-actin rev 5'-AGG AAGGCTGGAAAAGAGCC-3' IFN-α fwd 5'-CCTGCTGGCTGTGAAAT-3' IFN-β fwd 5'-TGTCCTCAACTGCTCTCAC-3' IFN-β rev 5'-CATCCAGGCGCTGTTGT-3' IL-1β fwd 5'-GTGGCTGTGGAGAAGCTGTG-3' IL-1β rev 5'-GAAGGTCCACGGGAAAGACAC-3' IL-6 fwd 5'-ACGGCCTTCCCTACTTCACA-3' IL-6 rev 5'-CATTTCCACGATTTCCGAGA-3' TNF-α fwd 5'-GCCTCTTCTCATTCCTGCTTG-3' TNF-α rev 5'-CTGATGAGAGGGAGGCCATT-3'

Mouse Tissue Histology and Staining

Mouse vaginal tissue was dissected and embedded in Tissue-Plus O.C.T. (Fisher HealthCare) then frozen on dry ice and kept at -80° C until processing. 10 μ m sections were cut with a Cryostar NX50 microtome (Thermo Scientific). Sections were air dried at room temperature, fixed in ice-cold acetone for 5 min, and washed under running water for 2 min. Slides were then incubated in Mayer's Hemalum solution (EMD Millipore, 109249) for 1 min and then washed under running water for 1 min. Slides were dipped in 70% ethanol for 2 min, then in 100% ethanol for 1 min, and incubated with eosin Y alcoholic, with phloxine (Sigma, HT110316) for 1 min. Slides were then dipped in 70% ethanol for 1 min, then in 100% ethanol for 1 min, then in 100% ethanol for 1 min, then in 100% ethanol for 1 min, then xylene for 1 min, and coverslipped with Permount mounting medium (Thermo Fisher). Sections were visualized and photographed using a Zeiss Axioskop 2 plus microscope.

Draining inguinal lymph nodes were excised from mice at time of euthanasia and placed in 24-well plates. Lymph nodes were then photographed using a desktop scanner at 1,200 dots per inch. Lymph node areas in pixels were quantified using Adobe Photoshop CC 2018.

Statistical Analysis

Errors bars denote SEM (n=5 mice per group) unless specified otherwise. Asterisks denote significant difference by two-tailed unpaired Student's t-test, *p < 0.05, ns or unlabeled, not significant.

RESULTS

Antiviral Effects of ZOTEN/HSV-2 Cocktail at the Primary Site of HSV-2 Infection

In order to maximize the virus neutralization potential of ZOTEN and study its antiviral and immune benefits we decided to generate a ZOTEN/HSV-2 cocktail by incubating the virus $[5 \times 10^5 \text{ PFU of HSV-2} \text{ (strain 333)}]$ with ZOTEN for 30 min. ZOTEN/HSV-2 was then used for the intravaginal infection of BALB/c mice. To study the effects of the cocktail we created 4 treatment groups of mice: HSV-2 infected, mock infected, ZOTEN/HSV-2 infected and ZOTEN/mock infected (**Figure 1**). The animals were monitored daily and the antiviral effects were measured for the next 7 days. To determine the presence of productive virus at the primary site of infection and local shedding of infectious virions, vaginal swabs were collected

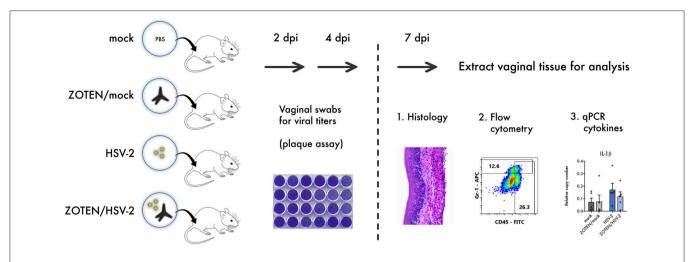


FIGURE 1 | Study design. 6–8 weeks old female BALB/c mice were infected with HSV-2 or mock infected in the presence or absence of ZOTEN. At 2 and 4 days post infection (dpi), mice genitals were swabbed to detect viral shedding using a plaque assay. At 7 dpi, mice were euthanized, and vaginal tissues were extracted and analyzed by histology, flow cytometry, and quantitative PCR (qPCR) to appreciate differences in cellular infiltration and local inflammation.

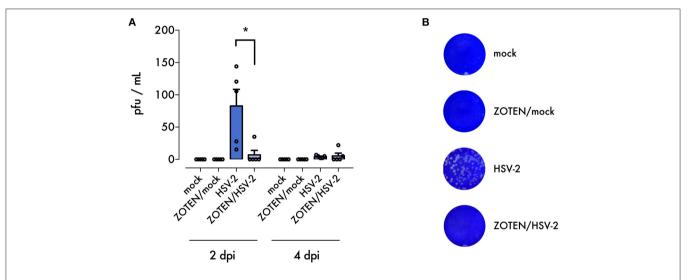


FIGURE 2 ZOTEN treatment reduces viral shedding. **(A)** Plaque assay results from vaginal swabs at 2 and 4 dpi. Error bars indicate SEM (*n* = 5 per group). Asterisk denotes significant difference by two-tailed unpaired Student's *t*-test, **p* < 0.05, ns, or unlabeled, not significant. **(B)** Representative images of crystal violet stained plaque assay results. Zones of clearing are noted in samples from untreated HSV-2 infected mice, indicating presence of replicating virus.

following genital infection with the 4 groups mentioned above. As shown in **Figure 2**, the viral titers recovered from these vaginal swabs were significantly lower in ZOTEN/HSV-2 group at 2 days post infection, with 4 out of 5 mice displaying no detectable virus. These findings confirm the potent antiviral activity displayed by ZOTEN and its ability to neutralize virus and decrease viral shedding as early as 2 days post infection (**Figures 2A,B**).

ZOTEN/HSV-2 Infection Restricts Local Inflammation and Cell Infiltration in Vaginal Tissue

To assess disease development, tissue inflammation or damage at the primary site of infection, vaginal tissue was excised at 7 days post infection and analyzed by three methods: histology, quantitative polymerase chain reaction (qPCR) and flow cytometry (Figure 1). Hematoxylin and Eosin (H&E) staining of the vaginal tissue was performed to quantify the phenotypic development of infection as well as activation of innate immune response (Figure 3A). It is evident that ZOTEN treated mice exhibit decreased signs of immune cell infiltration and inflammation, developing low or no apparent levels of acute HSV-2 infection. The thickness of the epithelium in ZOTEN/HSV-2 treated vaginal tissue is comparable to mock infected, as opposed to the apparently inflamed epithelium and increased cell infiltration in HSV-2 infected tissue. Looking beyond the primary site of infection, draining lymph nodes were also isolated to give an indication of the extent of the systemic immune response generated in each group. Lymph nodes isolated from HSV-2 infected mice were apparently larger than those of

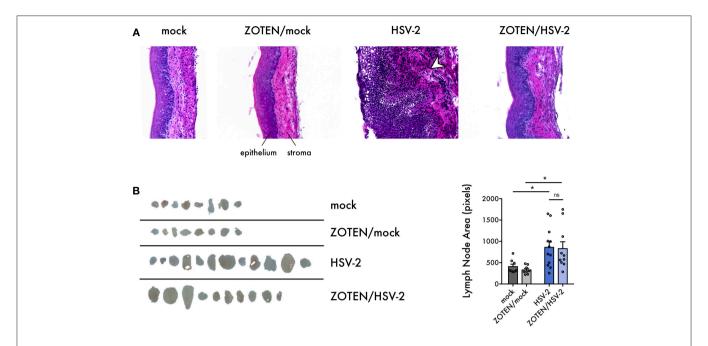


FIGURE 3 | Histological characterization of HSV-2 infection and ZOTEN treatment. **(A)** Representative images of hematoxylin and eosin stained vaginal tissue sections harvested from mice at 7 days post infection. Tissue epithelium and stroma are indicated. Arrowhead in HSV-2 panel indicates tissue infiltration and inflammation observed in infection. Images taken at 20X magnification. **(B)** Draining lymph nodes extracted at 7 days post infection. Areas of lymph nodes in pixels are quantified for each group at right. Error bars indicate SEM. Asterisks denote significant difference by two-tailed unpaired Student's *t*-test, **p* < 0.05, ns, or unlabeled, not significant.

mock infected mice, regardless of whether they received ZOTEN treatment (Figure 3B).

ZOTEN/HSV-2 Infected Female Mouse Genitalia Show Signs of Reduced Local Immune Response

Previously published work by our lab demonstrated ZOTEN's ability to exert adjuvant properties by showing increased levels of CD4 and CD8⁺ T cells in isolated splenocytes in response to ZOTEN treatment of HSV-2 infection (24). In this study, we sought to understand the nature of the elicited immune response at the primary site of infection and further identify acute disease development. The isolated vaginal tissues of varying treatment groups were subjected to flow cytometry and the presence of various immune cells were detected (Figure 4). The tissue was stained for CD45, Gr-1, CD3, CD49b, CD11c, and F4/80 positive cells. CD45+, Gr-1+, and F4/80+ cells showed trends of heightened levels in the presence of infection and interestingly displayed a similar trend of decreased levels with ZOTEN/HSV-2 treatment. CD45⁺ cells were significantly higher in HSV-2 infected mice, in comparison to mock infected, as well as ZOTEN/HSV-2 infected mice, in comparison to ZOTEN/mock treatment group. Similarly, Gr-1+ cells were detected at significantly higher levels in HSV-2 infected mice when compared to mock infected. A decrease in infiltration of Gr-1+ cells was observed between HSV-2 infected and ZOTEN/HSV-2 infected mice and the amount of Gr-1⁺ cells in the vaginal tissue of ZOTEN/HSV-2 infected cells were comparable to mock and ZOTEN/mock infected mice. CD49b⁺ and CD11c⁺ cells increased upon HSV-2 infection but remained at basal levels in the ZOTEN/HSV-2 group. Finally, relatively similar levels of CD3⁺ cells were observed in the four treatment groups. qPCR was also performed on the vaginal tissue to assess levels of pro-inflammatory cytokine transcripts at the local site of infection (**Figure 5**). While no discernible trends were observed among IFN- α , IFN- β , TNF- α , and IL-6, there was a slight decrease in IL-1 β transcript levels in ZOTEN/HSV-2 infected vaginal tissues further supporting the observation of decreased local inflammation (**Figure 5**).

DISCUSSION

HSV-2 infection causes significant disease worldwide, putting over 400 million people at risk of increased genital herpes and lifelong viral persistence in latently infected cells (11). HSV-2 most commonly results in painful ulcerations of genital mucosa and skin as well as increased psychological distress among carriers (19). HSV is also capable of infecting the central nervous system resulting in more severe disease development such as meningitis and encephalitis, which in some cases may be fatal (31). More recently, HSV-2 has received more attention as it has been associated with increased risk of HIV acquisition, making it a more relevant and critical virus to study (10, 32, 33). Current HSV-2 treatment options are not optimal as they exhibit problematic features such as developed drug resistance, toxicities and recurrences of infection. The majority of FDA approved drugs target the virus itself and are efficacious in restricting productive viral replication, however they lack the ability to entirely eliminate quiescent viral genomes and therefore cannot prevent

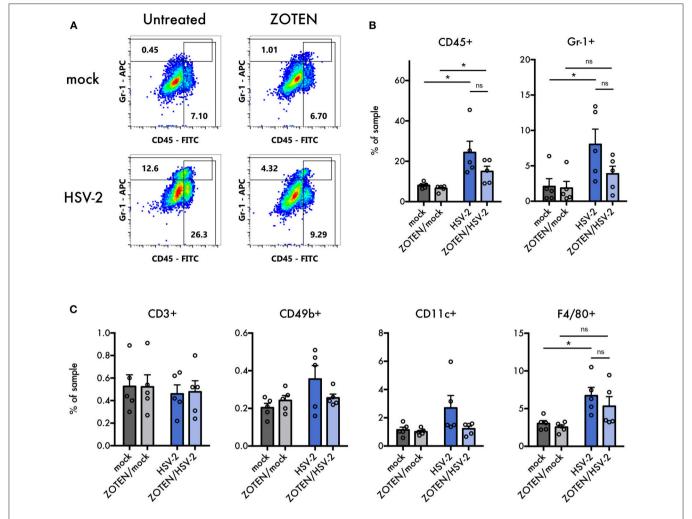


FIGURE 4 | Flow cytometry analysis of immune cell infiltration into vaginal tissues. **(A)** Representative flow cytometry plots of APC anti-Gr-1 vs. FITC anti-CD45. Values in gated regions indicate percentages of singlet non-debris events. **(B)** Quantification of flow cytometry analysis for CD45⁺ cells and Gr-1⁺ cells in vaginal tissues at 7 dpi. Error bars indicate SEM (n = 5 per group). **(C)** Quantification of flow cytometry analysis for CD3⁺, CD49b⁺, CD11c⁺, and F4/80⁺ cells in vaginal tissues at 7 dpi. Error bars indicate SEM (n = 5 per group). Asterisks denote significant difference by two-tailed unpaired Student's t-test, *p < 0.05, ns, or unlabeled, not significant.

reactivation from latency. Evidently, there is a critical need for a protective vaccine or an immunotherapeutic with a novel antiviral mechanism.

Viral survival in the host relies on the ability of the virus to evade host detection of viral determinants, block immediate host antiviral responses and induce responses favorable for its replication and shedding (16, 17). HSV is known to subvert various pathways in the cell such as DNA repair process, type I interferon (IFN) signaling, cell death and proliferation (17). Highly dynamic interactions between replicating HSV-2 and host mediated processes, like local immune responses in genital tissue, contribute to observed disease manifestations and viral persistence. An example observed is the host enzyme, heparanase, which has been identified as a key host protein that drives tissue destruction and viral pathogenesis (34–37). Exploiting tactics used by the virus in the host can provide an effective anti-HSV microbicide.

A microbivac like ZOTEN demonstrates unique and diverse antiviral mechanism that make it a great candidate for further development into a treatment/vaccination for HSV-2 genital infection. We have previously shown that ZOTEN traps the virus, inhibiting viral entry into the cell and simultaneously allowing for detection by immune cells such as antigen presenting cells. ZOTEN enhances anti-HSV-2 immunity and T cell responses and facilitates the development of memory T cells as well as neutralizing antibody response, acting as an immune booster (24, 38).

In this proof-of-concept study, we sought to elucidate short-term tissue specific antiviral efficacy and immune effects of a ZOTEN/HSV-2 cocktail. The cocktail helps to address two important questions. It sheds light on the virus neutralization potential of ZOTEN and more innovatively, shows its promise as a live virus vaccine platform, which reduces infection without compromising local immune responses. We studied

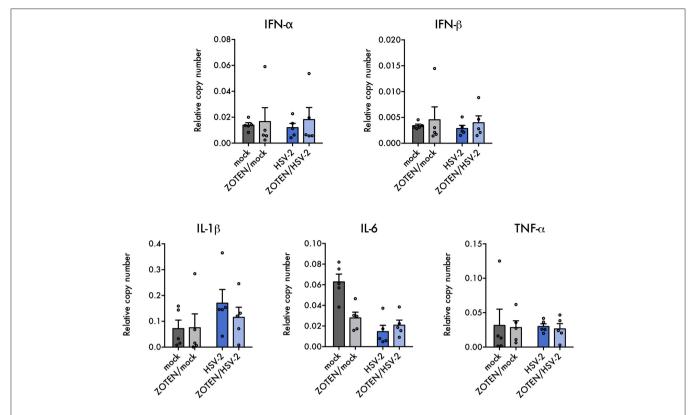


FIGURE 5 | Local cytokine expression in infection and ZOTEN treatment. Quantification of key antiviral type I interferon and pro-inflammatory cytokine transcripts in mice vaginal tissues. Copy numbers relative to b-actin are shown. Error bars indicate SEM (n = 5 per group).

the phenotype of infection, pathogenesis and resulting local immune response following genital infection of female BALB/c mice. The elicited immune response by ZOTEN/HSV-2 acts to decrease local cell infiltration and inflammation and therefore results in a global decrease of pathogenesis. To confirm this, we created 4 treatment groups of mice: HSV-2 infected, mock infected, ZOTEN/HSV-2 infected and ZOTEN/mock infected. To maximize our understanding of the events occurring at the primary site of infection, the excised vaginal tissue at 7 days post infection was divided in to 3 equal pieces and each section was subjected to different analysis.

First, we looked at the phenotype of infection by H&E staining (Figure 3A). Representative images of each animal group are shown with evident increased levels of cell infiltration, tissue inflammation and damage in HSV-2 infected mice as opposed to the other treatment groups. The vaginal epithelium of ZOTEN/HSV-2 infected mice was comparable in thickness and morphology as mock infected mice. Interestingly, ZOTEN/HSV-2 infected mice exhibited significantly larger draining lymph nodes than mock infected, comparable to HSV-2 infected mice without treatment, leading us to believe that presence of ZOTEN mediates an immune response similar to non-treated infection. However, ZOTEN treatment more so triggers the development of adaptive immunity and memory against the pathogen (Figure 3B). While further studies are needed, it appears that ZOTEN equips the host with heightened immune surveillance

against the virus, allowing it to fight off the infection while minimizing the inevitable side effect of disease development by innate immunity.

In hopes of better understanding the key players contributing to the changes in local immune response upon ZOTEN treatment, we looked at the different types of cells infiltrating the vaginal tissue by flow cytometry. CD45, Gr-1, CD3, CD49b, CD11c, and F4/80 were used as markers for leukocytes, neutrophils, T lymphocytes, natural killer cells, dendritic cells, and macrophages, respectively. A trend of decreased infiltration of CD45⁺, Gr-1⁺, and F4/80⁺ cells was observed in the vaginal tissue upon ZOTEN/HSV-2 genital infection. ZOTEN also restored basal levels of CD49b+ and CD11c+ cells. It is understood that neutrophils (expressing Gr-1) are a major component of the innate inflammatory infiltrate at the primary site of herpes infection (18). The observed trends of decreased CD45+ and Gr-1+ infiltrating cells in the vaginal epithelium in addition to lower levels of proinflammatory IL-1β transcripts further demonstrates the decreased local inflammation observed in ZOTEN/HSV-2 infected mice (Figures 4A,B, 5).

Tissue specific analysis of the application of ZOTEN has allowed for better understanding of how the infection is processed in the local tissue environment. HSV-2 infected mice, in the presence or absence of a prior ZOTEN treatment, demonstrate similar levels of activation of the immune system

however differ drastically in phenotype of local infection. This leads us to believe that while the immune response is activated in the presence of ZOTEN, local inflammation is limited and therefore clinical manifestations of infection are suppressed. Therefore, ZOTEN acts to bolster the immune system and equip the host with a better response to infection. ZOTEN shows to be a practical solution for instant benefit as a microbicide and future development of vaccine against HSV. In addition, our studies show the promise that ZOTEN can be developed as a live virus vaccine platform whereby the viral candidates for the vaccine can be preincubated with ZOTEN and then delivered via intravaginal or other routes. An optimized combination will not cause infection but elicit a protective and/or therapeutic immune response. While more studies are definitely needed, ZOTEN as a live virus vaccine platform is another out-of-the-box strategy, which may lead to new and more effective vaccine strategies.

DATA AVAILABILITY

All datasets generated for this study are included in the manuscript and/or the supplementary files.

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ETHICS STATEMENT

All animal experiments were reviewed by the UIC Animal Care Committee and the experiments were performed in adherence to the ARVO Statement for the Use of Animals in Ophthalmic and Vision research.

AUTHOR CONTRIBUTIONS

AA, LK, RS, TY, and YM performed the experiments. AA, LK, RS, and TY analyzed the results from the biological experiments and YM and RA analyzed the ZOTEN synthesis data. AA, LK, and DS conceived the study and wrote the manuscript.

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SOCS and Herpesviruses, With Emphasis on Cytomegalovirus Retinitis

Christine I. Alston 1,2 and Richard D. Dix 1,2*

¹ Department of Biology, Viral Immunology Center, Georgia State University, Atlanta, GA, United States, ² Department of Ophthalmology, Emory University School of Medicine, Atlanta, GA, United States

Suppressor of cytokine signaling (SOCS) proteins provide selective negative feedback to prevent pathogeneses caused by overstimulation of the immune system. Of the eight known SOCS proteins, SOCS1 and SOCS3 are the best studied, and systemic deletion of either gene causes early lethality in mice. Many viruses, including herpesviruses such as herpes simplex virus and cytomegalovirus, can manipulate expression of these host proteins, with overstimulation of SOCS1 and/or SOCS3 putatively facilitating viral evasion of immune surveillance, and SOCS suppression generally exacerbating immunopathogenesis. This is particularly poignant within the eye, which contains a diverse assortment of specialized cell types working together in a tightly controlled microenvironment of immune privilege. When the immune privilege of the ocular compartment fails, inflammation causing severe immunopathogenesis and permanent, sight-threatening damage may occur, as in the case of AIDS-related human cytomegalovirus (HCMV) retinitis. Herein we review how SOCS1 and SOCS3 impact the virologic, immunologic, and/or pathologic outcomes of herpesvirus infection with particular emphasis on retinitis caused by HCMV or its mouse model experimental counterpart, murine cytomegalovirus (MCMV). The accumulated data suggests that SOCS1 and/or SOCS3 can differentially affect the severity of viral diseases in a highly cell-type-specific manner, reflecting the diversity and complexity of herpesvirus infection and the ocular compartment.

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France
Deepak Shukla,
University of Illinois at Chicago,
United States
Homayon Ghiasi,
Cedars-Sinai Medical Center,
United States

*Correspondence:

Richard D. Dix rdix@gsu.edu

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INTRODUCTION

Herpesviruses skillfully manipulate their hosts by various mechanisms while viral lytic and latent cycles maintain a lifelong, Sisyphean struggle with host innate, and adaptive immune systems. Cells of innate and adaptive immunity are efficient producers of pro-inflammatory cytokines, chemokines, and cell surface receptors, and they rely heavily on cell-type-specific intracellular signaling pathways to differentiate and function properly. Upon infection, herpesviruses are recognized by circulating innate cells such as monocytes, macrophages, dendritic cells (DC), neutrophils, or natural killer (NK) cells (1), and by local resident innate cell types specialized in certain tissues, such as Müller cells and microglia (2) of the retina. Interactions between receptors and pathogens begin signaling cascades that result in progressively amplified, harmonious transcriptional stimulation of hundreds of downstream gene products, many of them cytokines released extracellularly to function in autocrine or paracrine positive feedback capacities.

of homeostasis being paramount for biological systems, this signaling also induces negative feedback agents such as suppressor of cytokine signaling (SOCS) proteins to aid in the prevention of damaging immunopathologies. The eight known SOCS members comprise a family of host proteins which, among their other functions, negatively regulate signaling pathways induced by antiviral and inflammatory cytokines, effectively increasing tolerance for specific cytokines signaling within specific cells [for reviews, see (3-6)]. Once activated, innate immune cells such as DCs or microglia can become professional antigen presenting cells, which instruct and activate adaptive immune cells such as B cells and CD4+ and CD8+ T lymphocytes to produce their effector functions against pathogens and pathogen-infected cells. During primary and lytic infection, herpesviruses nimbly evade sufficient aspects of innate and adaptive immunity to avoid complete clearance. Eventually they enter or are forced by the immune system into a state of latency during which the virus continues to modulate host immunity despite only a small subset of viral genes being detectable. Reactivation from latency to lytic infection then back to latency may then occur periodically throughout the life of the host [for reviews, see (1, 7-10)].

Despite the relatively large number of virus-encoded gene products contained within herpesviruses compared with other viruses, they remain obligate intracellular pathogens and therefore still rely on host-encoded gene products for survival and propagation. SOCS proteins are one such example of host-encoded proteins that are manipulated by many different types of viruses and other pathogens, as reviewed by others (5, 6). In addition to the viruses featured in these reviews, more herpesviruses also are now known to stimulate SOCS1 and/or SOCS3 during in vitro or in vivo infection. These include the human herpesviruses herpes simplex type 1 (HSV-1), varicella zoster virus (VZV), human cytomegalovirus (HCMV), Epstein-Barr virus (EBV), and Kaposi's sarcoma-associated herpesvirus (KSHV), as well as the animal herpesviruses gallid alphaherpesvirus 2 (GaHV-2, or Marek's disease virus, MDV), suid alphaherpesvirus 1 (SuHV-1, or pseudorabies virus, PRV), murine cytomegalovirus (MCMV), and murine gammaherpesvirus-68 (MHV-68) (11-23).

Herein we discuss these human and animal herpesviruses currently known to affect SOCS proteins in various in vitro and in vivo model systems, with particular emphasis on SOCS1 and SOCS3 expression during experimental MCMV retinitis, a mouse model used to study AIDS-related HCMV retinitis (24). AIDS-related HCMV retinitis is a blinding, degenerative disease of the retina that once threatened the bilateral vision of \sim 30% of AIDS patients (25). Despite the advent of antiretroviral therapies (ART) in the developed world, HCMV remains a significant opportunistic pathogen of AIDS patients worldwide. As with humans and AIDS, mice with murine AIDS (MAIDS) experience retrovirus-induced immune suppression and become susceptible to diseases of opportunistic pathogens (26). For many years our laboratory has used MAIDS-related MCMV retinitis as a clinically relevant mouse model with high face validity and predictive validity [per (27, 28)] to AIDS-related HCMV retinitis to elucidate the role of potential candidates contributing to this disease (29), including host SOCS proteins (21, 23). Thus, the purposes of this review are to explore briefly the model systems under which herpesviruses manipulate SOCS proteins and to review the effects of SOCS manipulation on virologic, immunologic, or pathologic outcomes, with a focus on experimental cytomegalovirus retinitis. Specialized therapeutic inhibition or mimicry of SOCS proteins, perhaps combined with immunotherapies or antiviral drugs, may become a viable tactic for more effectively combating herpesvirus pathologies.

SUPPRESSOR OF CYTOKINE SIGNALING (SOCS) FAMILY

Innate and adaptive immune cells secrete cytokines and chemokines to orchestrate a coherent, integrated immune response to protect the host against pathogens. During infection, cytokines initiate, execute, and resolve inflammatory responses, such that cytokine signaling is the crucial control switch between the initiation of the immune response and the maintenance of homeostasis in the periphery. Therefore, cellular negative feedback loops play an important role in maintaining the tight balance of cytokine secretion and cytokine inhibition, and SOCS proteins function in such a capacity.

SOCS Structure, Function, and Expression

SOCS proteins were first discovered in the mid-1990s as cytokine-induced inhibitors of signal transducers and activators of transcription (STAT) cell signaling pathways (30-33). The SOCS protein family currently contains eight known members: SOCS1 through SOCS7 and the cytokine-inducible Src homology 2 (SH2)-containing domain protein (CIS). These proteins are selectively upregulated in response to various cell signaling pathways (34) and subsequently act intracellularly as negative regulators of cell signaling (4). All SOCS proteins characteristically contain a C-terminal SOCS box, an internal SH2 domain, and a variable-length N-terminal region (4) (Figure 1). SH2 domains are conserved throughout most eukarya, excluding single-celled fungi, and they recognize and bind to specific phosphorylated tyrosine motifs on their target proteins (37). At least 110 unique human proteins contain SH2 domains (38), and specificity to their targets is achieved by primary and secondary binding sites within these SH2 domains (39). Immediately upstream of the SH2 domain is the extended SH2 sequence (ESS) which increases binding affinity to phosphotyrosine residues (40-42). The SOCS box is also a conserved sequence found within more than 70 different human proteins (43). This motif primarily functions to recruit cellular ubiquitination machinery, thus allowing such proteins to flag their specific substrates for proteasomal degradation (43). It achieves this by binding cellular Elongin B, Elongin C, Cullin5, and RING-box-2, thus forming an E3 ubiquitin ligase complex (4-6, 43). SOCS1 and SOCS3 additionally possess an N-terminal kinase inhibitory region (KIR) which can act as a pseudosubstrate to block the kinase activity of such proteins as Janus kinases (JAKs) (32, 44, 45). These SOCS proteins negatively regulate intracellular signaling pathways by several mechanisms,

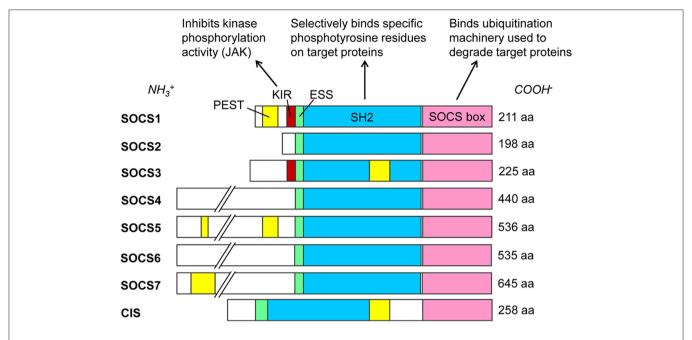


FIGURE 1 | SOCS family proteins and their domains. Src homology 2 (SH2) domains (blue) govern target protein specificity by recognizing phosphorylated tyrosine residues flanked by specific sequences such as those on cytoplasmic residues of cytokine receptors. SOCS1 and SOCS3 exclusively contain kinase inhibitory regions (KIR, red), which bind and inhibit JAK proteins. Extended SH2 sequences (ESS, green) enhance binding specificity and affinities to phosphotyrosine residues. SOCS box domains (pink) recruit cellular Elongin BC, Cullin5, and RING-box-2 to form an E3 ubiquitin ligase complex, ubiquitinating target proteins for proteasomal degradation. PEST motifs (yellow) greatly decrease the half-lives of the proteins; see (35, 36) for predicted PEST domain locations. Amino acid (aa) lengths for *Homo sapiens* SOCS proteins are from the National Center for Biotechnology Information (NCBI) database (February 2019).

including competitive binding of phosphotyrosine residues with various recruited STAT proteins, inhibition of JAK activity via KIR domains, or ubiquitination of SOCS-bound elements by the SOCS box, marking them for degradation (4, 5). In addition to these domains, SOCS1, SOCS3, SOCS5, SOCS7, and CIS each contain a sequence rich in proline (P), glutamic acid (E), serine (S), and threonine (T) known as a PEST motif (46), which decreases the half-life of the entire protein to about 2 h (42). The predicted locations for these PEST motifs vary, and to our knowledge no such predicted sequence has yet been found for SOCS2, SOCS4, or SOCS6 (35, 36).

Several different types of cell signaling pathways are capable of inducing SOCS (47-50), with JAK/STAT signaling driven by cytokines such as interferons (IFN) and interleukins (IL) being one of the best studied SOCS-inducing pathways (4). When transmembrane cytokine receptors on a cell surface recognize their cognate extracellular cytokines, they initiate intracellular phosphorylation cascades via specific combinations of JAK and STAT proteins, transcriptionally stimulating scores of gene products (51-53), including negative-feedback SOCS family proteins. Well-described cytokine receptor-JAK/STATgene target combinations are reviewed and summarized elsewhere (54, 55). Intracellular SOCS proteins then selectively inhibit components of JAK/STAT and other cell signaling pathways, within the specific cells expressing them (4, 33, 56–58) (Figure 2). Although some crosstalk occurs between individual SOCS members and their targets, the variations between SOCS protein SH2 domains equip them with preferential affinity to their respective substrates, as listed elsewhere (50). Receptor expression, cytokine milieus, and signaling pathways tend to differ greatly between cell types, even within the contexts of different tissues or microenvironments.

Many different cell types in various organs are capable of producing SOCS family proteins (33), and they are most amply produced by hematopoietic cells (59) of the innate and adaptive immune systems (4, 58). Some of these SOCS-expressing cell types include monocytes (60), macrophages (32, 61), DCs (62, 63), microglia (64), neutrophils (65), NK cells (66), CD4⁺, and CD8⁺ T cells (67, 68), and ocular Müller cells (69). SOCS proteins primarily function within the very cells which transcriptionally produce them, although cell-to-cell vesicular transport of SOCS proteins has been demonstrated from alveolar macrophages to adjacent epithelial cells (70).

SOCS1 and SOCS3

The importance of SOCS1 and SOCS3 in modulating immune responses is emphasized in knockout mice, as SOCS1-deficient mice die within 3–4 weeks of birth from massive IFN-related inflammation (71–73), and deletion of the SOCS3 gene is embryonically lethal (74). SOCS1 proteins are able to limit the surface expression of molecules that mediate the immune response, suppress inflammation by dampening expression of cytokines and chemokines, inhibit pathogen infiltration and replication, and prevent central nervous system demyelination. SOCS1 is quickly induced by IFN signaling and inhibits the specific JAK and STAT proteins involved during IFN signaling

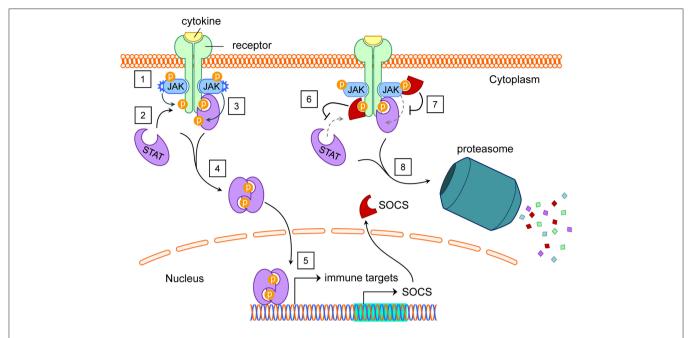


FIGURE 2 | SOCS induction by and inhibition of the JAK/STAT pathway. (1) Extracellular cytokines cause dimerization of their cognate transmembrane receptors. This brings intracellular receptor-associated JAK proteins into proximity to cross-phosphorylate each other and tyrosine residues on the receptors. (2) STAT proteins dock at phosphotyrosines on intracellular receptor subunits. (3) JAK proteins phosphorylate STAT proteins, activating them. (4) Activated STAT proteins undock from their receptors, dimerize, and translocate to the nucleus. (5) STAT proteins act as transcription factors for dozens of immune targets, including SOCS. (6) Functioning in the cytoplasm, SOCS proteins can bind various phosphotyrosines on intracellular receptors, blocking STATs from their native docking sites. (7) With their KIR domains, SOCS1 and SOCS3 can inhibit the kinase activity of JAK proteins, preventing tyrosine phosphorylation of STAT proteins. (8) SOCS boxes facilitate ubiquitination of SOCS-bound protein targets for proteasomal degradation. Abbreviations: suppressor of cytokine signaling (SOCS), Janus kinase (JAK), signal transducers and activators of transcription (STAT), kinase inhibitory region (KIR). See Akhtar and Benveniste (5).

(75, 76). In addition to its primary role in the regulation of components of the JAK/STAT pathway, SOCS1 is capable of regulating other cellular signaling pathways such as tolllike receptor (TLR) signaling and macrophage activation (47). Whereas inactivated macrophages produce low baseline levels of SOCS1 and SOCS3, induction of SOCS1 generally drives macrophages toward an M2 phenotype, and SOCS3 toward M1 (77, 78). SOCS1 also plays a dual role in CD4⁺ T-helper (T_H) cell differentiation (67, 79–81). As a key attenuator of type II IFN (IFN-γ) signaling, SOCS1 can inhibit IFN-γ-mediated STAT1 activation by targeting JAK2, thus suppressing the differentiation of the T_H1 lineage in CD4⁺ T cells (75, 82). SOCS1 is alternatively able to inhibit IL-4 signaling, thereby driving differentiation toward a T_H1 phenotype (67, 83). By comparison, SOCS3 is classically upregulated as a consequence of signaling by the IL-6 family of cytokines (33). Once induced, a major function of SOCS3 is then to inhibit the signaling of IL-6 family cytokines by targeting their common gp130 receptor (58, 84, 85). Furthermore, SOCS3 is a key regulator of IL-23-mediated STAT3 (79, 86) and of IL-12-mediated STAT4 activation (85), such that SOCS3 is also able to inhibit the development of CD4⁺ T_H1 and T_H17 cells (87), thereby promoting differentiation to the T_H2 lineage.

Both SOCS1 and SOCS3 have demonstrated transcriptional induction by type I IFNs, key immune regulators in mounting an antiviral response (88, 89). These cytokines play a role in

the activation of NK and T cells, and they induce cell death in virus-infected cells (90, 91). The type I IFN family consists of the many subtypes of IFN-α, as well as IFN-β, IFN-ε, IFN-κ, and IFN- ω (92). Almost all cell types are capable of producing type I IFNs in response to various stimuli (89, 90, 93). Plasmacytoid DCs (pDC) in particular are one of the highest contributors to the secretion of type I IFNs (90). Type I IFNs signal through the heterodimerization of the type I IFN receptor (IFNAR)-1 and IFNAR-2, which signal through the JAK/STAT pathway, mediated specifically by the JAKs Tyk2 and JAK1, and by STAT1, and STAT2 (90, 94). Unlike most dimerized STATs, the STAT1/STAT2 heterodimer must bind to an additional protein, interferon regulatory factor 9 (IRF9), and form the interferonstimulated gene factor 3 (ISGF3), before they are able to recognize the interferon-stimulated response element (ISRE) and begin transcription of ISGs (90). The more than 300 ISGs that have been identified to date (95) include SOCS proteins, particularly SOCS1, and, to a lesser extent, SOCS3.

In addition to this classical induction by cytokine signaling via the JAK/STAT pathway, SOCS proteins have also shown to be stimulated by alternative cell signaling pathways. Among these pathways are nuclear factor κB (NF-κB) and mitogen activated protein kinase (MAPK) signaling pathways through phosphorylation of c-Jun N-terminal kinases (JNKs) (96, 97). SOCS proteins can also be induced by stimulation of TLRs (48, 98, 99), which are expressed by many cell types, including

the retinal pigment epithelium (RPE) (100, 101) and Müller cells (102) of the eye. In macrophages and DCs, non-TLR sensor dectin-1 induces SOCS1 by MAPK/ERK, and SOCS1 modulates TLR9 signaling by inhibiting NF-κB (103). Stimulation of these pathways therefore may trigger the production of SOCS proteins directly or indirectly by the production of SOCS-inducing cytokines such as type I IFN.

SOCS2

Although the rest of the SOCS family (CIS, SOCS2, and SOCS4—SOCS7) remains less studied than SOCS1 and SOCS3, ever more research on these accumulates over time. SOCS2, briefly discussed below in the context of alphaherpesviruses, is stimulated within different cell types in response to signals from various hormones or cytokines, including growth hormone, insulin, IFN- α , and IL-6, possibly through STAT5 [reviewed in (6, 104)]. It is believed that SOCS2 and CIS primarily bind to phosphotyrosines on intracellular receptor residues to block STAT binding in a competitive manner (5). Among its other functions, SOCS2 negatively regulates the growth hormone receptor, and SOCS2-knockout mice are significantly (\sim 40%) larger than wild type mice (105). Like most other SOCS members, SOCS2 is also implicated in some types of cancer, albeit less abundantly so than other SOCS members.

HERPESVIRUSES

Herpesviridae Classification and Characteristics

Admittance into the Herpesviridae family of the taxonomic order Herpesvirales traditionally is based upon the virus structure: dsDNA within an icosahedral capsid surrounded by an amorphous tegument between the host cell-derived envelope encrusted with viral glycoproteins. Members of this family share the biological characteristics of replication within host cell nuclei, the establishment of latency, and ultimate destruction of lytically infected host cells. With notable exceptions, it is generally rare that herpesviruses cause severe disease in immunocompetent, endogenous hosts, with the majority of morbidities or mortalities occurring in the very young, very old, immune compromised, or non-native host. To date, there are nine known herpesviruses that infect humans; these are designated human herpesvirus (HHV)-1 through HHV-8, with a ninth member in the division of HHV-6 into HHV-6A and HHV-6B (106) as distinct herpesvirus species. The Herpesviridae family contains three subfamilies: Alphaherpesvirinae, Betaherpesvirinae, and Gammaherpesvirinae. Members of these subfamilies are phylogenetically classified based on genetic sequence homology but can also be generally distinguished by their respective cell or tissue preference for establishing latency, relative rate of replication cycle, and/or natural or experimental host restriction [reviewed in (1, 107–110)]. Classifications of select herpesviruses pertinent to this review are organized in Table 1.

Alphaherpesvirinae

The α -herpesviruses are characterized by their ability to establish latency in neurons, to infect a variety of host species, to

TABLE 1 | Taxonomic classifications of select members of the *Herpesviridae* family.

	Genus	Species name	Common name
α	Mardivirus	Gallid alphaherpesvirus 2 (GaHV-2)	Marek's disease virus (MDV)
	Simplexvirus	Human herpesvirus 1 (HHV-1)	Herpes simplex virus type 1 (HSV-1)
		Human herpesvirus 2 (HHV-2)	Herpes simplex virus type 2 (HSV-2)
	Varicellovirus	Bovine herpesvirus 1 (BoHV-1)	
		Bovine herpesvirus 5 (BoHV-5)	
		Human herpesvirus 3 (HHV-3)	Varicella zoster virus (VZV)
		Suid herpesvirus 1 (SuHV-1)	Pseudorabies virus (PRV)
β	Cytomegalovirus	Human herpesvirus 5 (HHV-5)	Human cytomegalovirus (HCMV)
	Muromegalovirus	Murid herpesvirus 1 (MuHV-1)	Murine cytomegalovirus (MCMV)
	Roseolavirus	Human herpesvirus 6A (HHV-6A) Human herpesvirus 6B (HHV-6B) Human herpesvirus 7 (HHV-7)	
γ	Lymphocryptovirus	Human herpesvirus 4 (HHV-4)	Epstein-Barr virus (EBV)
	Rhadinovirus	Human herpesvirus 8 (HHV-8)	Kaposi's sarcoma-associated herpesvirus (KSHV)
		Murid herpesvirus 4 (MuHV-4), isolate MHV-68	Murine gammaherpesvirus 68 (MHV-68)

Herpesviridae subfamilies: Alphaherpesvirinae (α), Betaherpesvirinae (β), Gammaherpesvirinae (γ). Classifications from the July 2017 International Committee on Taxonomy of Viruses (ICTV) and Pellett and Roizman (1) and Davison et al. (109).

replicate and spread relatively quickly, and to destroy infected host cells. This subfamily currently consists of five genera, two of which infect mammals: Simplexvirus and Varicellovirus. Pathologies of *Simplexvirus* HSV-1 include oropharyngeal lesions (cold sores), herpetic epithelial or stromal keratitis, herpes simplex encephalitis, and genital herpes (111), with the latter more frequently caused by HSV-2, another Simplexvirus. VZV of the Varicellovirus genus is the etiological agent of varicella (chickenpox) and herpes zoster (shingles). Also in this genus is suid alphaherpesvirus 1 (SuHV-1), or PRV, which causes fatal disease following natural infection of swine as well as a wide range of mammalian host species. In addition, bovine herpesvirus 1 (BoHV-1) and BoHV-5 are highly similar varicelloviruses (112) which cause significant infections of cattle (113, 114). The genus Mardivirus of the Alphaherpesvirinae subfamily contains gallid alphaherpesvirus 2 (GaHV-2), or MDV, which infects chickens and is responsible for significant losses in the poultry industry (115, 116).

Betaherpesvirinae

The β -herpesviruses generally replicate more slowly than other herpesviruses and display host species specificity, with a propensity to establish latency in lymphoid cells of hematopoietic origin. The genus *Roseolavirus* comprises HHV-6 and HHV-7, of which HHV-6B and HHV-7 have been shown to cause exanthem subitum (roseola, sixth disease) (106, 117). Of particular importance to this review are the genera *Cytomegalovirus*, which contains HCMV, and *Muromegalovirus*, which includes murid herpesvirus 1 (MuHV-1), or MCMV. HCMV and MCMV represent a central focus of this report and are discussed more thoroughly in following sections.

Gammaherpesvirinae

The γ -herpesvirus subfamily contains viruses that are species-specific, generally prefer B or T lymphocytes for replication, and establish latency within lymphoid tissue. This subfamily contains four genera, of which *Lymphocryptovirus* contains EBV, and *Rhadinovirus* includes KSHV (HHV-8) and MHV-68, an isolate of *murid herpesvirus* 4 that is widely used in experimental model systems (1).

Herpesvirus Immune Evasion: HCMV and MCMV

The balance between virulence and the host immune response sways the outcome of any viral infection. Just as the host has an arsenal of mechanisms for sensing, stopping, and clearing viral infection, viruses have as many mechanisms for evading, escaping, and producing productive infections in the host. Herpesviruses undergo lytic and latent life cycles for the lifetime of their hosts, and they are particularly adept at manipulating the innate and adaptive immune responses by a multitude of mechanisms. As HSV-1 is a quintessential example of the α-herpesviruses, HCMV and its mouse counterpart MCMV are well-studied examples of the β -herpesviruses. HCMV and MCMV, like many herpesviruses, modulate their host cells by interfering with signaling pathways important to the innate or adaptive immune response (110). As HCMV and MCMV represent a major focus of this review, they are depicted in this section as examples of herpesvirus immune evasion.

Integral to the first-responding cells of innate immunity is the vast family of pattern recognition receptors (PRR) which are capable of detecting common non-self, pathogen-associated molecular patterns (PAMPs) (118). PAMPs are highly-conserved molecules which are usually indispensable to the pathogens with which they are associated (91, 118, 119). Many types of PRRs have been identified so far, including TLRs, retinoic acid-inducible gene I (RIG-I)-like receptors (RLRs), nucleotide oligomerization domain (NOD)-like receptors (NLRs), C-type lectin receptors (CLRs), and absent in melanoma 2 (AIM2)-like receptors (120, 121). In general, activation of any of these PRRs leads to one or more well-characterized cell signaling pathways responsible for the upregulation of pro-inflammatory cytokines, including type I IFNs (120). Among these pathways are NF-κB and MAPK signaling pathways through phosphorylation of JNKs (96, 97), as well as inflammasome/caspase-1-dependent IL-1β maturation (122). Infection with herpesviruses such as HCMV

or MCMV has the capacity to stimulate and/or to modulate several of these PRRs (110). For instance, MCMV infection of monocytes and other cell types stimulates TLR2/myeloid differentiation primary response 88 (MyD88) (123), TLR3/TIR-domain-containing adapter-inducing interferon- β (TRIF), and TLR9/MyD88 (124) signaling. Macrophages and their progenitor cells (monocytes, bone marrow cells) highly express PRRs and are major players during systemic HCMV or MCMV dissemination and latency (125–133).

As major players in the innate immune response, macrophages exhibit divergent activation phenotypes in response to various stimuli. These have very generally been categorized into M1 classically-activated macrophages and M2 alternatively-activated macrophages (134), so called for their association with CD4⁺ T_H1 or T_H2 polarization, respectively. In general, M1 macrophages are activated via exposure to IFN-γ alone or together with tumor necrosis factor (TNF)-α, PAMPs such as TLR4-recognized lipopolysaccharide (LPS). They express TNF-α, IL-6, IL-1, and IL-12 upon activation, and through production of these pro-inflammatory cytokines and nitric oxide, they exhibit a pro-inflammatory phenotype (135). Alternatively-activated M2 macrophages have grown to include all non-classically-activated macrophages and therefore display a diverse range of activation phenotypes. An M2 phenotype is generally induced by exposure to IL-4 or corticosteroids, results in the production of anti-inflammatory IL-10 and IL-1 receptor antagonist, and participates in anti-inflammatory or pro-angiogenic activities (135). These macrophage polarizations exhibit extreme plasticity, however, and are not as clearly defined as originally thought. Monocytes infected with HCMV, for instance, display a hybrid M1/M2 activation phenotype, simultaneously showing pro-inflammatory and pro-angiogenic properties, but with a propensity mostly toward the M1 phenotype (136–139).

Also integral in early control of herpesvirus infection are NK cells. These granulocytic cells are highly effective at destroying cells that fail to display sufficient amounts of major histocompatibility complex (MHC) class I (MHC-I), which presents intracellularly-derived antigens to MHC-I-restricted immune cells such as CD8 $^{\rm +}$ T cells (140). The cytotoxic effector function of NK cells also requires signaling by activating receptors and/or signaling by cytokines such as type I IFN or IL-12 (141). Activated NK cells produce high amounts of IFN- γ and use an arsenal of cytotoxic molecules like perforin or granzyme B to fulfill their cytotoxic functions (142). NK cells play a protective role in response to systemic HCMV and MCMV infections (110, 143) and are primarily responsible for immediate control of infection.

In addition to the immediate response of NK cells of the innate immune system, large numbers of MHC-II-restricted CD4 $^+$ T cells as well as MHC-I-restricted CD8 $^+$ T cells of the adaptive immune system specifically target HCMV or MCMV antigens during viral infection (110, 142, 144). More so than the HCMV-or MCMV-specific antibody response of B cells, T cells keep the virus in check throughout the life of the host and play a role in the balance between persistent infection and latency (141, 142). The importance of CD4 $^+$ and CD8 $^+$ T cells in controlling lifelong

HCMV or MCMV infection is underscored by the profound susceptibility to cytomegalovirus-derived pathologies that occur during depletion or dysfunction of these cells (24, 25, 107, 108, 110, 145–152).

HERPESVIRUSES AFFECTING HOST SOCS PROTEINS

Because of the immunomodulatory effects of SOCS proteins, it is not surprising that infectious microbes may take advantage of host SOCS expression. Indeed, SOCS1 and/or SOCS3 exploitation by such viruses as human immunodeficiency virus (HIV) (153-156), hepatitis B virus (157), hepatitis C virus (158, 159), Semliki forest virus (56), respiratory syncytial virus (160), coxsackievirus (161), Ebola virus (162), influenza A virus (163), HSV-1 (164-166), and EBV (12) has been beautifully reviewed elsewhere (5, 6). As Akhtar and Benveniste foresaw, more viruses affecting SOCS proteins have been discovered, many of them herpesviruses. In addition to HSV-1, these include the human herpesviruses VZV (17), HCMV (14), and KSHV (13), as well as the animal herpesviruses MDV (15, 19), PRV (20), MCMV (11, 16, 18, 21, 23), and MHV-68 (22) (Table 2). In addition to these, recent reports discuss the effects of SOCS2 gene knockout during infection with HSV-1 (171), HSV-2 (172), or BHV-5 (173). It is likely that still more viruses affecting SOCS proteins will be discovered in the future.

Human Herpesviruses and SOCS1 or SOCS3

The consequences of virally manipulated SOCS1 and SOCS3 expression during HSV-1 infection are probably thus far the best studied among herpesviruses. After hepatitis C virus, HSV-1 is the second virus reported to stimulate host SOCS3 (164). In the human amnion cell line FL (174), this SOCS3 induction occurs very early, within 1 h post-infection (hpi) and coincides with reduction in type I IFN signaling downstream of JAK phosphorylation (164). The same group soon after reported that this is cell-type-specific, as SOCS3 is upregulated within 1 hpi (HSV-1 strain VR3) in the human T-cell leukemia cell line TALL-1 and the T-lymphoblastoid cell line CCRF-CEM, but not in human U937 or THP-1 monocytic cell lines, nor in an EBV-negative clone of the Burkitt's lymphoma B-cell line AKATA (165). This SOCS3 stimulation in FL cells is partly dependent on activation of JAK3 (165). Furthermore, siRNAtargeted suppression of SOCS3 results in lower HSV-1 virus titers in FL cells. Taken together, these studies provide strong evidence that during HSV-1 infection of FL cells, JAK3 signaling stimulates SOCS3, which then modulates the antiviral effects of IFN- α/β signaling, thus facilitating greater viral replication (165). Although this group found no stimulation of SOCS1 within 1 hpi in these cell types with HSV-1 strain VR3, they later detected both SOCS1 and SOCS3 transcriptional stimulation by RT-qPCR in FL cells at 4 hpi that is dependent on the HSV-1 UL13 protein kinase (167). Still others (166) later reported that HSV-1 strain syn17⁺ stimulates SOCS1 expression between 1 and 6 hpi in HEL-30 keratinocytes but not L929 fibroblasts,

TABLE 2 | Herpesviruses that manipulate host SOCS expression.

Virus	socs	Cell/tissue type	Effect	References
HSV-1	↑SOCS1	HEL-30 (not L929), J774A.1 at M0, FL	↓IFN-γ signaling, ↑viral replication	(166–168)
	↑SOCS3	FL, TALL-1, CCRF-CEM (not U937, THP-1, AKATA)	↓IFN-α/β signaling, †viral replication	(164, 165)
VZV	↑SOCS1	MRC-5, HaCaT		(17)
	↑SOCS3	MRC-5, HaCaT, THP-1	↓IL-6 production, †viral gene expression	
HCMV	↑SOCS1 ↑SOCS3	Human MoDC		(14)
EBV	↑SOCS1 ↑SOCS3	HK-1, NP69 PBMC	↓JAK/STAT ↓IFN-α/β positive feedback signaling	(12, 169)
KSHV	↑SOCS3	Primary human endothelial cells	↓neutrophil recruitment ↓IFN-γ/STAT1 signaling, ↓MHC II, CIITA	(13, 170)
MDV	↑SOCS1	Thymus, spleen, and skin of chickens	Unknown	(15, 19)
PRV	↑SOCS3	RAW264.7		(20)
MCMV	↑SOCS1	BMM, IC-21, MEF, mouse eyes during	↑Severity retinitis correlation	(11, 18, 21, 23)
	↑SOCS3	experimental MCMV retinitis		,
MHV-68	↑SOCS1	BMM, RAW264.7 (but not MLE-12, NIH3T3)	↓IFN-γ signaling ↑viral replication	(22)

↑ increases; ↓ decreases. Cells: HEL-30 mouse keratinocytes, L929 mouse fibroblasts, J774A.1 mouse macrophages, FL human amnion cell line, TALL-1 T-cell leukemia cell line CCRF-CEM T-lymphoblastoid cell line, U937 and THP-1 human monocytes, AKATA EBV-negative clone of the Burkitt's lymphoma B-cell line, MRC-5 human lung fibroblasts, HaCaT human keratinocytes, monocyte-derived dendritic cell (MoDC), HK-1 and NP69 human nasopharyngeal epithelial cell lines, primary human peripheral blood mononuclear cells (PBMC), RAW264.7 mouse (BALB/c strain) macrophages, primary mouse bone marrow macrophages (BMM), IC-21 mouse (C57BL/6 strain) macrophages, MLE-12 mouse lung epithelial cells, NIH3T3 mouse fibroblasts.

cell lines derived from mouse strain C3H. Importantly, this correlates with the ability of IFN- γ to protect L929 cells but not HEL-30 cells from HSV-1-induced cell death, with inhibition of STAT1 α activation downstream of IFN- γ signaling, and with transcriptional activation of the SOCS1 promoter (166). In primary human astrocytes and neurons, SOCS1 expression during HSV-1 infection is significantly reduced by exposure to type III IFN (IFN- λ) in primary human astrocytes and neurons (175). This cell type specificity for virologic and/or immunologic outcomes is a common theme with herpesviruses, with some outcomes even limited to specific cell activation phenotypes. For instance, HSV-1 infection stimulates SOCS1 in unactivated (M0) J774A.1 mouse macrophages (BALB/cN strain), but not in M1 nor M2 activated macrophages (168).

The α -herpesvirus VZV of the *Varicellovirus* genus initially infects the lungs then disseminates through the blood to cause skin lesions characteristic of varicella (chicken pox). The virus

establishes lifelong latency in dorsal root ganglia, where it may reactivate to cause herpes zoster (shingles) (176). Primary infection elicits an innate immune response characterized by stimulation of IFN- α and IFN- γ (17, 176) that is kept in check by multiple viral mechanisms (177). In immunocompetent individuals, adaptive immunity follows, and although anti-VZV antibodies are abundantly produced by B cells, an effective Tcell response is more important for control of severe disease (178), as with many herpesviruses. During experimental in vitro infection of permissive cell lines, VZV stimulates SOCS1 and, to a greater extent, SOCS3 in HaCaT human keratinocytes and MRC-5 human lung fibroblasts, and it also stimulates SOCS3 but not SOCS1 in THP-1 human monocytes (17). Suppression of SOCS3 by siRNA significantly reduces viral gene expression and greatly increases IL-6 production during VZV infection of MRC-5 cells (17).

The β-herpesvirus HCMV persistently infects about 80% of the worldwide population without usually causing disease in immunocompetent individuals (110, 179). As with most herpesviruses, most severe HCMV pathologies present only during immune suppression, as in HIV/AIDS patients or solid organ recipients, or underdevelopment of immunity (congenital cytomegalovirus) rather than in immunocompetent hosts. AIDSrelated HCMV retinitis, for instance, causes vision loss and blindness in ~30% of untreated AIDS patients (110, 152, 180-183). Upon primary infection, HCMV disseminates via the blood to various organs and establishes latency in circulating monocytes and bone marrow cells (129). Monocyte-derived DCs infected with HCMV (TB40/E or VHLE strains with endothelial cell tropism) stimulate SOCS1 and SOCS3 compared with uninfected cells (14). SOCS3 upregulation in these cells occurs via HCMV stimulation of IL-6/STAT3 signaling, and once stimulated, SOCS3 but not SOCS1 inhibits STAT5 activation downstream of the granulocyte-macrophage colony-stimulating factor (GM-CSF) receptor (14). GM-CSF/STAT5 signaling in monocytic cells drives differentiation toward DCs, and inhibition of this pathway in already-differentiated DCs by HCMV-driven SOCS3 changes their phenotype from CD1a⁺ to CD1a⁻, rendering them inefficient at presenting lipid antigens to T cells (14). Genome sequence analysis of human epithelial HEK293 cells stably expressing the HCMV viral protein US27 showed stimulation of SOCS2 and SOCS5, but not SOCS3, compared with nontransfected HEK293 cells (184), suggesting that the HCMV-encoded G-protein coupled receptor protein US27 may not contribute to SOCS3 stimulation. Like many other herpesviruses, the HCMV genome contains homologs presumably purloined from their hosts (185), such as HCMVencoded vIL10 (186). HCMV vIL10 stimulates SOCS3 in HeLa cells (187) and monocytes (188). These studies demonstrate pathways whereby HCMV indirectly stimulates SOCS1 and/or SOCS3 in various cell types, which then functionally change host and/or bystander cells to contribute to viral immune evasion.

EBV is a γ -herpesvirus in the genus *Lymphocryptovirus* that ubiquitously infects most of the world's population, frequently without symptoms, and establishes latency in B cells (189). Along with causing most cases of infectious mononucleosis,

EBV also is associated with many types of cancer such as nasopharyngeal carcinoma and Burkitt's lymphoma (189, 190). Although the virus efficiently infects B-cell lines *in vitro*, experimental infection of epithelial cells has been more difficult, requiring innovative strategies to develop such model systems (191–193). During persistent EBV infection of the HK-1 and NP69 human nasopharyngeal epithelial cell lines, signaling pathways including STAT3 and NF-κB are activated compared with uninfected cells, resulting in transcriptional upregulation of downstream targets, including SOCS1 and SOCS3 (169). During EBV infection of human PBMCs, the viral Zta or ZEBRA protein stimulates SOCS3, thereby downregulating JAK/STATs involved with IFN-α/β positive feedback signaling (12).

KSHV (HHV-8), an oncogenic γ -herpesvirus, is the etiological agent of Kaposi's sarcoma (194), a neoplasm of endothelial cells that is characterized by dysregulated angiogenesis and massive inflammation, found primarily in patients with HIV/AIDS (195). During latency, KSHV expresses latency-associated nuclear antigen (LANA) that contains a virally-encoded SOCS box motif, which binds to host cell ubiquitination machinery and flags target proteins including tumor suppressor p53 for proteasome degradation (196). Not only does KSHV encode its own SOCS box-containing protein, it also indirectly induces host SOCS3 in endothelial cells. When infected with KSHV, immortalized human TIME dermal microvascular endothelial cells (DMVECs) significantly induce SOCS3 over uninfected cells or cells infected with UV-inactivated virus at 24, 48, and 96 hpi (197). Like other herpesviruses, KSHV also encodes many proteins homologous with host proteins as well as its own viral-encoded microRNA sequences (195). KSHV-encoded microRNA miR-K12-3 and miRK-12-7 stimulate IL-6 and IL-10 in RAW264.7 mouse macrophages and human myelomonocytic leukemia MM6 cells (198). KSHV-infected primary human endothelial cells repress neutrophil recruitment through stimulation of host IL-6 and SOCS3 (13), and SOCS3 stimulation also suppresses MHC II expression on these cells by suppression of IFN-γ/STAT1 signaling and the downstream class II transactivator (CIITA) (170). Therefore, KSHV and other herpesviruses contain multiple strategies to evade immune surveillance, including stimulation of host SOCS1 and/or SOCS3 by multiple mechanisms.

Animal Herpesviruses and SOCS1 or SOCS3

MDV (GaHV-2) in the *Mardivirus* genus is an oncogenic α-herpesvirus of chickens. MDV is the etiological agent of Marek's disease, characterized by immunosuppression, neurological disorders, and CD4⁺ T-cell lymphoma with subsequent solid tumors (115, 116). Transmission occurs through inhalation or ingestion of contaminated dust and dander from feather follicle epithelium (199) of the skin of infected chickens. The virus infects many cell types, including lymphocytes, which disseminate through the blood to various organs, including the thymus and spleen (115, 116). Analyses of whole genome arrays have shown that 2–4 days following systemic MDV infection of chickens, SOCS1 and SOCS3 are stimulated in thymus and spleen tissues, with greater upregulation occurring in chicken strains that are

more susceptible to MDV (15). Transcriptional stimulation of host SOCS1 and SOCS3 was also found in skin samples of MDV-infected chickens at 20 and 30 days post-infection (19). The specific effects of SOCS1 and/or SOCS3 stimulation during MDV infection are yet unknown.

PRV (SuHV-1) is a *Varicellovirus* endogenous to swine but can infect many different animal and cell types. It therefore has been widely used in various animal model systems, including as a neural tracer (200). In a recent study using PRV infection of RAW264.7 mouse macrophages as an oxidative stress model to measure the antioxidant qualities of *Dunaliella salina* alga extract, it was incidentally reported that PRV induces expression of SOCS3 in these cells at 12 and 24 hpi (20). To our knowledge, thus far the impact of SOCS3 stimulation on PRV infection or pathology remains unknown, as does the effect of PRV on SOCS1 expression.

Mouse-specific salivary gland virus (201, 202), now called MCMV, is in the *Muromegalovirus* genus of the β -herpesvirus subfamily. It frequently is used in experimental mouse models and has contributed greatly to our understanding of infection and pathogenesis of its human-specific counterpart, HCMV (108, 203). HCMV and MCMV both establish latency in circulating monocytes and bone marrow cells (129). SOCS1 and SOCS3 are stimulated very early after in vitro MCMV infection of bone marrow macrophages (BMM) (11) as well as IC-21 mouse macrophages and mouse embryonic fibroblast (MEF) cells (18). This stimulation and its temporal patterns are dependent on host cell type and on the mouse strain (C57BL/6 or BALB/c) used for propagation of the MCMV stocks (18). In addition to these in vitro models, we have observed in our laboratory that after intraocular (subretinal) MCMV inoculation of immunocompromised mice during experimental MCMV retinitis, SOCS1 and SOCS3 mRNA (16, 23) and protein (21) are upregulated in retinitis-susceptible eyes. As a major topic of focus in this review, the effects of SOCS1 and/or SOCS3 stimulation in this model are discussed in greater detail in a subsequent section of this review.

MHV-68 (or yHV-68) of the Rhadinovirus genus natively infects rodents such as mice and voles (204, 205). Because of its genomic and physiologic similarities with both EBV and KSHV, MHV-68 infection of mice is a useful animal model to study pathogen-host interactions of these human yherpesviruses (206, 207). It persistently infects lung epithelial cells and establishes latency in B cells, macrophages, and DCs (208). In yet another demonstration of cell type specificity, SOCS1 mRNA and protein are induced upon MHV-68 infection of mouse BMMs and RAW264.7 mouse macrophages, but not MLE-12 mouse lung epithelial cells, NIH3T3 fibroblasts, or MEF cells (22). Transcription of viral genes is likely required for SOCS1 stimulation as UV-inactivation of the virus abrogates this effect. Viral induction of the TLR3/NFκB pathway induces SOCS1, which then inhibits the antiviral effects of IFN-y through inhibition of pSTAT1, resulting in increased viral titers (22). Suppression of SOCS1 during MHV-68 infection restores the antiviral qualities of IFN- γ signaling (22). None of these cell types produced SOCS3 stimulation during MHV-68 infection.

Alphaherpesviruses and SOCS2

In addition to these findings with SOCS1 and SOCS3, a few studies also explore the effects of SOCS2 during α -herpesvirus infection. Following intracranial injection with HSV-1, SOCS2deficient mice are more resistant to HSV-1 encephalitis, neuroinflammation, and immune cell infiltration to the brain compared with wild type C57BL/6 mice (171), suggesting that SOCS2 contributes to the severity of this disease. HSV-2, the causative agent of genital herpes, has long been debated to have a putative involvement in oncogenesis, particularly as a cofactor in cervical cancer, but this remains unproven (209). In LTEP- α -2 and SPC- α -1 human lung cancer cell lines experimentally infected with HSV-2, the virally-encoded microRNA Hsv2-miR-H9-5p targets and inhibits SOCS2, thereby driving experimental tumor metastasis in these cell lines (172). BHV-5 in the Varicellovirus genus natively infects cattle but can establish productive infection in rabbits and mice, which are frequently used as animal models to study neurological disease caused by this virus (173). Unlike HSV-1 infection, infection with BHV-5 exacerbates meningoencephalitis in SOCS2-knockout mice compared with wild type animals (173), suggesting a protective role during intracranial BHV-5 infection. Although it remains unknown whether HSV-1 or BHV-5 stimulates or dampens host SOCS2 expression in these models, SOCS2 nevertheless plays a multivariate role in the pathologies of these herpesviruses.

CYTOMEGALOVIRUS RETINITIS AND SOCS

Despite the development of antiretroviral therapies to treat HIV infection, AIDS-related HCMV retinitis remains a major sight-threatening disease worldwide (110, 152, 180–183). Understanding the pathogenesis of this disease is essential for developing new, safe, and effective treatments for its prevention or management in the clinical setting, yet much remains unknown about the virologic and immunologic mechanisms contributing to its pathology. The pathogenesis of AIDS-related HCMV retinitis involves the complex orchestration of cytomegalovirus infection during AIDS-mediated progressive destruction of the immune system, within the context of retinal cells in the eye.

Vision is facilitated by a complex system whose gross anatomy, microanatomy, biophysical, and biochemical properties are critical to its function. Disruption of any one of thousands of components of this system could lead to visual impairment or blindness. Light first encounters the cornea, which acts as a powerful lens to focus light through the liquid-filled anterior chamber, through the aperture of the pupil, and into the crystalline lens. The lens focuses light with greater precision through the viscous vitreous gel and onto the parfait-like layers of the neurosensory retina at the back of the eye. Photoreceptors in the retina detect photons of light and transmit signals through first-order, second-order, and third-order neurons into ganglion cell axons that exit the eye as the optic nerve. The specialized neuronal cells of the retina are supported by networks of Müller cells, astrocytes, and microglia, as well as by the RPE,

a specialized layer of phagocytic, multifunctional epithelial cells (210). As part of the posterior segment of the eye and an extension of the brain, the retina is considered an immune-privileged site (211) primarily because it does not elicit a typical inflammatory immune response to the introduction of antigens (212, 213). Thus, irreplaceable neuronal tissue is somewhat protected from the damaging effects of inflammation and immunopathogenesis.

AIDS-Related HCMV Retinitis

When the immune privilege of the ocular compartment fails, inflammation causing severe immunopathogeneses and permanent, sight-threatening damage may occur, as in the case of AIDS-related HCMV retinitis. Prior to the era of antiretroviral therapies, this progressive necrosis of the retina is estimated to have occurred in $\sim\!30\%$ of HIV/AIDS patients with CD4 $^+$ T-cell counts fewer than 50 cells/µL blood (25, 180, 181, 214–216). Antiretroviral therapies targeting HIV have greatly reduced the number of new cases of AIDS-related HCMV retinitis in developed countries (151, 180) but have failed to eliminate them completely (215). This disease therefore remains a significant clinical problem worldwide.

Although HCMV is ubiquitous in the population and relatively mild as an infectious disease of immunocompetent individuals, it can become a severe opportunistic pathogen during the immune suppression that occurs when HIV infection progresses to AIDS. It is likely that during AIDS-related HCMV retinitis, HCMV reactivates from latency and travels to the eye hematogenously within monocytes or macrophages, as ophthalmoscopic examination of the retina reveals the characteristic foci of dense retinal whitening that follow retinal blood vessels and may be accompanied by hemorrhage (151). Failure to treat AIDS-related HCMV retinitis results in blindness of most or all of the affected eye, usually followed within 1 year by vision loss in the contralateral eye (110, 152, 180-183). The mechanisms of blindness involve destruction of the retina itself, retinal detachment, or a uveitis that can occur with reconstitution of the immune system associated with well-tolerated antiretroviral therapies (immune recovery uveitis, IRU) (151, 180). Current treatment strategies for HIV/AIDS patients presenting with HCMV retinitis target HCMV replication through lifelong administration of antiviral drugs such as ganciclovir, cidofovir, or foscarnet that can control but not eradicate the virus, slowing but not reversing HCMV-induced ocular damage (217–221). Unfortunately, frequent administration of these drugs has led to an increase in drug-resistant strains of HCMV (222). Vaccination has been one of the most effective methods for controlling other problematic infectious diseases, but attempts to engineer a suitably efficacious vaccine against HCMV thus far have been unsuccessful (223, 224).

Mouse Models of Experimental Cytomegalovirus Retinitis

Because the species-specificity of HCMV precludes its ability to establish productive infection in animal models or cells (225), MCMV is commonly substituted in research laboratories to

investigate cytomegalovirus infection and pathogenesis in mouse models (108, 203) because of high face validity and predictive validity (27). Such research with MCMV has significantly improved our collective understanding of HCMV characteristics and pathogeneses, including the involvement of immune cell types such as CD8⁺ T cells and NK cells in controlling infection (110).

As with humans and HCMV, immunologically normal mice are generally resistant to MCMV retinitis (24, 147, 226, 227), depending on mouse strain (228, 229), viral load, and route of viral inoculum (230-232). Establishment of an immunesuppressed state together with delivery of a substantial amount (10⁴ plaque forming units, pfu) of MCMV directly into the subretinal space of the eye overcomes this resistance, consistently manifesting high frequencies (75–100%) of experimental MCMV retinitis (29, 150, 230) in a manner dependent upon viral load (230) and mouse strain (24, 150, 228-233). Two successful immunosuppression strategies to achieve susceptibility to MCMV retinitis include systemic delivery of corticosteroid drugs (150, 230, 234) or a mixture of mouse-specific retroviruses designated lymphoproliferative-bone marrow 5 (LP-BM5) (235, 236) that induces MAIDS after 8-10 weeks in C57BL/6 mice (26, 237, 238).

The strain of mouse used during experimental MCMV retinitis studies impacts susceptibility to MCMV infection and to the MAIDS-producing LP-BM5 retrovirus mixture. BALB/c mice are more susceptible than C57BL/6 mice to systemic MCMV infection (228, 231, 239-242), and this appears to affect the incidence of experimental retinitis in the corticosteroid model. During corticosteroid-induced immune suppression, the frequency of MCMV retinitis in BALB/c mice is about 90% (150), compared with 50% in C57BL/6 mice (23, 233). BALB/c mice, however, are more resistant than C57BL/6 mice to the induction of MAIDS by LP-BM5 (26, 243), as C57BL/6 mice reach latephase MAIDS within 10 weeks whereas a year or longer is required for BALB/c mice to progress to late-stage MAIDS. For this reason, although BALB/c mice are generally used for experimental MCMV retinitis models with corticosteroidinduced immune suppression, C57BL/6 mice are used for MAIDS models. Importantly, the frequency of experimental MCMV retinitis after subretinal MCMV injection in C57BL/6 mice with MAIDS is 80-100% (24, 226, 227), comparable with the frequency in drug-immunosuppressed BALB/c mice (150).

Just as later stages of AIDS in humans correlates with greater susceptibility to HCMV retinitis, so mice with late-stage MAIDS at 10 weeks (MAIDS-10) are more susceptible to MCMV retinitis than mice with early- or mid-stage MAIDS around 4 weeks (MAIDS-4). Importantly, SOCS1 and SOCS3 are highly stimulated following subretinal MCMV infection in the retinitis-susceptible eyes of MAIDS-10 mice, but not in the MCMV-infected retinitis-resistant eyes of MAIDS-4 mice (16, 21). In C57BL/6 mice with corticosteroid-induced immune suppression, however, subretinal MCMV infection does not significantly alter SOCS1 or SOCS3 protein expression and only mildly stimulates SOCS3 mRNA (23). To our knowledge, the effect of subretinal MCMV infection on SOCS1 and SOCS3 expression in the

eyes of BALB/c mice during corticosteroid-induced immune suppression has not been reported to date.

In the absence of MCMV infection, these two different techniques to accomplish immune suppression also differ in their types of dysfunctional immune cells and the timing of immune cell demise (23). One of the major differences between these models is the number and function of macrophages. MAIDS, without MCMV infection, causes reduced Mac1⁺ (CD11b⁺) macrophage population percentages and activation frequencies at MAIDS-4 (237, 244), with increased macrophage numbers between MAIDS-8 and MAIDS-12 (245). Macrophage populations in MAIDS mice are driven toward an alternatively-activated proangiogenic phenotype that is between classically-activated M1 and alternatively-activated M2. They have decreased TNF- α and IFN- α production but increased IL-1β and IL-6 production in response to LPS (246, 247). By contrast, corticosteroids such as methylprednisolone acetate, in the absence of MCMV infection, very quickly suppress or destroy most of both the innate and adaptive immune systems, including macrophages (248). Whatever macrophages remain tend to be driven toward the M2 alternatively-activated phenotype, in a similar manner as macrophages exposed to IL-4, and they avidly produce IL-10, but not TNF-α, IL-1, or IL-6 (134, 135). Therefore, whereas MAIDS mice experience a functional change in macrophage phenotype after weeks (245-247), drug-induced immune suppression decreases macrophage populations within days (248). Corticosteroids also decrease the overall number and function of CD4+ and CD8+ T cells [~93% depletion, (234, 248, 249) and generally dampen the immune response by suppressing the expression, release, and/or function of inflammatory cytokines such as IFN- γ TNF- α , and IL-2 (249). This rapid, acute decline of the immune system is not observed during MAIDS, which slowly progresses through distinct phases of immune cell dysfunction. Whereas corticosteroid treatment causes apoptosis in leukocytes and lymphocytes therefore decreasing the overall number of these populations (248, 249), MAIDS causes aberrant proliferation of B and T lymphocytes (250, 251) that results in increases in these cell populations coupled with retrovirus-induced cellular dysfunction (26, 251, 252). By late-stage MAIDS, NK cells (253), and neutrophils (254) are also dysfunctional, and macrophage phenotypes are irregular (245–247).

Throughout the many years that these mouse models have been studied, both drug-induced and retrovirus-induced immune suppression strategies during subretinal MCMV infection have contributed to our collective theoretical knowledge of MCMV retinitis and our clinical knowledge of HCMV retinitis. While the drug-induced immune suppression model yields relatively faster results, it bypasses the many nuances and complexities of retroviral immune suppression that the MAIDS model alone bridges to clinical relevance.

MAIDS-Related MCMV Retinitis and SOCS

AIDS of humans and MAIDS of mice are both caused by species-specific retroviruses and share many immunologic and pathologic features (26, 237). Both syndromes are characterized by progressive generalized lymphadenopathy, polyclonal B-cell

TABLE 3 | AIDS-related HCMV retinitis vs. MAIDS-related MCMV retinitis.

	AIDS-related HCMV retinitis	MAIDS-related MCMV retinitis			
Retrovirus-Induced Immune Suppression					
Macrophages among targeted cell types	Yes	Yes			
Polyclonal B-cell activation	Yes	Yes			
Hypergammaglobunemia	Yes	Yes			
Splenomegaly	No	Yes			
T _H 1-to-T _H 2 cytokine shift	Yes	Yes			
Diminished CD4 ⁺ and CD8 ⁺ T-Cell:					
Numbers	Yes	No			
Functions	Yes	Yes			
Cytomegalovirus Retinitis Histologic Characteristics					
Foci of cytomegalic cells	Yes	Yes			
Hemorrhage	Yes	Yes			
Transition zones between normal and necrotic retina	Yes	Yes			
Full-thickness retinal necrosis	Yes	Yes			

Reviewed in Jolicoeur (26) and Watson (237).

activation (250), diminished CD4+ T-cell and CD8+ T-cell functions (251), and a cytokine shift from a TH1 origin to T_H2-associated cytokines (236, 255, 256). Although profound splenomegaly also occurs in MAIDS mice, this overall increase in splenic cell counts is associated with dysfunctional immune cells (257). By MAIDS-10, B cells (247, 258), CD4⁺ and CD8⁺ T cells (245, 251, 259), NK cells (253), and neutrophils (254) are dysfunctional, and macrophage phenotypes are irregular (245-247). Mice with late-stage MAIDS (8-12 weeks) develop a retinitis at 8-10 days following subretinal MCMV injection that exhibits histopathologic features similar to those found in AIDS-related HCMV retinitis (24, 260), including full-thickness retinitis, cytomegalic cells, and transition zones of histologically normal to necrotic retina. Table 3 summarizes the similarities and differences between the retroviruses causing AIDS or MAIDS, and between HCMV retinitis and MCMV retinitis during each, respectively.

Immunologically normal C57BL/6 mice and MAIDS-4 C57BL/6 mice are resistant to MCMV retinitis (0% frequency). Mice with MAIDS-8 to MAIDS-12, however, are susceptible (80–100%) to MCMV retinitis following subretinal (24, 226, 227), but not systemic (232), MCMV inoculation. Importantly, retinitis susceptibility does not correlate with ocular viral titers, because MCMV replication in the ocular compartment at 6–10 days after subretinal inoculation reaches equivalently high levels ($\sim 3 \times 10^4$ pfu/eye) in retinitis-resistant MAIDS-4 mice as those in retinitis-susceptible MAIDS-10 mice (227, 261). By comparison, immunologically normal mice receiving the same amount of subretinally-injected MCMV typically produce only $\sim 10^2$ pfu/eye (24). Thus, high intraocular MCMV titers alone are insufficient for retinitis, and susceptibility to intraocular MCMV replication precedes susceptibility to retinitis in this model (227).

Thus far mechanisms of humoral immunity (262), cellular immunity (263, 264), cell death pathways (261), and several

cytokines have been studied during onset and development of retinal disease in the MAIDS model of MCMV retinitis. Among the putative SOCS-inducing cytokines examined in this model are TNF- α (227, 261), IFN- α/β and IL-6 (21), IFN- γ (21, 227), IL-2 (265, 266), IL-12 (266), IL-4 (226, 267), IL-10 (267), and IL-17 (16). In addition, SOCS1 and SOCS3 are highly stimulated following MCMV infection in retinitis-susceptible MAIDS-10 eyes, but not MCMV infected retinitis-resistant MAIDS-4 eyes (16, 21). In MAIDS-10 eyes with MCMV retinitis, SOCS1 and SOCS3 are produced by infiltrating macrophages and granulocytes, as well as resident microglia and Müller cells (21). Uninfected bystander cells as well as MCMV-infected cells of the retina also abundantly produce SOCS1 and SOCS3 (21), a phenomenon that also has been reported in MCMV-infected IC-21 macrophages (18) and in HCMV-infected monocyte-derived DCs (14). Systemic MCMV in immunocompetent mice without MAIDS moderately stimulates splenic SOCS1 transcripts and SOCS-inducing cytokines IFN-γ and IL-6, but this stimulation decreases in amplitude as MAIDS progresses (21). Furthermore, there is a decreased intraocular stimulation of SOCS1 and SOCS3 during experimental MCMV retinitis during corticosteroidinduced immune suppression that correlates with reduced severity of retinitis (23). Thus, during in vivo MCMV infection, substantial and extended SOCS1 and SOCS3 stimulation appears only in the eye (21) and is correlated with more severe MCMV retinitis (23). Stimulation of pro-inflammatory and antiviral cytokines such as TNF- α and IFN- γ in the eyes of mice with severe MAIDS-related MCMV retinitis fails to control viral replication, but concurrent stimulation of anti-inflammatory cytokines like IL-10 and IL-4 is not sufficient for protection against ocular immunopathogenesis in this disease model (21). Although many questions remain, SOCS1 and/or SOCS3 may play promising roles in the balance of this phenomenon, potentially revealing themselves as novel therapeutic targets to improve the management and/or prevention of AIDS-related HCMV retinitis.

SOCS1 or SOCS3 as Potential Therapeutic Targets During Cytomegalovirus Retinitis

Several strategies for inhibiting or enhancing SOCS1 or SOCS3 gene expression or protein activity in the context of infectious or inflammatory diseases, including over-expression or inhibition gene therapies via viral vectors, have been developed and tested *in vitro* and *in vivo* with promising results, as summarized elsewhere (6). One attractive approach to control the functions SOCS1 and/or SOCS3 includes therapeutic use of smallmolecule protein antagonists or mimetics of SOCS1 and/or SOCS3 proteins.

Although stimulation of SOCS1 and SOCS3 during experimental MAIDS-related MCMV retinitis suggests that one or both of these contribute to the severity of the disease, at this time it remains unknown whether SOCS1 and/or SOCS3 inhibition or overexpression would improve the clinical outcome of AIDS-related HCMV retinitis. If SOCS1 and/or SOCS3 contribute to the pathogenesis of this disease, then their inhibition in HIV/AIDS patients with HCMV retinitis

could prevent further damage to affected eyes and/or protect the contralateral eye from vision loss. One such SOCS-sequestering small synthetic peptide is pJAK2[1001–1013] (LPQDKEYYKVKEP), which includes the phosphorylated activation loop of JAK2 (44, 268) and antagonizes both SOCS1 and SOCS3. This peptide has shown efficacy against HSV-1 infection in keratinocytes (166) and protects against lethal doses of vaccinia virus, encephalomyocarditis virus, and influenza A virus in mice (269, 270). Because SOCS1 and SOCS3 dampen the ability of cytokines to propagate effective signals within their target cells, inhibition of SOCS1 and/or SOCS3 coupled with immunotherapy treatments such as antiviral IFNs (271) could improve the efficacy of such treatments.

It remains a possibility that the immunosuppressive effect of SOCS1 and/or SOCS3 may play a protective role against a potential immunopathology of experimental MCMV retinitis or AIDS-related HCMV retinitis. If overexpression of SOCS1 and/or SOCS3 reduces retinitis severity, SOCS1 and/or SOCS3 mimetic peptides or overexpression treatment strategies could be efficacious against this disease, as with experimental autoimmune uveitis (EAU) (272, 273). This seems to be the case for HSV-1 infection in the eye, where the role of SOCS1 during HSV-1 infection appears to be protective despite in vitro HSV-1 infection stimulating SOCS1 and SOCS3 very early to increase viral load and cytopathology in different cell types (166, 175). In transgenic rats overexpressing SOCS1 in the retina, however, intraocular HSV-1 (McKrae strain) infection is reduced or delayed compared with wild type rats (274). These SOCS1-overexpressing rats bred to a Lewis strain background also display reduced severity during interphotoreceptor retinoid binding protein (IRBP) antigen-induced (retina-specific) EAU (275). In a mouse model of IRBP antigen-induced EAU, treatment with the cell-penetrating SOCS1-KIR-derived peptide (272, 273) reduces severity of disease. EAU is also less severe in mice containing a conditional SOCS3 knockout in CD4⁺ T-cells (276). The anti-inflammatory role of SOCS1 and/or SOCS3 functioning with cell-type-specificity within the complexity of the eye may therefore protect the precious cells of the retina during immunopathologies such as intraocular HSV-1 infection or autoimmune uveitis. Further studies utilizing knockdown or overexpression of SOCS1 or SOCS3 would elucidate this possibility for experimental MCMV retinitis and/or AIDS-related HCMV retinitis.

CONCLUDING REMARKS

Host manipulation strategies among herpesviruses, diverse and redundant, share many similarities, such as stimulation of host SOCS1 and/or SOCS3. The virologic, immunologic, and pathologic effects of SOCS1 or SOCS3 stimulation during herpesvirus infection frequently depend on cell type, virus strain, and host or host organ system. Such parameters reflect the complexities of the diverse cells and organ systems directly or indirectly involved with herpesvirus infection, disease, and latency. Although it remains unclear whether viral stimulation of SOCS1 and/or SOCS3 is protective or pathogenic in the

eye during AIDS-related cytomegalovirus retinitis, these host proteins may yet prove useful therapeutic targets for treatment or prevention of this sight-threatening disease, as well as other disease of herpesvirus etiology.

AUTHOR CONTRIBUTIONS

CA composed and RD conceptualized this review. Both authors contributed to manuscript revision and approved the submitted version.

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Bovine Herpesvirus 1 Counteracts Immune Responses and Immune-Surveillance to Enhance Pathogenesis and Virus Transmission

Clinton Jones*

Department of Veterinary Pathobiology, Center for Veterinary Health Sciences, Oklahoma State University, Stillwater, OK, United States

Infection of cattle by bovine herpesvirus 1 (BoHV-1) can culminate in upper respiratory tract disorders, conjunctivitis, or genital disorders. Infection also consistently leads to transient immune-suppression. BoHV-1 is the number one infectious agent in cattle that is associated with abortions in cattle. BoHV-1, as other α -herpesvirinae subfamily members, establishes latency in sensory neurons. Stressful stimuli, mimicked by the synthetic corticosteroid dexamethasone, consistently induce reactivation from latency in latently infected calves and rabbits. Increased corticosteroid levels due to stress have a two-pronged effect on reactivation from latency by: (1) directly stimulating viral gene expression and replication, and (2) impairing antiviral immune responses, thus enhancing virus spread and transmission. BoHV-1 encodes several proteins, bICP0, bICP27, gG, UL49.5, and VP8, which interfere with key antiviral innate immune responses in the absence of other viral genes. Furthermore, the ability of BoHV-1 to infect lymphocytes and induce apoptosis, in particular CD4+ T cells, has negative impacts on immune responses during acute infection. BoHV-1 induced immune-suppression can initiate the poly-microbial disorder known as bovine respiratory disease complex, which costs the US cattle industry more than one billion dollars annually. Furthermore, interfering with antiviral responses may promote viral spread to ovaries and the developing fetus, thus enhancing reproductive issues associated with BoHV-1 infection of cows or pregnant cows. The focus of this review is to describe the known mechanisms, direct and indirect, by which BoHV-1 interferes with antiviral immune responses during the course of infection.

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*Correspondence:

Clinton Jones clint.jones10@okstate.edu

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BOHV-1 IS AN IMPORTANT VIRAL PATHOGEN

Bovine herpesvirus 1 (BoHV-1) is an α -herpesvirinae subfamily member that causes significant economical losses to the cattle industry (1). Three well-defined subtypes exist, BoHV-1.1, BoHV-1.2a, and BoHV-1.2b (2b) (2). Subtype 1 virus isolates are prevalent in Europe, North America, and South America: these subtypes are frequently detected in cattle suffering from infectious bovine rhinotracheitis (IBR) and the respiratory tract of aborted fetuses. Subtype 2a strains are prevalent in Brazil and are associated with respiratory and genital tract infections, including IBR, infectious pustular vulvovaginitis (IPV), balanopostitis (IPV), and abortions (3). Subtype 2b strains, which are

frequently isolated in Australia or Europe (4), are associated with respiratory disease and IPV/IPB, but not abortion (3, 5). The seroprevelance of BoHV-1 ranges from 14 to 90% depending on the age of cattle and geographical location (6, 7). Serological testing and removal of infected animals has eliminated BoHV-1 from Denmark, Switzerland, and Austria (8).

BoHV-1 is the most frequently diagnosed cause of viral abortion in North American cattle (9). Exposure of a susceptible herd to BoHV-1 can result in abortion storms ranging from 25 to 60% of cows undergoing abortion. Commercially available modified live vaccines also induce abortions in pregnant cows. Furthermore, several studies concluded that naïve heifers vaccinated with an inactivated BoHV-1 vaccine are more likely to have a normal estrous cycle and significantly higher pregnancy rates relative to heifers vaccinated with a modified live (MLV) vaccine (9–13).

The incubation period for the genital forms of BoHV-1 is 2–6 day and initial clinical signs are frequent urination and a mild vaginal infection (14). It is also common to observe swollen vulva or small papules followed by erosions and ulcers on the mucosal surface. In bulls, similar lesions occur on the penis and prepuce. If secondary bacterial infections occur, inflammation of the uterus and transient infertility with purulent vaginal discharge occurs for several weeks. BoHV-1 infection, virulent field strains or modified live vaccines, of sero-negative heifers can target the ovary and corpus luteum during estrus and early in gestation (9).

Bovine respiratory disease complex (BRDC), a poly-microbial disease initiated by stress and/or virus infection, is the most economically important disease that affects beef and dairy cattle. Annual BRDC losses in the U.S. are \sim \$1 billion (15–18). A gram negative bacterium, Mannheimia haemolytica (MH), exists in the upper respiratory tract of healthy ruminants (19, 20). Following stressful stimuli or co-infections with other viruses (21), this commensal relationship is disrupted and MH becomes the predominant organism that causes life threatening bronchopneumonia in many BRDC cases (22-25). BoHV-1 infection frequently causes upper respiratory tract disease (26, 27), high fever, conjunctivitis, and erodes mucosal surfaces of the upper respiratory tract. Consequently, colonization of MH occurs in the lower respiratory tract (22, 23, 25), thus enhancing interactions between the MH leukotoxin, bovine peripheral blood mononuclear cells, and neutrophils (28, 29). Co-infection of calves with BoHV-1 and MH consistently leads to pneumonia (30). Finally, a BoHV-1 protein that is required for virus entry was identified as a significant BRDC susceptibility gene in Holsteins (31) confirming BoHV-1 is an important BRDC cofactor.

THE BOHV-1 LATENCY-REACTIVATION CYCLE IS IMPORTANT FOR VIRUS TRANSMISSION

Acute Infection Leads to High Levels of Virus Shedding

Acute BoHV-1 infection of cattle is initiated on mucosal surfaces and results in high levels of programmed cell death (32, 33). Acute infection leads to high levels of virus production and

secretion in ocular, oral, nasal, or genital cavities for 7-10 days after infection. BoHV-1 gene expression during productive infection is operationally divided into three distinct phases: immediate early (IE), early (E), or late (L) (32, 33). IE gene expression is stimulated by VP16, a tegument protein (34, 35). Thus, IE mRNA expression does not require de novo protein synthesis. Two IE transcription units exist: IE transcription unit 1 (IEtu1) and IEtu2. IE transcription unit 1 (IEtu1) encodes two transcriptional regulatory proteins, bICP0 and bICP4, because a single IE transcript is differentially spliced and then translated into bICP0 or bICP4 (36-38). The bICP0 protein is also translated from an E mRNA (E2.6) because a separate E promoter drives expression of the bICP0 E transcript (36-39). The bICP0 protein has similar properties as HSV-1 encoded ICP0 (40), including a RING finger that is crucial for stimulating viral promoters and productive infection (41, 42). bICP4 is likely to possess similar functions as the HSV-1 encoded ICP4. bICP4 autoregulates the IEtu1 promoter, but activates the bICP0 E promoter.

E gene expression requires *de novo* protein expression, including bICP0 and bICP4, which transactivate E viral promoters. In general, the E proteins encode proteins that promote DNA synthesis. Example of early viral proteins include the DNA polymerase, thymidine kinase, small and large subunits of the ribonucleotide reductase, dUTPase, and origin binding protein. In general, the E proteins are non-structural.

The L genes are divided into two classes: Gamma-1 and Gamma-2 genes. Transcription of Gamma-1 genes requires *de novo* protein synthesis, including bICP0 and bICP4, but does not require viral DNA replication. Transcription of Gamma-2 genes requires *de novo* protein synthesis, including bICP0 and bICP4, and abundant expression requires viral DNA replication. In general, L proteins encode structural proteins and their synthesis culminates in virion assembly and release.

Summary of Latency-Reactivation Cycle

Viral particles enter the peripheral nervous system via cell-cell spread. If infection is initiated within the oral, nasal, or ocular cavity, the primary site for latency is sensory neurons in trigeminal ganglia (TG). Viral gene expression (43) and infectious virus (44) are detected in TG from 2 to 6 days after infection. Lytic gene expression is then extinguished, and surviving infected neurons harbor viral genomes (establishment of latency).

Abundant expression of the viral encoded latency related (LR) gene occurs in latently infected neurons, but infectious virus is not readily detected (maintenance of latency) (32, 33, 45–48). LR-RNA overlaps the bICP0 gene (49, 50), has two open reading frames (ORF1 and ORF2), two reading frames lacking an initiating ATG, and encodes two micro-RNAs. A LR mutant virus strain with three stop codons at the N-terminus of ORF2 has reduced virus shedding from the eye, TG, or tonsils of infected calves (44, 51, 52). LR-encoded proteins are expressed late during productive infection when infected with wild-type (wt) or LR-rescued virus, but have reduced or no expression after infection with the LR mutant virus (53, 54). Wt BoHV-1, but not the LR mutant virus, reactivates from latency (44).

The anti-apoptosis activity of ORF2 (41, 55–57) and the micro-RNAs, which interfere with bICP0 expression (58) regulate the latency-reactivation cycle.

The synthetic corticosteroid dexamethasone (DEX) initiates reactivation from latency in latently infected calves or rabbits 100% of the time (27, 32, 33, 44, 47, 59). Within 6h after latently infected calves are treated with DEX, viral regulatory proteins (ICP0 and VP16) (60, 61) and lytic cycle viral RNA expression are detected in TG neurons (62, 63). Within 3 h after DEX treatment, 11 cellular genes are induced more than 10-fold in TG (64). Pentraxin 3, a regulator of innate immunity and neuro-degeneration, is stimulated more than 30-fold at 3 or 6 h after DEX treatment. Two transcription factors, promyelocytic leukemia zinc finger (PLZF) and Slug are induced more than 15-fold 3 h after DEX treatment, which can enhance productive infection. Additional DEX induced transcription factors, SPDEF (Sam-pointed domain containing Ets transcription factor), Krüppel-like transcription factor 15 (KLF15), KLF4, KLF6, and GATA6, stimulate productive infection and certain key viral promoters. The finding that four KLF family members are stimulated during DEX induced reactivation from latency is intriguing because KLF family members resemble the Sp1 transcription factor family and both family of transcription factors interact with GC rich motifs, reviewed in Bieker (65) and Kaczynski et al. (66). The BoHV-1 genome is GC rich and many viral promoters contain Sp1 consensus binding sites and other GC rich motifs suggesting specific KLF transcription factors bind to viral sequences and stimulate viral transcription during early stages of reactivation from latency.

The IEtu1 promoter that drives bICP0 and bICP4 expression is stimulated by DEX and contains two consensus GR binding sites that are bound by the activated GR (67, 68). The GR and KLF15 are frequently expressed in the same TG neuron during reactivation and cooperatively stimulate productive infection and IEtu1 promoter activity. A host cellular factor 1 (HCF-1), which forms a complex with VP16 and Oct1 to bind to the IE enhancer core via the TAATGARAT motif, is important for GR mediated activation of the IEtu1 promoter suggesting glucocorticoid induction of viral reactivation may proceed via an HCF-1-GR mechanism in the absence of the viral IE activator VP16 (69). Stress-mediated activation of key viral promoters is predicted to be a very early event during reactivation from latency; then viral transactivators activate all other viral genes and virus production occurs. Hence, stress has a two-pronged effect on reactivation from latency by directly activating viral gene expression and indirectly enhancing viral spread via immunosuppression (70–72).

IMMUNE RESPONSE TO BOHV-1 FOLLOWING ACUTE INFECTION

Cattle acutely infected with BoHV-1 develop an innate immune response (73–76); however, efficient virus replication and spread occurs. For example, virus neutralizing antibodies are detected after acute infection that recognize envelope glycoproteins, including gB, gC, gD, and gH (77, 78). Cytotoxic T cell responses

to viral glycoproteins occur in cattle following infection (79–81). Infection of cultured cells also induces inflammasome formation (82), consistent with inflammation in the nasal cavity and upper respiratory tract during acute infection.

Although the host immune response clears virus after acute infection, viral infection impairs immune-recognition on several levels impairs: (1) cell-mediated immunity (83–86), (2) CD8+ T cell recognition of infected cells (68, 87–89), (3) CD4+ T cell functions because BoHV-1 infect these cells and rapidly inducing apoptosis after viral entry (90, 91), and (4) interferon responses (92–95). The known viral genes that antagonize immune responses are discussed below (see **Figure 1** for a schematic that summarizes how viral genes impair immune responses).

VIRAL PROTEINS INTERFERE WITH INNATE IMMUNE RESPONSES AND IMMUNE-SURVEILLANCE

The amino-terminus of the bICP0 protein contains transcriptional activation domains, a nuclear localization signal (NLS) necessary for efficient transcriptional activation (99), and a C₃HC₄ zinc RING finger that is conserved in all ICP0 proteins (100, 101). Point mutations within the C₃HC₄ zinc RING finger domain of bICP0 interfere with transactivation of a simple viral promoter (99), stimulation of productive infection (41, 102), and reduces IFN-β promoter activity (92–95). bICP0 co-localizes with and disrupts the anti-viral promyelocytic leukemia (PML) protein-containing nuclear domains (41, 101). PML bodies are comprised of numerous proteins, which regulate the cell cycle, apoptosis, senescence, stress, DNA damage, and innate immune responses (103). Many DNA viruses reorganize or dissolve PML bodies, thus increasing viral replication. Interferon treatment increases components of PML bodies, Sp100, and PML for example (104, 105) and PML bodies increase beta-interferon (IFN- β) expression (106).

bICP0 inhibits IFN-β promoter activity in transient transfection studies (92, 94) by reducing IRF3 (interferon regulatory factor 3) protein levels. The RING finger of bICP0 (107) is an E3 ubiquitin ligase suggesting it mediates IRF3 degradation in a proteasome dependent manner. bICP0 also interacts with IRF7 and impairs activation of IFN-β promoter activity, but does not reduce IRF7 protein levels (94). IRF3 and IRF7 are transcription factors that stimulate IFN-β promoter activity (96-98). IRF3 directly binds several consensus DNA binding sites, including an ISRE (IFN response elements), and can activate IFN-stimulated promoters in the absence of IFN (108, 109). A recent study concluded PML regulates intrinsic and innate immune responses to HSV-1 infection, which is ablated by ICP0 (110). The ability of bICP0 to reduce IFN-β promoter activity correlates with IRF3 degradation, IRF7 interactions, and dissolving PML bodies.

The BoHV-1 bICP27 protein is expressed from an early promoter and based on similarity with the HSV-1 ICP27 is expected to shuttle RNA from the nucleus to the cytoplasm and regulate transcription (111). HSV-1 encoded ICP27 regulates IFN expression (112) by interfering with activation of the stimulator

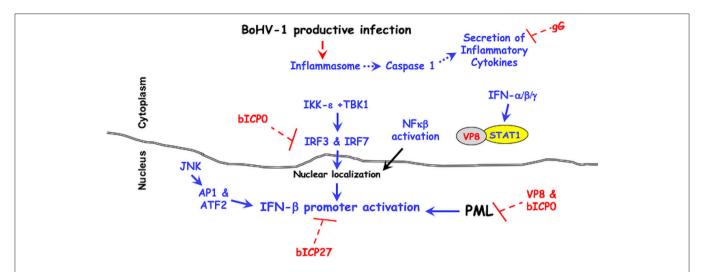


FIGURE 1 | BoHV-1 encoded immune-evasion genes that promote productive infection. Cellular mechanisms leading to innate immune antiviral signaling pathways are denoted in blue. Red lettering denotes viral genes that counteract antiviral signaling pathways. It is well-established that two protein kinases (IKK-ε +TBK1) activate the transcription factors (IRF3 and IRF7), which are required for activating the IFN- β promoter (96–98). The JNK protein kinase (c-Jun N-terminal kinases) activates the AP1 (activating protein 1) and ATF2 (activating transcription factor 2), which are also required for activating the IFN- β promoter (96–98). For further details, see the text.

of interferon genes (STING) by tank binding protein kinase 1 (TBK1) (113). Interestingly, bICP27 reduces bovine IFN- β 1 and IFN- β 3 promoter activity in transfected cells (114). Bos Taurus encodes three functional IFN- β genes; all have anti-viral activity but each gene contains a unique promoter (115, 116).

Glycoprotein G (gG) promotes cell to cell spread (117) and maintains adherence of infected cells (118). gG is a unique viral glycoprotein because it can exist in three isoforms: a full-length membrane-bound form, a smaller membrane-bound form, and a secreted form. gG interferes with chemokine binding to their specific receptors and glycosaminoglycans (119). Although it is not known what role gG plays during acute infection of calves, the ability of chemokines to control the migratory patterns and positioning of immune cells (120) would likely be altered by gG.

The BoHV-1 UL49.5 ORF, also known as glycoprotein N (gN), is a 96 amino acid protein (121). The BoHV-1 and pseudorabies virus UL49.5 proteins interfere with processing of the transporter-associated antigen processing (TAP)-mediated transport of cytosolic peptides into the endoplasmic reticulum because UL49.5 renders the TAP complex susceptible to proteolytic degradation (122, 123). Peptide transport by TAP is crucial for MHC class I antigen presentation and recognition of infected cells by CD8⁺ T cells (122, 124–126). Infection of calves with a UL49.5 BoHV-1 mutant leads to increased levels of virus neutralizing antibody and cellular immune responses when compared to the parental wild-type virus (127).

VP8, the most abundant tegument protein in the virion, enhances growth in cultured cells and is required for pathogenesis in calves (128). VP8 interacts with DDB1 (DNA damaging-binding protein 1) that is associated with a E3 ubiquitin ligase complex (129), and remodels PML nuclear bodies (130). Recent studies demonstrated VP8 interacts with STAT1 (Signal transducer and activator of transcription 1) and prevents STAT1 from entering the nucleus (131). Stat1 is bound to the IFN-γ receptor and upon IFN-γ binding to

its receptor (Jak1 and Jak2) phosphorylates specific tyrosine residues on STAT1. STAT1 subsequently enters the nucleus and stimulates GAS (IFN- γ activated sequences) setting off a second wave of IFN- γ (132). Following IFN- α or IFN- β stimulation, STAT1 forms a heterodimer with STAT2 and this heterodimer binds an ISRE element and activates transcription (133). VP8 also interferes with IFN- β signaling activity by reducing an interferon sensitive response element (ISRE) responsive promoter in transfected or infected cells. Thus, VP8 is a potent IFN antagonist that can interfere with host innate immune responses in the absence of *de novo* viral protein synthesis.

CONCLUSIONS/DISCUSSION

BoHV-1 is a very successful pathogen because it encodes several genes that impair intrinsic and innate immune responses throughout productive infection (see **Figure 1**). VP8 is likely the initial anti-viral protein that impairs antiviral IFN responses because high levels of VP8 are present in the tegument of incoming viral particles. bICP0, which is encoded by the IEtu1 promoter, would be an early interferon antagonist. bICP27 via unknown mechanisms interferes with IFN- β promoter activation. Three late proteins (gG, UL49.5, and VP8) would further antagonize immune-recognition. In summary, the presence of viral proteins in the virion and expression of viral proteins throughout productive infection allows for high levels of virus production during acute infection and reactivation from latency in cattle.

AUTHOR CONTRIBUTIONS

The author confirms being the sole contributor of this work and has approved it for publication.

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Subversion of Immune Response by Human Cytomegalovirus

A. Raj Kumar Patro*

Infectious Disease Biology Group, Institute of Life Sciences (ILS), Bhubaneswar, India

Human cytomegalovirus (HCMV) is the most common cause of congenital infections and is an important pathogen in immunocompromised individuals. Despite a robust host immune system, HCMV able to replicate, evade host defenses, establish latency for life. A significant portion of HCMV genome dedicated to encode gene products for modulation of host immune response. Growing number of HCMV gene products are being recognized to play role in immune evasion. Information on viral immune evasion mechanisms by which HCMV persists in host will be useful in devising antiviral intervention strategies and development of new vaccines. This minireview provides a brief overview of immune evasion strategy adapted by HCMV by utilizing its gene products in modulation of host immune response.

Keywords: HCMV (human cytomegalovirus), immune evasion, pathogenesis, superinfection, vaccine

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*Correspondence:

A. Raj Kumar Patro rajkumarpatro@yahoo.com

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INTRODUCTION

The human cytomegalovirus (HCMV) is a ubiquitous β -herpesvirus that establishes lifelong persistent infection following introduction to an immunocompetent host. Primary infection in a healthy individual leads to mild febrile illness, whereas HCMV causes serious complications in immunosuppressed subjects, especially in transplant recipients and in immunocompromised patients (1, 2). Human cytomegalovirus is the most common cause of congenital infections leading to neurodevelopmental sequelae. Each year, 20,000–40,000 children are born with congenital human CMV infection in the US, of which 10–15% develops permanent sequelae including sensorineural hearing loss (3–5). Furthermore, substantial fraction of the asymptomatic children develops late onset hearing loss. In an attempt to reduce these disabilities and loss of life, as well as the associated economic cost, the Institute of Medicine of National Academy of Sciences, USA have ranked the development of HCMV vaccine as a highest priority (6, 7).

Decades of research on cytomegalovirus has provided novel insight in understanding the host immune response and evasion strategies adapted by the virus. HCMV has dedicated more than half of its genome encoding for modulation of host response to infection (8, 9). This mini-review article discusses on current understanding of HCMV gene products in modulation of host immune response with an emphases on the immune evasion by interference in antigen presentation and activation of NK cells, viral strain diversity and superinfection in immune subject.

MODULATION OF IMMUNE RESPONSES BY HCMV GENE PRODUCTS

The virus has co-evolved with its host organism for 200 million years (9, 10). HCMV has a large genome size of 236 kb with unique long (UL) and unique short (US) regions flanked by terminal repeats and internal repeats. The genome has been annotated and encodes 167 gene products, as

well as non-coding RNAs, microRNAs, and with an extensive alternate mRNA splicing. However, recent report suggested that HCMV encode to have more than 750 translated ORFs (11). More than 40 HCMV gene products are recognized to have a role in modulating the host immune response following infection (12, 13). Both the innate and adaptive arms of the immune system play a crucial role in controlling HCMV infection (12, 14). Despite a robust host immune system, HCMV is able to establish latency and once infected the HCMV remains in the host for life. The virus remains latent in the myeloid progenitor cells during its dormant phase; however on stimulation, or when the immune system is suppressed, the virus can once again become active (15). The battle between the host immune system and the virus continues throughout life, with HCMV having evolved multiple mechanisms to evade the host immune response. The divergence of the immune response and incomplete viral control may be attributed to the diversity of immune modulators encoded by HCMV gene products [Figure 1, Table 1]. Many of these gene products are homologs of host genes involved in the immune response.

To eliminate the virus, the host needs to have an effective immune system. After viral infection, host antigen presenting cells must present viral antigen to the immune cells in order to stimulate effector cells to eliminate the virus. However, HCMV has devised strategies to limit this presentation. NK cells are normally responsible for immediate control of viral infections; however, there are number of HCMV gene products that block NK cell mediated recognition. Approximately, there are 12 HCMV gene products, US20, UL16, UL17, UL18, UL40, UL43, UL140, UL83, UL141-UL144, and UL148, known to control NK cell modulation (Table 1). HCMV UL16, UL17, UL40, UL140, and UL142 genes all encode products that downregulate NK cell activity by imitating the host HLA class I. For example, UL40 encodes a canonical ligand for HLA-E and negatively regulates NK cells, which results in down-regulation of activating ligand CD155 (20). Individuals with impaired NK cell function, succumbs to severe herpesvirus infections (31). In addition, HCMV gene products UL18 and UL83 (pp65) encode for an MHC-I homolog, modulate expression of other HCMV genes and inhibit NK cell lysis (12, 20). Furthermore, the HCMV microRNA miR-UL122 acts to suppress host MICB surface expression (13, 20, 29).

As is a common characteristic of herpes viruses, HCMV is able to interfere with the class I MHC molecule involved in antigen presentation to CD8+ T cells. HCMV establishes persistent infection by producing host homologous molecules that prevent recognition and interfere with antigen presentation, subverting the cytotoxic T lymphocytes (CTLs). Viral antigens are normally presented by the MHC class I proteins on the infected cell surface. HCMV gene products obstruct peptide translocation to the ER lumen and stimulate degradation of the MHC class I proteins before they can reach the cell surface. For example, the HCMV US3 gene product degrades the MHC class I heavy chain by interacting with Tapasin and retaining the class I molecule at the site of synthesis, in the ER. In addition, the US2 and US11 gene products relocate the heavy chain of MHC class I into the ER for proteosomal degradation. Similarly,

another gene product of HCMV, US6, prevents peptide loading by inhibiting the binding of ATP to TAP, thereby preventing the transport of peptides through the TAP pore. The combined functions of the HCMV gene products US2, US3, US6, and US11, therefore, lead to peptide transport blockade, retention of MHC class I in the ER and ultimately proteasomal degradation. In addition, the gene product US2 interferes with MHC class II signal transduction by degradation of MHC class II proteins. US2 targets the class II DR and DM α chains for degradation in the cytosol, thereby preventing antigen presentation to CD4+ T lymphocytes (12, 14, 16, 32).

In addition to the above, the HCMV UL83 gene product, pp65 blocks the processing of immediate early-1 in the proteasome by phosphorylation. Besides, the tegument Protein UL82 evades antiviral immunity by inhibiting stimulator of interferon (STING) signaling (21) and may be responsible for induction of latency (15, 22). Recently, Nightingale et al. reported that the HCMV gene product UL145 facilitates degradation of the antiviral factor helicase like transcription factor (HLTF) by recruiting the host Cullin4 E3 ligase complex, and captures Cullin3 to invoke the strategy of immune evasion (27). Additionally, the HCMV late gene product UL111A encodes cmvIL-10, a homolog of human IL-10, which is expressed during viral latency, and causes a state of immune suppression (23). The cytokine Interleukin-10 has an immunosuppressive role on several effector cells of the immune system. The HCMV gene product cmvIL-10 exerts an immunosuppressive effect on the host by modulating the expression of the MHC class I and II molecules and interfering with dendritic cell (DC) function (24). In a murine model of CMV, following productive infection with CMV both *in vitro* and *ex vivo*, the virus reduced the expression of MHC as well as co-stimulation of DC. This eventually led to loss of expression of IL-2 and IL-12 and hindrance of DC differentiation (33-35). A recent report by Wang et al also demonstrated that the HCMV UL148 gene product suppresses co-stimulation and expression of the cell adhesion molecule CD58, endorsing cellular immune defense evasion by impairing NK and T cell activation (28). This work was further supported by HCMV UL148 mediated tropism and immune evasion by unfolded protein response (36). In Rhesus model, Rh159, a homolog of HCMV UL148 involved in retention of distinct set of costimulatory molecules and involved in NK cell evasion (37). HCMV UL148 gene products encode for avoidance of killing of HCMV infected cells from NK cells by down regulating MICA (38).

HCMV possesses a unique challenge, as it is able to superinfect in a subject already infected with the virus, even in the presence of a strong specific immune response. Several studies have demonstrated congenital HCMV infection in offspring of immune mothers because of reinfection with a different strain of virus (39–43). Further, congenital infected infant born to immune mother may develop sequelae similar to infants born to mother with primary infection during pregnancy. It has also been observed that infection with more than one strain of HCMV is common in nature (39, 40, 44). HCMV strain polymorphism could contribute to immune evasion. Since HCMV glycoproteins are highly polymorphic, antibody response to one strain may

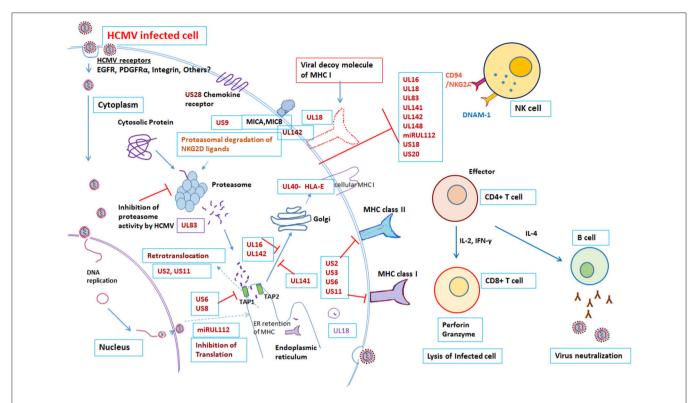


FIGURE 1 | Modulation of Immune response by human cytomegalovirus. Overview of the interactions between HCMV and the immune system. Red "T" bars indicate inhibition. Blue arrows indicate activation. Detail mechanisms explained in the text.

not efficiently neutralize infection with a different strain and this could enable to superinfection (45-47). In addition to interference in antigen presentation, the CMV gene products US2, US3, US6, and US11 encode for human homologs that interfere with the function of CD8+ T cells. This allowed viral replication and super-infection with a different strain of virus in a rhesus macaque model. This was confirmed, by the observation that US2-11 mutant virus, although able to produce infection, was unable to super-infect (17). However, further studies are needed to decipher the detailed mechanisms of the CTL response in contending with the combined action of these HCMV gene products. The large genome size of HCMV enables it to utilize an array of genes for host immune evasion, which allows long-term association and adaption of the virus in the host. In an immunocompetent host, viral latency is critical for its survival. After primary infection, the virus persists for a lifetime regardless of pre-existing immunity. During latency, the viral genome is maintained in the host without active replication and retains the capacity to reactivate in response to activation signals (48). Studies have linked various latency-associated determinants to HCMV latency (15), however, the detailed mechanisms of immune evasion during latency and how the virus persists in the host for life remains elusive. Deciphering these mechanisms could provide clues to allow us to prevent reactivation of this latent virus in congenital and transplant setup. Further, a note of caution is required; HCMV is strictly species specific. Since much of our understanding on cytomegalovirus biology is derived from in vitro cell culture studies and animal models, it is necessary to test these immune evasion functions in the appropriate setting. For instance, the UL18 gene product of HCMV encoding an MHC class I homolog was proposed to block NK cell activity by binding with KIR receptors; however, later studies have found it to enhance killing of infected fibroblasts by NK cells (12).

Further, extensive genetic variability has been observed in clinical isolate of HCMV (4, 40, 49-51), and even within a single host (4, 44, 52-54). High throughput sequencing of HCMV clinical isolates reveals that intrahost HCMV populations were as variable as seen in RNA virus quasispecies (52, 53). Viral strain diversity, differences in culture systems and population heterogeneity, make the generalization of genetic information difficult. In addition, a recent report showed that HCMV seroprevalence is related to a shift in immune phenotype along an age axis (55). This immunotypes varies in younger vs. elder individuals (55-57). In due course of evolution with the host, HCMV has been significant in shaping host immune system (57). HCMV also affects the host in response to infection with other pathogen. In HCMV seropositive children and in aging individuals have negative impact to Influenza; however, in younger individuals HCMV infection enhance immune response to influenza (58). Viral strain diversity could limit effective antiviral function, and the evasion strategy adapted by HCMV further complicates the development of an effective vaccine (45, 59). This underscores the need for large-scale genetic and immunological profiling studies, which could provide

TABLE 1 | HCMV gene products involved in modulation of host immune response.

HCMV Gene Product	Effect on host immune system & mechanism of evasion	Reference(s)
US2, US3, US6, US11	MHC class –I down regulation and impairment of expression; Further reduction in HCMV antigen presentation to CD8+ cells; Evasion of CD8+ T cell Immunity; Superinfection	(16, 17)
JS2, HCMV Immediate Early/ Early	MHC class –II down regulation; Further reduction in HCMV antigen presentation to CD4+ cells	(12, 18)
JS18 and US20	Interfere with B7-H6 surface expression involving endosomal degradation; escapes immune recognition by NK cells	(19)
JL18	Expression of human MHC class –I homolog; downregulate CTLs; Ligand decoy for NK receptors	(14, 16)
JL16	Regulation of NK cell ligand NKG2D; NK cells function impairment	(18)
JL40	NK cell evasion; HLA-E Over expression	(20)
JL83 (pp65)	IE-I sequestration; inhibit proteasome processing; Reduce action of NKp30; hinders antiviral gene expression	(21)
E2 (immediate early) gene product	Overexpression of anti-apoptotic FLIP protein	(16, 18)
JS28 (viral GPCR)	Targeting chemokine receptor; reduced inflammatory response	(12)
JL82 (pp71)	The tegument protein binds with stimulator of interferon genes to inhibit antiviral response.	(21, 22)
JL111A	HCMV encodes cmv IL-10, an homolog of human IL-10, thereby modulate immune system results in immune suppression	(23, 24)
JL141	CD155 down regulation	(14)
JL142	Inhibition of MICA	(12, 18)
JL36	Inhibition of pro-apoptotic recruitment of pro-caspase 8 to the DISC Decline in phagocytic activity (infected APCs)	(12)
JL37	Inhibition of pro-apoptotic Bcl-2 family Bak and Bax protein Apoptosis inhibition	(18)
JL97	Along with HCMV pp65 mediated immune evasion; Protein Kinase UL97 Forms a Complex with the Tegument Phosphoprotein pp65	(14, 25)
E gene products	Induction of TGF- β : HCMV induce transcription & release of TGF- β	(26)
JL138	Latency associated; Sensitizes cells to TNF- α signaling	(15)
JL141- UL144	Encodes for homolog of TNFR; This HCMV encoded gene product inhibits cell surface expression of CD155 and CD112 (NK cell activating ligands) and the death receptor for the TNF family ligand TRAIL	(8, 14)
JL145	degradation of helicase like transcription factor- (HLTF) by recruitment of Cullin4/DDB ligase complex	(27)
JL146	Chemokine; role in inflammatory response	(14)
JL148	Suppression of CD58; Potent Modulator of CTL Function	(28)
miR-UL112	Escape from NK cell by down regulation of MICB; recognition from T cells by NKG2D decreased	(29, 30)

List of HCMV gene products involved in immune evasion.

[US, Unique short; UL, Unique long; miR, Micro RNA; MHC, major histocompatibility complex, TAP, Transporter associated with antigen processing; NK cells, natural killer cells; CTL, cytotoxic T cell I; LIR-1, Leukocyte Immunoglobulin-like receptor 1; HLA, human leukocyte antigen; IE, Immediate early; FLIP, FLICE-inhibitory protein; FLICE, cysteine proteases (caspase-8/MACH/Mch5), CRP- C-reactive protein, MICA, MHC class I polypeptide-related sequence A; un, unknown; DISC, death-inducing signaling complex; APC, Antigen presenting cells; Bak- BCL2 Antagonist/Killer, Bax- BCL2 Associated X, Bcl-2- B-cell lymphoma 2; pp65, phospho protein 65; TGF-β, Transforming growth factor -β; TNFR, tumor necrosis factor receptor; Cullin4/DDB, Cullin-4A-DNA Damage-binding Protein; CD, cluster of differentiation].

a decisive correlation on the nature of protective immune responses (56, 59–61).

HCMV has devised multiple strategies to interfere with antigen presentations and escape from CTL response, but this does not abrogate with the development of CTL response by host. This underscores the critical role of CD8+ T cells in HCMV infected cells as targets for immune clearance. Studies from adaptive transfer of HCMV specific CTL, in bone marrow transplant subjects, provide protection from HCMV disease (62). The complex interaction between the HCMV immune-evasins and host factors contributes to the levels of viral persistence in host (63). Information on viral

immune evasion mechanisms by which HCMV persists in host will be useful in devising antiviral intervention strategies and development of new vaccines. Deletion of immune evasions could be a novel strategy for virus attenuation for vaccine candidate without compromising CD8T cell response (64). Hansen et al reported that Simian immunodeficiency virus (SIV) protein expressing rhesus cytomegalovirus vector elicits SIV specific CD8+ T cells which recognizes unusual, diverse epitopes and results in immune clearance (65, 66). Thus, CMV vectors, genetically altered for diverse CD8+ T cell response could be useful for effective prophylactic and therapeutic vaccination (9, 65–68). Further, this could be useful in ultimately

designing an effective vaccine that could protect primary as well as reinfections.

CONCLUSIONS

In conclusion, human cytomegalovirus is a master of disguise. HCMV has evolved mechanisms to replicate and evade the host immune system by targeting the host cell machinery. Information on the host cell receptor targeted by this virus and the mechanisms utilized to operate cellular processes and evade the host immune system will provide clues to viral pathogenesis. An increasing number of HCMV gene products have been reported to play roles in immune evasion. These gene products sophistically orchestrate to modulate the host immune system, thereby allowing persistent and latent infection and life-long existence in the host. Information on viral escape mechanisms will be useful in rational design of antiviral drugs and should bring us one step closer to development of an effective vaccine.

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AUTHOR CONTRIBUTIONS

The author confirms being the sole contributor of this work and has approved it for publication.

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