# Chapter 12 Kaposi's Sarcoma-Associated Herpesvirus: Pathogenesis and Host Immune Response

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# Introduction

Kaposi's sarcoma-associated herpesvirus (KSHV) (also known as human herpesvirus 8 or HHV-8) was first discovered by Drs. Yuan Chang and Patrick Moore in 1994 in Kaposi sarcoma lesions from HIV-infected individuals [1]. Since its discovery, KSHV has also been linked to two lymphoproliferative diseases, primary effusion lymphoma (PEL) and multicentric Castleman's disease (MCD) [2, 3]. More recently, KSHV has been found to be associated with an inflammatory condition called KSHV-inflammatory cytokine syndrome (KICS) [4, 5].

Kaposi sarcoma (KS) lesions are highly angiogenic and the skin lesions are visibly red due to the high degree of vascularization. The vessels in KS lesions are prone to fluid leakage and extravasation of red blood cells. KS progresses through different stages that include patch, plaque, and nodular. The lesions contain inflammatory cells and slit-like neovascular spaces. The elongated, spindle-shaped cells in these lesions are thought to be endothelial in origin. These cells are all infected with KSHV and are thought to be the drivers of KS pathogenesis. Spindle cells display many markers of the endothelial cell lineage, including factor XIII, CD31, CD34, and CD36 [6]. Interestingly, KSHV infection of vascular and lymphatic endothelial cells reprograms their transcriptional profile towards a lymphatic or vascular lineage, respectively, thus giving rise to pleiotropic marker expression in these spindle cells [7–10].

Kaposi sarcoma is named after the Hungarian dermatologist, Moritz Kaposi, who identified these lesions as "Idiopathisches multiples Pigmentsarkom der Haut," or idiopathic multiple pigmented sarcoma of the skin [11]. The KS lesions seen by

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Kaposi were found on elderly Mediterranean men and are known as "classic KS." KS is common in certain geographical regions such as in Mediterranean countries and parts of Africa [12, 13]. Before the advent of HIV, KS was rare; however, following the AIDS epidemic, KS was identified as one of the most common AIDS-defining cancers. Currently, there are thought to be four classes of KS:

- 1. Classic KS
- 2. Endemic or African KS
- 3. Iatrogenic KS associated with immunosuppressive therapies in transplant patients
- 4. Epidemic or AIDS-related KS

In contrast, PEL is an expansion of B cells in the pericardial, pleural, and peritoneal spaces, although PEL can also occur in solid organs. Unlike KS, the KSHVinfected B cells in PEL have a clonal origin [14, 15]. Each PEL cell contains many copies of the KSHV episome. Another B cell disorder linked to KSHV infection is the plasmablastic variant of MCD [16]. In AIDS patients, MCD can manifest as an aggressive malignancy that is almost always associated with KSHV infection [3]. The most newly recognized disease associated with KSHV is KICS. KICS is similar to KSHV-MCD in that KICS patients have elevated viral interleukin-6 (vIL-6), human IL-6, and IL-10 levels and high KSHV viral titer compared to KS patients. Unlike KSHV-MCD, KICS patients do not suffer from proliferating plasmacytoid B lymphocytes in the lymph node [4, 5].

# Virion Structure and Viral Genome

KSHV virions comprise an electron-dense nucleocapsid that is surrounded by a lipid bilayer envelope. A proteinaceous layer called the tegument, which exists between the capsid and the envelope, contains multiple proteins and viral RNA transcripts [17–19]. The virion contains multiple glycoproteins including gB, gH, gM, gL, gN, ORF68, and K8.1 [17]. KSHV has an icosahedral capsid that is symmetric (T=16) with 20 triangular faces [20–22]. The capsid is made up of six proteins, including the major capsid protein (MCP, ORF25), a heterotrimer triplex protein containing one copy of ORF62 and two copies of ORF26, the small capsid protein (ORF65), scaffold protein (ORF17.5), and protease (ORF17). The capsomers comprise hexamers and pentamers of MCP. Each capsid contains 150 hexons and 12 pentons and these are interconnected by 320 copies of the triplex heterotrimer [21, 23–25]. The viral genomic DNA is linear [26] and is located inside the capsid.

Sequencing of the KSHV genome revealed its similarity to other members of the gammaherpesvirus family. The gammaherpesviruses are divided into two groups: the  $\gamma$ 1 or lymphocryptoviruses, which includes Epstein–Barr virus (EBV), and the  $\gamma$ 2 or rhadinoviruses, which includes KSHV [27, 28]. The genome is 165–170 kb

long with 140 kb of unique coding sequence flanked on either side by repetitive terminal repeat sequences [27]. The KSHV ORFs are numbered consecutively from left (ORF 1) to right (ORF 75). ORFs unique to KSHV are denoted by a "K" designation [28, 29]. The KSHV genome also encodes many noncoding RNAs, including microRNAs [29–32] and other noncoding RNAs, e.g., PAN [33–36].

# Viral Entry

KSHV encodes three glycoproteins, gB, gH, and gL, which can mediate membrane fusion [37]. KSHV is thought to bind to the cell via a number of different cellular receptor proteins. KSHV gB, gH, ORF4, and gpK8.1A bind heparin sulfate [38-42]. It is likely that heparin sulfate binding allows for a concentration of virions on the cell membrane, which may help to increase the concentration of viruses that can interact with cell surface receptors. KSHV gB contains an integrin-binding RGD (Arg-Gly-Asp) motif that enables virus entry [38, 39, 43] by interacting with  $\alpha V\beta 3$ and  $\alpha V\beta 5$  integrins on cells [44]. In activated B cells, dendritic cells (DCs), and macrophages, dendritic cell-specific intercellular adhesion molecule 3 (ICAM-3)grabbing non-integrin (DC-SIGN; CD209) can also bind KSHV [45, 46]. Collectively, heparan sulfate, integrins, and DC-SIGN are all thought to interact with KSHV and contribute to binding of the virus to the cell. xCT, a 12-transmembrane glutamate/cysteine exchange transporter protein, can also serve as a receptor [47]. xCT is part of the CD98 (4F2 antigen) complex that contains a glycosylated heavy chain and several 45-kDa light chains. Ephrin receptor tyrosine kinase A2 (EphA2) has also been identified as a cellular receptor. Binding of EphA2 to the viral glycoprotein dimeric complex gH-gL results in the phosphorylation and endocytosis of EphA2 in epithelial and endothelial cells [48]. EphA2 has also been shown to be a master regulator of macropinocytosis in human dermal microvascular endothelial cells by facilitating the recruitment of various signaling molecules to the entry site and by regulating the activation of KSHV-induced signaling molecules [49]. KSHV primarily enters cells by clathrin-mediated endocytosis [50-53] (Fig. 12.1), although it can also enter through macropinocytosis [52]. Virus binding to the cell initiates a host cell signaling cascade that allows the virus to modulate the cellular microenvironment to its advantage. Binding of KSHV to cell surface receptors such as integrins stimulates the phosphorylation and activation of focal adhesion kinase (FAK), which in turn activates other proteins including PI3K, Src, Rho GTPases, and Diaphanous 2 [40, 43, 51, 54–63]. Activation of PI3K and Rho GTPase causes rearrangement of the cytoskeleton and formation of lamellipodia (Rac), stress fibers (RhoA), and filopodia (Cdc42). Priming of the microtubules enables the delivery of viral capsids to the nuclear membrane [57, 61]. KSHV also activates the mitogenactivated protein kinase (MAPK) pathway, specifically ERK1/2, as well as the NFkB pathway; both of these pathways help initiate viral gene expression in infected cells [40, 56, 58, 62, 64].



**Fig. 12.1** Viral entry. The various stages of KSHV entry are depicted. The virion binds various cellular receptors and primarily enters the cell by clathrin-mediated endocytosis. Signaling initiated by virion binding modulates the cytoskeleton to facilitate delivery of the virion to the nucleus. After the KSHV genome enters the nucleus, the decision to enter the latent or lytic phase of the viral lifecycle occurs

# **Cellular Targets of Infection and the Viral Lifecycle**

In vitro, KSHV can infect a wide range of cell types including fibroblasts, keratinocytes, B lymphocytes, monocytes, plasmacytoid dendritic cells (pDCs), endothelial cells, and epithelial cells [45–47, 50, 64–75]. However, in vivo, KSHV is known to infect B cells and endothelial cells [76–78], epithelial cells [79–81], and monocytes [82].

KSHV has two phases to its lifecycle: latency and viral lytic replication (Fig. 12.2). During latency, the viral genome exists as a circular episome that is tethered to the host chromosomes via a viral protein named latency-associated nuclear antigen (LANA). Viral gene expression is restricted and only a small number of viral genes are expressed. In contrast, during lytic replication nearly all viral genes are expressed, which allows for amplification of viral genomes and the subsequent assembly, egress, and dissemination of progeny virions. The lytic switch protein, ORF50 or Replication and Transcription Activator (RTA), is the master switch that controls KSHV reactivation [83, 84]. In cell culture, chemicals such as sodium butyrate, histone deacetylase



inhibitors, and phorbol esters reactivate the virus [85]. Other triggers include cytokines such as oncostatin M, interferon- $\gamma$ , and hepatocyte growth factor. Hypoxia, or oxygen deprivation, as well as terminal differentiation of B cells induced by X-box-binding protein 1 (XBP-1) expression can also reactivate KSHV [86–89]. Finally, activation of toll-like receptors (TLRs) 7 and 8 by microbes can induce KSHV reactivation from latently infected cells [90]. Host cellular factors such as the tousled-like kinases (TLKs) can also control KSHV reactivation from latency. Depletion of TLKs in KSHV latently infected cells results in viral reactivation [91]. Chromatin organizing factors such as cohesins have a regulatory role in maintaining KSHV latency by binding and repressing transcription of the immediate early gene cluster. Depletion of cohesions in PEL cells results in RTA expression and viral replication [92]. Spontaneous reactivation from latency occurs both in cell culture and in vivo and the primary site of lytic virus replication in humans is the oropharynx [73, 93–96]. Clinical data demonstrates that shedding of virus during periodic bouts of lytic reactivation is intermittent and usually asymptomatic [94, 97].

#### Viral Latency

The KSHV latent genes are encoded by a major latency locus that is transcribed in all latent KSHV-infected cells (Fig. 12.3). This locus encodes LANA, viral cyclin (v-cyclin), v-FLICE-inhibitory protein (v-FLIP), and the kaposins (K12). The LANA, v-cyclin and v-FLIP genes are under the control of the LANA promoter [98–100]. The three kaposin transcripts (A, B, C) are driven by the kaposin promoter, which can also generate a bicistronic transcript for v-cyclin and v-FLIP [101]. Twelve virally encoded pre-miRNAs are also transcribed using this promoter [30–32, 102, 103]. All of these latent genes are expressed in KS and PEL cells [104, 105]. Additionally, PEL cells express v-IRF3 (also called LANA-2) during latency [106].



**Fig. 12.3** The latency locus of KSHV. The latent genes include Orf73/LANA, Orf72/vCyclin, Orf71/vFLIP, and Kaposin/K12. The KSHV latency locus also expresses a number of viral premicroRNAs that are processed into 18 mature microRNAs

# LANA

Latency-associated nuclear antigen (LANA), the major latency protein, plays a critical role in latent viral replication. LANA simultaneously binds the viral episome (via the latent origin of replication in the terminal repeats) and cellular histones H1, H2A, and H2B [107–114], thus tethering the episome to host chromosomes. Latent viral DNA replication is performed by the host's DNA polymerase. Therefore, during cell division, viral genomic DNA undergoes replication and segregation concurrently with host chromosomes, allowing distribution of viral genomes to daughter cells [113–115].

Aside from its function in replication and maintenance of the KSHV latent genome, LANA promotes tumorigensis by altering cellular pathways involved in cell proliferation and survival. LANA extends the life span of endothelial cells [116]. LANA transgenic mice display splenic follicular hyperplasia and enhanced germinal center formation [117], B cell lymphomas, and an increased response to antigen stimulation [118]. LANA binds p53, and cells that express LANA have reduced activation of p53-dependent reporter genes [119]. However, most PEL respond to p53-activating DNA damaging agents [120]. LANA also binds the tumor suppressor Rb resulting in functional inactivation of Rb and increased E2F-dependent reporter gene activation [121].

LANA also interacts with GSK-3 $\beta$ , which phosphorylates and inactivates  $\beta$ -catenin through ubiquitin-mediated proteosomal degradation [122]. LANA's binding to GSK-3 $\beta$  induces its relocation to the nucleus, which allows  $\beta$ -catenin to accumulate in the cytoplasm. This allows for the transcription factor LEF to move into the nucleus to activate expression of cyclin D and c-myc [122]. LANA can also increase c-Myc protein stability [123, 124]. Moreover, LANA contributes to tumorigenesis by inducing chromosome instability. LANA interacts with the spindle checkpoint protein, Bub1, and dysregulates its activity leading to irregular chromosome replication [125].

As a nuclear protein, LANA has transcriptional effects on the Rb/E2F pathway [126–128]. Although LANA can activate transcription of certain genes [126–128], LANA is predominantly a repressor of transcription [111, 129, 130]. LANA interacts

with RBP-J $\kappa$  (also called CBF-1 or CSL) and is targeted to RBP-J $\kappa$  sites in the ORF50 promoter to repress RTA transcription [131]. LANA also associates with the cellular transcription repressors Krüppel-associated box domain-associated protein-1 (KAP1) and Sin3A to repress the lytic promoter RTA during primary KSHV infection, thereby promoting the establishment of latency [132, 133].

# vCyclin

vCyclin shows homology to cellular cyclin D. vCyclin binds and activates cdk6 in a similar fashion as its cellular homolog [134]. vCyclin can also induce phosphorylation of histone H1, p27, nucleophosmin (NPM), Id-2, and cdc25a [135–137]. vCyclin promotes S-phase entry and can overcome Rb-mediated cell cycle arrest mediated by cdk inhibitors [138]. Phosphorylation of p27 by vCyclin-cdk6 targets p27 for degradation thereby inhibiting the regulation of cdk6 by p27 [139, 140]. vCyclin also opposes senescence and G1-arrest induced by vFLIP (see section on vFLIP)-activated NFκB by resisting cdk inhibitors and by targeting p27 for degradation [141]. Interestingly, vCyclin can also bind cdk9 resulting in increased phosphorylation of p53 and subsequent cell cycle arrest [142]. vCyclin transgenic mice develop lymphomas only in animals deficient for p53 [143, 144]. vCyclin transgenic mice also display severe lymphatic dysfunction and develop chylous ascites [145]. Therefore, vCyclin is not sufficient to induce tumorigenesis, but it contributes to cellular transformation by promoting cell cycle progression and proliferation when cells are in a contact-inhibited state [146].

#### vFLIP

KSHV vFLIP or K13 is the viral homolog of cellular FLIP (FLICE [protein FADDlike interleukin-1 beta-converting enzyme, now called caspase-8] inhibitory protein). vFLIP contains two death effector domains (DEDs) that allows for homotypic protein–protein interactions with other DED-containing proteins. Overall, vFLIP has been shown to inhibit Fas-dependent apoptosis [147–149], with the exception of one report [150]. vFLIP upregulates the NFkB signaling pathway [151–155] and can bind NEMO (also called IKK $\gamma$ ) in PEL cells [156–158]. This complex activates IKK, resulting in IkB phosphorylation and the release of active p65-p50 NFkB heterodimers [159]. Binding of vFLIP to the adaptor NEMO and activation of NFkB are essential for protecting cells against death receptor-induced cell death [160]. Moreover, vFLIP enhances interferon regulatory factor 4 (IRF4)-mediated gene transcription [161] and induces the expression of IL-1 $\beta$ , IL-18, and caspase-1 transcripts via NFkB [162]. Expression of vFLIP protects B cells from B cell receptorinduced apoptosis by NFkB activation [163]. Transgenic vFLIP mice displayed an increased incidence of lymphoma and enhanced responses to mitogenic stimuli [150, 164]. A separate line of vFLIP transgenic mice displayed B cell-derived tumors and lymphadenopathy with an increased number of lambda light chain-expressing plasmablasts, similar to MCD [149].

# Kaposin/K12

The kaposin locus encodes three proteins: kaposins A, B, and C [165]. Kaposin A is a small transmembrane protein that can transform cells in vitro [166, 167]. Kaposin B activates the p38 MAPK signaling pathway by direct interaction with the kinase MK2, a p38 substrate [168]. This results in the stabilization of cytokine and growth factor mRNAs [168]. Kaposin B also induces phosphorylation of STAT3 and MK2-mediated phosphorylation of TRIM28 thus relieving STAT3 repression from TRIM28 and enhancing inflammation [169].

#### Viral miRNAs

The KSHV pre-miRNAs produce 18 mature miRNAs [170]. Both host and viral mRNAs are targeted by the KSHV miRNAs. KSHV miRK9-3p (also called miRK9\*) targets the expression of the viral RTA protein [171] while several viral miRNAs including miR-K12-1, miR-K12-3-3p, miR-K12-6-3p, and miR-K12-11 target thrombospondin, an anti-angiogenic protein [172]. One KSHV miRNA, miRK11, shares seed sequence identity with a lymphoid-specific host miRNA (miR155) that modulates B cell differentiation [173-175]. Deletion of a 14-miRNA cluster from the viral genome increased viral lytic replication due to lowered NFkB activity [176]. Thus, the KSHV miRNAs modulate KSHV viral latency and lytic replication. KSHV miRNAs also regulate cell transformation and tumorigenesis by preferentially targeting pathways related to cancer including the NFκB pathway. KSHV mIR-K1 targets and reduces IκBα levels thereby facilitating NFkB activation, cell growth, and survival. Several KSHV miRNAs are implicated in promoting cell growth and survival by modulating levels of various host proteins. Moreover, some KSHV miRNAs regulate the levels of cellular proteins involved in the immune response and angiogenesis [177–179].

# Viral Lytic Cycle

Like other herpesviruses, the lytic program of KSHV also displays a temporal order of gene expression: immediate early, delayed early, and late genes.

The RTA protein encoded by KSHV ORF50 is the key lytic switch protein that controls reactivation from latency and initiates lytic replication. Ectopic expression

of RTA alone can induce reactivation from latency [83, 180, 181] and deletion or inactivation of RTA prevents reactivation from latency [84, 182]. ORF50 is an immediate-early protein as it is transcribed in the presence of cycloheximide, meaning no other viral protein synthesis is required for ORF50 expression [83, 183, 184]. ORF50 is the first transcript to be made during reactivation following chemical induction of PEL with TPA [181, 185]. This is because the ORF50 promoter is induced by TPA and lytic induction is associated with demethylation of the ORF50 promoter [186, 187]. ORF50, K8, and K8.1 genes are all part of a polycistronic transcript.

KSHV RTA has an amino-terminal DNA-binding domain (DBD) and a carboxyterminal activation domain. ORF50 can bind to and activate many different KSHV viral promoters as well as the two origins of lytic replication, OriLyt-L and OriLyt-R [188]. The RTA/ORF50-binding sites are called RTA-response elements (RREs), although many of the RREs share limited sequence homology [189–199]. Although ORF50 can directly bind DNA to transcriptionally activate promoters, it can also interact with other cellular transcription factors such as RBP-J $\kappa$  [192]. RBP-J $\kappa$  recognition sites are found in several ORF50-responsive gene promoters [189, 192, 196, 199–201]. ORF50 can also bind the transcription factors C/EBP $\alpha$  [190, 202], Oct-1 [203], and STAT-3 [204]. Additionally, ORF50 can interact with factors involved in chromatin modification such as CBP and histone deacetylase 1 [205], the chromatin remodeling complex SWI/SNF, and the TRAP/Mediator complex, which enables interaction of RNA pol II with many transcription factors [206].

The spliced isoform of plasma cell transcription factor X box-binding protein 1 (XBP-1s) can also govern the switch from latency to lytic replication [88, 89]. XBP-1s is not present in PEL, but the induction of hypoxia or endoplasmic reticulum stress gives rise to XBP-1s and subsequent induction of the lytic cycle [89, 207]. In addition to ORF50, ORFs K8, ORF45, and K4.2 are also classified as immediate early genes, although some reports classify them as delayed early (DE) genes.

DE genes encode transcripts that are sensitive to cycloheximide (since their expression depends on activation of their promoters by IE proteins) but resistant to viral DNA synthesis inhibitors. DE proteins include the viral DNA polymerase, thymidine kinase, ribonucleotide reductase, ssDNA-binding protein, and polymerase processivity factor, which prepare the infected cell for the onset of viral DNA replication. Several other DE proteins function in nuclear-cytoplasmic transport of viral RNAs (ORF57), modulation of signal transduction (K1, K15, and vGPCR), and immune evasion (K3/MIR1 and K5/MIR2).

The delayed early lytic phase is followed by viral DNA replication. The core replication machinery is directed to the replication origins on the viral genome called oriLyts. The KSHV genome contains two oriLyt regions: the left-hand origin (oriLyt L) which lies between ORFs K4.2 and K5, and the right-hand element (ori-Lyt R) which lies between ORFs K12 and 71 [208, 209]. Viral genome replication is thought to occur in a rolling circle mechanism and linear genomes are produced and packaged into nascent capsids. The viral replication machinery comprise the KSHV viral DNA polymerase, helicase, polymerase processivity factor, primase,

primase-associated factor, and single strand-binding protein [210]. Following DNA replication, late gene expression ensues. Most late genes encode structural proteins such as capsid proteins and envelope proteins [99, 104, 211, 212].

# Host Response to KSHV Infection and the Viral Counter Response

An innate immune response occurs following KSHV infection due to the detection of KSHV by various host cellular proteins including TLRs, IFI-16, and RIG-I like receptors, TLRs are the first line of defense against infecting microbes. TLRs detect pathogen-associated molecular patterns (PAMPs) present on the invading microbe and initiate signaling cascades leading to the activation of type I interferon (IFN) and NFkB and the production of proinflammatory cytokines [213]. TLRs can be expressed endosomally or on the cell surface. KSHV activates TLR3 during infection of primary human monocytes leading to the upregulation of TLR3 expression and its downstream mediators, including IFN-β1 and CXCL10 [75]. In human pDCs, which are the body's chief IFN-producing cells, viral infection activates TLR9, a DNA sensor [65]. KSHV is also sensed by another innate immune protein, the interferon gamma-inducible factor IFI-16, and IFI-16 colocalizes with the KSHV genome in the nucleus [214] and forms an inflammasome resulting in the production of IL-1 $\beta$  during primary and latent infection [162, 214]. The double stranded RNA sensor retinoic acid-inducible gene 1 (RIG-I) and its adaptor mitochondrial antiviral signaling protein (MAVS) also sense KSHV infection. Primary infected KSHV cells that have been depleted of RIG-I and MAVS have increased KSHV and reduced IFN- $\beta$  transcription [215].

To counter the host-mediated immune response, KSHV encodes many gene products that thwart various arms of the host immune response. Several KSHV proteins are able to ablate the activation and function of type I IFNs produced in response to microbial infection. Activation of the innate immune response leads to the activation of cellular interferon regulatory factors (IRFs), e.g., IRF3 and IRF7, type I interferon (IFN $\alpha$  and IFN $\beta$ ), and inflammatory cytokines. IFN $\alpha/\beta$  secreted from the infected cell can bind to IFN $\alpha$  and IFN $\beta$  receptors expressed on neighboring cells. IFN receptor activation induces signaling that stimulates transcription of many different IFN-sensitive genes (ISGs), and the cellular IRFs themselves.

The KSHV genome encodes four homologs of cellular IRFs. vIRF-1, -2, -3, and -4 were named based on their order of discovery. vIRF-3 is latently expressed but the other vIRFs (vIRF-1, -2, and -4) are mainly expressed during the lytic cycle. Although primarily a lytic gene, vIRF-1 can also be transcribed in latently infected KS cells [216, 217], vIRF-1 is transcribed in latently infected KS cells [105, 195]. vIRF-1, -2, and -3 cannot bind IRF-binding motifs in type I IFN and ISG promoters since they do not contain the DBDs of cellular IRFs (Fig. 12.4). vIRF-1 inhibits IFN activation in response to Sendai virus infection [216, 218] and dimerizes with cellular IRF1 and IRF3 to prevent their activation of IFN promoters. vIRF-1 can bind and sequester the



**Fig. 12.4** The KSHV vIRFs. KSHV encodes four vIRFs that share varying amounts of homology with cellular IRFs. One function of the vIRFs is to block cellular IRF function and interferon activation that is initiated by the host cell's immune response to the virus

coactivator, CBP/p300, away from cellular IRFs, thereby inhibiting CBP/p300 histone acetyltransferase activity on IRF-driven promoters [217, 219, 220]. vIRF-2 inhibits cellular IRF1- and IRF3-mediated transcription [217, 221], IFN $\beta$  promoter activity [222], ISG56 activation [221], and ISRE transactivation [221]. Similar to vIRF-1 and vIRF-2, vIRF-3 can inhibit transactivation of the IFN- $\alpha$ 4 and IFN- $\alpha$ 6 promoter [223, 224]. vIRF-3 also inhibits IFN $\gamma$ -mediated activation of the GAS promoter and CIITA promoters PIV and PII [225]. Downregulation of the CIITA promoters results in reduced major histocompatibility complex class II (MHC II) expression [226] and a hampered adaptive immune response.

Two other KSHV proteins that are not IRF homologs can also thwart cellular IRF signaling. ORF50 induces IRF7 degradation and ORF45 can bind IRF7 and prevent its phosphorylation and nuclear translocation [227, 228]. An ORF45-deleted virus was less able to replicate compared to wild-type virus [229, 230].

Two viral proteins, ORFs K3 and K5, inhibit presentation of MHC-I [231]. K3 and K5 encode for *m*odulators of *i*mmune *r*ecognition (MIR1 and MIR2, respectively). K5/MIR2 downregulates only HLA-A and HLA-B, while K3/MIR1 downregulates all four HLA allotypes (HLA-A, -B, -C, -E) [232, 233]. The KSHV MIR proteins functionally resemble the cellular MARCH protein family. This is a family of ubiquitin ligases that ubiquitinate cellular glycoproteins and target them for



Fig. 12.5 The KSHV MIRs and vCCLs. K3 and K5 encode the KSHV MIRs, which can ubiquitinate and induce the degradation of a number of immune receptors including MHC class I, ICAM-1, B7-2, and IFN $\gamma$ R1. The KSHV-encoded viral chemokines (vCCLs) block Th1 responses and augment Th2 responses

lysosomal destruction [234]. The MIRs also downregulate CD1d, an MHC-related protein that presents lipids and glycolipids to classical T and nonclassical NK T cells [235]. Additionally, K5/MIR2 (but not K3) can downregulate ICAM-1 and the costimulatory molecule B7-2 (CD86) [236, 237], which are proteins that exist on antigen-presenting cells and function in activating CD4-positive T cells. K5-driven downregulation of these proteins prevents helper T cell costimulation [236] and inhibits Natural Killer (NK) cell cytotoxicity [237]. Furthermore, K3 and K5 downregulate the interferon gamma receptor 1 (IFN-gammaR1) [238] and K5 reduces surface expression of the NKG2D ligands MHC class I-related chain A (MICA) and MICB, as well as the NKp80 ligand activation-induced C-type lectin (AICL) [239] (Fig. 12.5).

KSHV also encodes multiple CC chemokines: vCCL1 (formerly known as v-MIP-I), vCCL-2 (vMIP-II), and vCCL-3 (v-MIP-III) [240]. KSHV vCCL-1 signals through CCR8, vCCL-2 signals through CCR8 and CCR3, and vCCL-3 signals through CCR4 [241–243]. These viral chemokines activate receptors that are mainly present on Th2 cells, leading to a Th2-polarized response (Fig. 12.5). Moreover, vCCL-2 can interact with other chemokine receptors including CCR1, CCR2, CCR5, CXCR1, CXCR2, and CXCR4; however, binding of vCCL-2 to these

receptors inhibits, rather than activates, signal transduction in the presence of each receptor's chemokine ligands [241–243]. KS lesions comprise more Th2 T cells (CCR3+) than Th1 T cells (CCR5+) which aligns with these observations [244]. As well as binding T cell receptors, binding of vCCL-2 to CX3CR1 and CCR5 on NK cells inhibits binding to natural ligands resulting in reduced NK cell migration [245]. The viral chemokines can also induce angiogenic responses and activate vascular endothelial growth factor (VEGF) [246, 247].

Another viral protein that inhibits the inflammatory response is KSHV ORF63. This protein shows some homology to the nucleotide binding and oligomerization, leucine-rich repeat (NLR) family of proteins [248]. Activation of the NLR-dependent inflammasome complex results in the autocatalytic processing of procaspase-1 to caspase-1. Activated caspase-1 subsequently cleaves the precursors of the proinflammatory cytokines pro-IL-1 $\beta$  and pro-IL-18 into their biologically active forms: IL-1 $\beta$  and IL-18, respectively [249]. ORF63 binds NLRP1, and prevents its association with procaspase-1, thereby inhibiting the processing of procaspase-1 and subsequent processing of pro-IL-1 $\beta$  and pro-IL-18 [248].

KSHV K14 encodes a glycoprotein of the immunoglobulin superfamily that shows homology to cellular CD200 (also known as OX2). Cellular CD200 is a negative regulator of inflammation [250]. One report demonstrated proinflammatory signaling by K14 [251], but other studies found that K14/vOX2 represses induction of myeloid activation by suppressing TNF- $\alpha$  production by activated macrophages, decreasing MCP-1 and IL8 production, and blocking the secretion of histamine from activated basophils [252, 253]. In human primary monocyte-derived macrophages, K14 expression decreases cytokine production and phagocytic activity only in the context of IFN- $\gamma$  activation [254]. Expression of K14 in antigen presenting cells (APC) leads to the suppression of antigen-specific T-cell responses. These T cells make less IFN- $\gamma$  and express less CD107a, a component of cytotoxic granules and an indication of cytotoxic killing after exposure to K14-expressing APC [255].

# Viral Genes Involved in Cell Survival and Transformation

In addition to the genes and miRNAs described above in the section on viral latency, some other viral proteins that play roles in cell survival, signaling, and proliferation are described below and depicted in Fig. 12.6.

# K1

K1 is a type I transmembrane protein located at the left end of the KSHV genome. K1 is found in the ER and on the cell membrane. Its amino terminus is glycosylated and the C-terminal cytoplasmic tail contains an immunoreceptor tyrosine-based



Fig. 12.6 The KSHV K1, K15, and vGPCR transmembrane proteins. Multiple cellular signal transduction pathways are activated by the expression of the viral proteins K1, K15, and vGPCR. These signaling pathways include MAPK, NF $\kappa$ B, PI3K/Akt/mTOR, and PLC $\gamma$ , and their activation leads to increased production of growth factors and cytokines, cell proliferation, and cell survival

activation motif (ITAM) [256] that when phosphorylated can activate downstream signaling events including PLC $\gamma$  activation and calcium release [256, 257]. K1 is constitutively active and its aggregation leads to ITAM phosphorylation, Syk kinase recruitment, and increased NFATc and AP-1 activity. Moreover, the phosphorylated K1 tail can interact with Syk, PI3-kinase, lyn, RAS-GAP, PLC-γ 2, vav, and cbl [257-259]. PI3K activation results in the phosphorylation and activation of Akt kinase [259], the cell survival kinase involved in activation of pro-apoptotic factors, e.g., FOXO, Bad. K1-expressing cells are more resistant to apoptosis induced by Fas ligand or the expression of FOXO proteins [259]. K1 interacts with endoplasmic reticulum-associated Hsp40 (Erdj3/DnaJB11) and heat shock protein 90-beta (Hsp90beta), and these interactions are important for K1's effect on cell survival [260]. In B cells, K1 prevents surface transport of the B cell receptor (BCR) [261]. K1 has been shown to transform rodent fibroblasts [262] and K1 transgenic animals display lymphomas and sarcomas [263] and activated Lyn kinase [264]. K1 upregulates the secretion of angiogenic factors such as VEGF and matrix metalloproteinase-9 [265] in epithelial and endothelial cells. In addition to B cells, K1 can activate the PI3K/Akt/mTOR pathway in endothelial cells, which results in immortalization of primary human umbilical vein endothelial cells (HUVEC) in culture [266]. Thus, K1 contributes to angiogenesis and cell survival.

# vGPCR

KSHV encodes a viral G protein-coupled receptor (vGPCR) that is a member of the seven transmembrane G protein-coupled chemokine receptor family [267]. vGPCR displays constitutive signaling activity, although its activity can be augmented by chemokines such as GRO- $\alpha$  and inhibited by chemokines like CXCL10/IP10 [268, 269]. vGPCR signaling activates the PI3K/Akt/mTOR, NF $\kappa$ B, and MAPK pathways [270–277]. vGPCR augments angiogenesis and cell proliferation and vGPCR expression transforms cells [278–280]. vGPCR transgenic mice develop focal angioproliferative lesions similar to KS [281–283]. vGPCR is thought to aid transformation through a paracrine mechanism [284]. vGPCR activates IKK $\epsilon$  leading to phosphorylation of NF $\kappa$ B. Nude mice injected with vGPCR-expressing cells deficient in IKK $\epsilon$  fail to develop tumors suggesting that IKK $\epsilon$  is essential for vGPCR-induced tumorigenesis [285]. vGPCR also activates expression of many cellular genes including Rac1 [286] and VEGF [271, 279].

# K15

K15 lies at the right end of the viral genome and encodes another transmembrane signaling protein. K15 was initially named latency-associated membrane protein (LAMP) [287] and while it is thought to be expressed at low levels during latency [288], it is highly upregulated during the lytic cycle. K15 mRNAs are generated from alternatively spliced transcripts that include 8 or fewer exons resulting in four different isoforms [287, 289]. All spliced isoforms encode the carboxy-terminal cytoplasmic tail and are connected to a varying number of transmembrane domains. The full-length K15 protein contains 8 exons and 12 transmembrane domains. K15 localizes to the cell membrane and is often present in lipid rafts [290]. The K15 cytoplasmic region contains signaling motifs that, when phosphorylated, inhibit BCR signal transduction [289]. A TRAF-binding site in the cytoplasmic tail allows K15 to interact with TRAFs 1, 2, and 3 to constitutively activate NFkB and MAPK signaling pathways [287, 290]. K15 also contributes to angiogenesis. KSHVinfected endothelial cells induce the formation of angiogenic tubes upon reactivation; whereas, cells infected with K15-deficient KSHV fail to form tubes. K15 recruits PLCy leading to the activation of calcineurin/NFAT-1 and increased expression of RCAN1, a gene involved in angiogenesis [291]. Finally, K15 can activate the expression of cytokines and chemokines including IL-8, IL-6, CXCL3, CCL20, CCL2, IL-1  $\alpha/\beta$ , and Cox-2 [292] (Fig. 12.6).

# vIL-6

vIL-6 is a viral homolog of human IL-6 (hIL-6). It is different from hIL-6 since it does not need to bind to the gp80 subunit of the IL-6 receptor complex to initiate gp130 signal transduction [293-296]. vIL-6 contributes to pathogenesis by influencing multiple pathways and cellular proteins involved in proliferation, apoptosis, and angiogenesis. vIL-6 shares the anti-apoptotic functions of hIL-6 on B cells, and can prevent apoptosis in response to pro-apoptotic stimuli [297-299]. Depletion of vIL-6 in PEL cells inhibits cell growth [300]. vIL-6 can localize to the endoplasmic reticulum (ER) where it is thought to signal in an "intracrine" fashion. The interaction of vIL-6 and gp130 in the ER is important for maintaining PEL cell growth and viability via the activation of ERK 1 and 2 and STAT 1 and 3. vIL-6 also enhances the expression of DNA methyltransferase 1 (DNMT1) that induces irregular DNA methylation. Treating cells with a DNMT inhibitor results in reduced cell proliferation and migration [300-304]. vIL-6 can increase angiogenesis by upregulating VEGF [246, 305, 306]. Furthermore, vIL-6 expression induces angiopoietin 2, a proangiogenic and lymphangiogenic factor [307]. vIL6-expressing cells induce large tumors in mice and vIL6-transgenic mice develop MCD-like disease [308].

# Conclusions

KSHV is an oncogenic herpesvirus associated with three different human malignancies. KSHV encodes an arsenal of viral proteins that help the virus evade the host immune response and stay hidden inside infected cells for the lifetime of the host. KSHV also encodes many viral proteins that can modulate cellular signaling pathways to facilitate angiogenesis, cell proliferation, and survival. By manipulating these cellular signaling pathways, KSHV creates an environment that is beneficial for the survival of the virus, which may inadvertently lead to transformation of the cell.

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