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## Molecular Biology of KSHV in Relation to HIV/AIDS-Associated Oncogenesis

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### 2.1. Introduction

Discovered in 1994, KSHV is a human oncogenic gammaherpesvirus [1]. KSHV is causatively associated with several malignancies, including Kaposi's sarcoma (KS), primary effusion lymphoma (PEL), multicentric Castleman's disease (MCD), and KSHV inflammatory cytokine syndrome (KICS), most of which are commonly found in HIV-1-infected individuals [1, 2, 3, 4].

KS is a multifocal mesenchymal neoplasm characterized by neo-angiogenesis, inflammatory infiltration, and spindle-shaped tumor cells that express mixed cellular markers, including vascular and lymphatic endothelial, mesenchymal, and hematopoietic precursor cells [5]. Early stage of KS primarily affects mucocutaneous tissues but advanced stage of KS is often involved with visceral organs [5]. KS is one of the most common malignancies in AIDS patients. While the advent of antiretroviral therapy has substantially reduced the incidence of KS in Western countries, it has stabilized or even rebound in recent years in some populations, and continues to be the most common cancer in some African regions [6]. Hence, KS remains to be one of the most important malignancies in AIDS patients causing significant morbidity and mortality.

PEL is a rare and aggressive non-Hodgkin's B cell lymphoma clinically characterized by lymphomatous effusions in body cavities usually without tumor masses [7]. PEL often occurs in advanced AIDS patients with a decreased CD4 T cell count at diagnosis. Approximately, half of PEL patients have KS or are at risk for developing KS. PEL is resistant to conventional chemotherapy with a short median survival of less than 6 months [7].

MCD is a polyclonal B cell lymphoproliferative disorder characterized by inflammatory symptoms, including fever, cachexia, lymphadenopathy, splenomegaly, cytopenia, and hypoalbuminemia [8]. MCD in the setting of HIV is typically associated with KSHV infection and is usually fatal without treatment. Furthermore, there is no established standard of treatment for KSHV-associated MCD [8].

KICS is a newly described severe systemic inflammatory symptom associated with elevated viral loads and cytokine production [4]. The symptoms of KICS are similar to MCD but without any pathological evidence of MCD. KICS patients have poor prognosis, stressing the need for better understanding of its biology [9].

To dissect the biology of KSHV-associated malignancies and discover new approaches for potential therapy, extensive studies of KSHV from the aspects of virology to its associated pathogenesis have been done in the last three decades. Here, we present an update of literature review of KSHV in the following topics: (1) primary infection, (2) life cycle, (3) immunity, (4) tumorigenesis, (5) inflammation, and (6) metabolism. Because of space constraint, we can't describe all studies in detail and cite every reference. However, several excellent reviews have been published in the last few years and readers are advised to refer to those articles and the previous edition of this book chapter for additional information [5].

## 2.2. KSHV Primary Infection

KSHV has a broad cellular tropism and infects numerous cell types in vivo and in vitro, including endothelial cells, B cells, monocytes, macrophages, epithelial cells, keratinocytes, mesenchymal stem cells, and neurons [10, 11, 12, 13, 14]. Following primary infection, KSHV eventually establishes latency in all the cell types examined so far. While KSHV establishes latent infection without any active lytic replication in some cell types, it has an early full productive replication phase shortly after primary infection in others [15, 16]. To better understand the mechanism that controls KSHV latency and lytic replication following primary infection, it is necessary to identify cell types and conditions that support early lytic replication and the associated cellular pathways.

### 2.2.1. Attachment, Entry, and Cellular Receptors

KSHV enters the host cell and delivers its genome into the nucleus through a series of events tightly regulated by diverse viral and host factors [17, 18]. These events include attachment to the host cell surface, binding to specific entry receptors, and internalization through fusion of viral envelope with the membrane of intracellular vesicles following receptor-mediated endocytosis [17, 18].

The attachment of KSHV to the host cell is through interactions between viral glycoproteins (gB, gH, and gpK8.1) and cell surface molecule heparan sulfate, a linear polysaccharide ubiquitously expressed at the extracellular matrix [19, 20, 21, 22]. Following attachment, KSHV binds to the specific entry receptors, including integrins, DC-SIGN, xCT, and ephrin type-A receptor 2 (EphA2), and activates a cascade of signaling pathways to promote receptor-mediated endocytosis [17, 18].

Integrins are a large family of cell adhesion receptors, widely expressed in various cell types, including endothelial cells and B cells. KSHV was the first herpesvirus demonstrated to utilize integrins as entry receptors [13]. An integrin binding RGD motif (arginine–glycine–aspartic acid) of glycoprotein gB mediates its interactions with integrins  $\alpha 3\beta 1$ ,  $\alpha V\beta 3$ , and  $\alpha V\beta 5$  expressed on the surface of human foreskin fibroblasts (HFF), human dermal

microvascular endothelial cells (DMVEC), human monocytic THP-1 cells, human fibrosarcoma HT1080, Vero cells, and HEK-293T cells [13, 23, 24, 25].

Dendritic cell-specific intercellular adhesion molecule-3-grabbing non-integrin (DC-SIGN) is a C-type lectin expressed by dendritic cells (DCs), macrophage subpopulations, and activated B lymphocytes. KSHV uses DC-SIGN as a binding and entry receptor to infect human myeloid DCs, macrophages, and activated B cells [26, 27]. While blocking binding of KSHV to DC-SIGN does not affect virus attachment to the cells, it inhibits KSHV infection in human monocytic THP-1 cells [23].

Human cysteine/glutamate exchange transporter system  $x_c^-$  (xCT) is an amino acid transporter that imports L-cystine and exports L-glutamate across plasma membrane [28]. xCT mediates KSHV cell fusion and virion entry [29]. xCT interacts with  $\alpha 3\beta 1$  integrin to form a complex, which triggers downstream signaling cascades essential for viral gene expression during primary infection of DMVEC [24].

Eph2A, a receptor protein tyrosine kinase (RTK), serves as an entry receptor through direct interaction with gH/gL glycoprotein complex [12, 30]. Eph2A plays an important role in regulating macropinocytosis and trafficking of KSHV through its association with signaling molecules (e.g., FAK, Src, and c-Cbl) in the lipid raft (LR) regions during primary infection of DMVEC [31]. In contrast, KSHV infection of HFF induces association of integrins with Eph2A in non-LR regions, suggesting a crucial role of Eph2A in KSHV entry through clathrin-mediated endocytosis [32].

### 2.2.2. Internalization and Intracellular Trafficking

KSHV infects most types of cells through clathrin-mediated endocytosis and macropinocytosis. Clathrin-mediated endocytosis is an endocytic portal into cells through which cargos are taken up using clathrin-coated vesicles. KSHV enters human umbilical vein endothelial cells (HUVEC), HFF, HEK293 cells, and BJAB cells via clathrin-mediated endocytosis [33, 34, 35]. During infection of HUVEC, KSHV particles are co-localized with early endosome antigen (EEA1) and late endosome/lysosome marker (LAMP1) [34]. By electron microscopy, KSHV virions are present in the endocytic vesicles in HFF cells [33], and KSHV entry is sensitive to inhibitors of clathrin-mediated endocytosis [33, 34].

KSHV utilizes macropinocytosis as the major route to enter DMVEC [36]. Inhibition of membrane blebbing, an important event in macropinocytosis, significantly blocks KSHV entry [37]. It is identified that ESCRT-0 component Hrs regulates KSHV entry and ESCRT-I protein Tsg101 plays a role in the trafficking of virus particles in DMVEC [38, 39].

Studies on other cell types further suggest that KSHV entry is cell type-dependent. KSHV enters THP-1 via clathrin- and caveolae-mediated endocytosis but not macropinocytosis [23] while KSHV enters primary B lymphocytes by DC-SIGN-mediated endocytosis [26].

Upon internalization, the intracellular transport of KSHV particles relies on the cytoskeletons. In HUVEC, KSHV is co-localized with actin filaments during early infection and induces dynamic actin cytoskeleton rearrangements. Disruption of actin dynamics significantly inhibits KSHV trafficking [34]. In addition, KSHV infection modulates

microtubule polymerization to promote the trafficking of viral capsids in HFF [40]. Disruption of microtubule formation or impairing dynein-directed retrograde microtubule transport strongly reduces KSHV trafficking [40].

### 2.2.3. Regulation of Cellular Signaling Pathways During Primary Infection

KSHV dysregulates multiple signaling pathways to promote primary infection [18]. Interactions between KSHV and cell surface receptors activate focal adhesion kinase (FAK) signaling in several cell types [41]. Activated FAK is vital for many processes including cytoskeleton rearrangement and endocytosis, which facilitate virus entry [42]. Calcium and integrin binding protein 1 (CIB1), an enhancer of FAK, ERK1/2, and PAK kinases [43, 44], facilitates Eph2A-related signaling and regulates KSHV entry and macropinocytosis [45]. c-Cbl, a multifunctional E3 ubiquitin ligase, is induced by KSHV to promote virus entry in endothelial cells [37, 46, 47]. In addition, KSHV infection induces reactive oxygen species (ROS) to promote virus entry and subsequent viral gene expression [48].

Primary KSHV infection activates ERK, JNK, p38 MAPK pathways to promote virus entry, viral gene expression, and productive viral replication [49, 50, 51]. KSHV infection suppresses dual-specificity phosphatase-1 (DUSP1) to activate MAPK signaling, facilitating viral gene expression, pro-inflammatory factor secretion, and cell invasiveness [52]. In HUVEC, KSHV activates MSK/CREB1 signaling pathway in an ERK- and p38-dependent manner to regulate viral lytic replication at the postentry stage [53]. Endogenous activity of AMPK, which maintains cellular homeostasis, inhibits KSHV lytic replication [54]. Activation of AMPK activity decreases while inhibition of AMPK increases KSHV lytic replication during primary infection of HUVEC [54]. In addition, KSHV infection leads to sustained NF- $\kappa$ B induction, which regulates viral and host cell gene expression and possibly affects the establishment of latent infection [55]. Nuclear factor erythroid 2-related factor 2 (Nrf2) is activated by KSHV infection through an ROS-dependent pathway [56]. Knockdown of Nrf2 decreases early lytic gene expression but increases latency-associated nuclear antigen (LANA) expression in the infected cells, indicating its crucial role in viral gene expression [56].

### 2.2.4. Viral Gene Expression During Primary Infection and the Establishment of Viral Latency

Viral gene expression profiles during KSHV primary infection are heavily dependent on the types of cells infected [57, 58, 59]. In cells that support productive KSHV infection (e.g., HUVEC), the expression of latent transcripts precedes the cascade of lytic genes [57]. Latent transcripts are sustained at high levels throughout infection. The lytic transcripts are expressed in the order of immediate early (IE), early (E), and late (L) transcripts, and reach peaks at around 54 h post infection (hpi). After 54 hpi, the levels of lytic transcripts decline while latent transcripts continue to increase, leading to the switch from lytic replication to viral latency [57]. In cells such as CD14<sup>+</sup> monocytes, HFF, and DMVEC that support minimal lytic activities without producing infectious virions during KSHV primary infection, the expression of lytic transcripts is weak and transient (within 24 hpi) while latent transcripts are expressed throughout the infection process [58, 59].

The establishment of latency is an essential step for persistent infection and induction of KSHV-associated malignancies. One hallmark of KSHV latency is the global repression of viral lytic genes. During primary infection, the chromatin-free KSHV genome undergoes biphasic chromatinization with an initial transcriptionally active euchromatin phase characterized by high levels of the H3K4me3 and H3K27ac activating histone marks, followed by a heterochromatinization phase featured by decreased levels of activating histone marks and increased levels of repressive marks H3K27me3 and H2AK119ub [60, 61, 62]. The euchromatin-to-heterochromatin transition corresponds with the expression switch of viral lytic to latent genes and depends on the recruitment of polycomb repressive complexes 1 and 2 (PRC1 and PRC2) to lytic promoters by LANA [63].

KSHV triggers DNA damage response (DDR) signaling inducing phosphorylation of DDR-associated proteins, ataxia telangiectasia mutated (ATM) and H2AX, during primary infection of endothelial cells [64]. Inhibition of ATM or H2AX activation leads to over 80% reduction in the nuclear viral DNA copy number, indicating an essential role of the DDR proteins for the establishment of KSHV latency during primary infection [64].

### 2.3. KSHV Life Cycle

Following an acute phase of infection with or without active lytic replication, KSHV enters latency, which is essential for the development of KSHV-associated malignancies [65]. Upon stimulation by specific intracellular and extracellular signals, latent KSHV is reactivated into lytic replication which culminates in virion production and cell death [65].

#### 2.3.1. The Latency Locus

The KSHV latency locus encodes LANA, viral homologues of the cellular FLICE-like inhibitory protein (vFLIP) and cyclin D (vCyclin), Kaposin A, B, and C, and 12 precursor microRNAs (pre-miRNAs). Transcription of the latent locus occurs from LANA promoters (LT1 and LT2) and Kaposin promoter. LT1 drives the expression of LANA, vCyclin, and vFLIP whereas LT2 drives the expression of vCyclin and vFLIP [66, 67, 68]. The LANA promoter is bidirectional and can drive the expression of upstream lytic genes such as surface glycoprotein vOX2 and viral G-protein coupling receptor (vGPCR) during reactivation [69]. Of the 12 pre-miRNAs, miR-K1 to -K9 and -K11 form a cluster region located between vFLIP and Kaposin while miR-K10 and miR-K12 are in the Kaposin coding region or 3'UTR, respectively [70]. In addition to the latency locus, KSHV encodes another latent protein viral interferon regulatory factor 3 (vIRF-3) located outside the latency locus, which is expressed in PEL but not in KS cells [71].

#### 2.3.2. KSHV Latency and Latent Nuclear Antigen (LNA) or Latency-Associated Nuclear Antigen (LANA)

LANA (LNA) is a KSHV latent protein discovered as an immunodominant antigen and has been used for detecting KSHV infection [72, 73, 74]. LANA is approximately 1162aa in length with a proline-rich N terminal and repeats regions (CRs) composed of glutamine (Q), glutamic acid (E), and aspartic acid (D) [75]. The CRs can be further divided into three distinct regions: CR1 (aa 321–429), CR2 (aa 430–768), and CR3 (aa 769–937), with CR3

containing a leucine zipper domain. CR1 is involved in immune evasion by inhibiting major histocompatibility complex class I (MHC-I) peptide presentation in *cis* [76] while CR2 and CR3 decrease LANA synthesis and enhance its stability [77]. Although its predicted size is 135 kDa, LANA is resolved as double bands of 226–234 kDa in SDS-PAGE [72]. The second band is the result of a 76 aa truncation in the C-terminal region [78]. Besides the two bands, multiple bands between 150 and 180 kDa are present in KSHV-infected cells due to noncanonical translation initiation [79].

LANA is a multifunctional protein and its key function is to maintain the cellular persistence of KSHV episome [65]. During latency, the KSHV genome replicates once in each cell cycle, and the copy number is stable (40–150 copies/cell in PEL cells) [80, 81, 82]. Without LANA, KSHV is unable to establish and maintain its episome in mammalian cells [83]. LANA has an essential nuclear localization signal (NLS) at its N-terminus (aa 24–30) and a second one at the C-terminus, and is detected in dot-like pattern by immunohistochemistry or immunofluorescence [73, 74, 84]. The N-terminus also has a chromosome binding site (CBS) (aa 5–13), which interacts with histones H2A/H2B whereas the C-terminus has a DNA binding and a dimerization domain (DBD), which allows LANA to bind to LANA-binding sites (LBS) located within KSHV terminal repeat (TR) region [85, 86, 87, 88].

LANA interacts with chromatin-associated proteins such as heterochromatin protein 1 $\alpha$  (HP1), KSHV LANA-interacting protein 1 (KLIP1), methyl CpG-binding protein (MeCP2), bromodomain protein 4 (Brd4), RING3/Brd2, kinetochores-associated proteins as centromere protein F (CENP-F), budding uninhibited by benzimidazoles (Bub-1), and nuclear mitotic apparatus protein (NuMA) [89, 90, 91, 92, 93, 94]. Furthermore, LANA is associated with nucleophosmin (NPM), and the origin recognition complexes (ORCs) [95]. Some of these interactions are essential for KSHV genome segregation to daughter cells and repression of KSHV lytic replication. LANA silences the replication and transcriptional activator (RTA) promoter and interacts with RTA to inhibit its transactivation function [96]. Deletion or disruption of LANA abolishes the establishment of KSHV latency and increases the expression of KSHV lytic genes and production of infectious virions [83, 97]. Hence, LANA is the predominant regulator in maintaining latency by mediating episome replication, proper segregation to daughter cells, and repressing KSHV lytic replication program [65]. LANA also contributes to KSHV latency by promoting host cell proliferation and survival, which will be detailed in a later section.

### 2.3.3. Epigenetic Silencing and Regulation of KSHV Latency

To silence the expression of viral lytic genes, the KSHV genome undergoes epigenetic remodeling during latency. The KSHV genome is heavily methylated and contains histone repressive marks and HDACs [61, 62, 98, 99, 100, 101, 102]. To mediate viral genome replication, LANA binds to the latent origin of replication in the TR, which also harbor ORC, MCM, CDC6, PARP1, and hyperacetylated histones [100, 103, 104, 105]. During latency, the spread of transcription beyond the latent locus is arrested by H19/Lgf2 insulators recruited to the CTCF-binding site, which also harbors CTCF, cohesins, RAD21, SMC1 and SMC 3 [106, 107], mediating viral chromosome conformation, expression of latent genes, and silencing of lytic genes [108, 109, 110]. In addition to LANA, vFLIP and miR-K1

promote KSHV latency by activating the NF- $\kappa$ B pathway [111, 112]. Several KSHV miRNAs inhibit RTA expression by direct targeting and silencing or indirect activation of cellular pathways including Rbl2, DNMTs, NFIB, and IKK $\epsilon$  [113, 114, 115, 116, 117]. These cellular factors could cause chromatin remodeling of KSHV genome. KSHV miRNAs also target several other viral genes, which could regulate viral latency [118].

#### 2.3.4. Reactivation of KSHV from Latency

The mechanism of KSHV reactivation is involved with complex interactions of viral genes, cellular factors, and extracellular signals. During reactivation, the quiescent state of the KSHV genome is disrupted and undergoes epigenetic remodeling, resulting in the expression of viral lytic genes and production of infectious viral particles [119].

#### 2.3.5. Viral Genes Required for Reactivation

KSHV lytic genes can be broadly divided into three classes: IE, E, and L genes. IE gene expression is not dependent on de novo translation of any proteins, whereas E and L genes require de novo expression of proteins. Late genes are also dependent on viral DNA replication. Here, we will discuss several viral lytic genes that are important for viral lytic replication.

RTA is an IE gene. Expression of RTA is essential and sufficient for KSHV reactivation [120, 121]. RTA transactivates numerous viral genes, including itself, by binding to the palindromic RTA-responsive element (RRE) [122, 123, 124, 125, 126]. RTA cooperates with cellular factors such as Sp1, Oct-1, XBP-1, RBP-Jk, and C/EBP $\alpha$  to transactivate genes [127, 128, 129, 130, 131]. As an E3 ubiquitin ligase, RTA targets numerous repressors of viral lytic replication for degradation [132, 133, 134, 135]. RTA binding to origin of lytic replication (oriLyts) is required for viral DNA replication [136, 137]. Several isoforms of RTA, which possess transactivation activities weaker than the canonical isoform, have been identified but the regulation of their expression as well as their specific target genes remain unclear [138]. Hence, RTA's complex functions are not fully understood despite it is known as the master regulator of KSHV lytic replication.

mRNA transcript accumulation (MTA) is an E gene required for KSHV reactivation [139, 140]. MTA interacts with RTA to enhance RTA expression [141]. Importantly, MTA mediates viral transcript processing by hijacking splicing and nuclear export factors such as TREX for efficient viral gene expression, particularly for intronless viral transcripts [142]. However, MTA's role in nuclear export is controversial [143]. MTA interacts with an RNA stem-loop structure termed the MTA-responsive element (MRE) [144, 145]. Of interest, MTA protects vIL6 from miRNA-mediated degradation though the exact mechanism remains unknown [146]. To promote translation, MTA interacts with PYM to shuttle transcripts to the 48S transcription pre-initiation complex [147]. Taken together, MTA enhances viral gene expression by hijacking cellular RNA processing events and translation.

K-bZip encoded by ORF-K8 is an E gene. K-bZip is a leucine zipper protein with multiple functions [148]. It interacts with RTA and inhibits RTA transactivation of several viral genes, notably ORF57, ORF-K15, itself, and RTA autoactivation [149]. K-bZIP interacts with HDAC1/2 to silence viral promoters [150] and this repressive function depends on its

SUMO modification of KSHV genome and heterochromatin histone demethylase JMJD2 [151, 152, 153, 154]. K-bZIP supports lytic DNA replication by overcoming LANA's repression of the OriLyts [136, 155]. Furthermore, viral protein kinase (vPK/ORF36) co-localizes with K-bZIP at oriLyts and phosphorylates K-bZIP to prevent its sumoylation, thus reducing its transcription repression activity [156]. Taken together, K-bZIP contributes to viral DNA replication and repression of lytic genes during lytic replication.

### 2.3.6. Factors Involved in KSHV Reactivation

KSHV reactivation from latency is accompanied by dynamic chromatin remodeling [101, 102]. Inhibition of class II HDACs, EZH2, or DNA methylation with small molecules is sufficient to induce KSHV reactivation [101, 102, 157]. During reactivation, the KSHV episome gains activating histone marks (H3K4me3, acH3) and loses repressive histone marks (H3K9me3, H3K27me3, H4K20me3) [157]. This is facilitated by RTA, which recruits CBP/p300 and SWI/SNF to promote H3K27Ac on lytic promoters [158]. Inhibition of SIRT1, a class III HDAC and NAD<sup>+</sup> sensor, results in expression of lytic genes thus linking epigenetics to the cellular metabolic state [98, 99]. In fact, high glucose suppresses SIRT1 leading to KSHV reactivation [159].

KSHV infection often occurs in the context of immunosuppression [160]. How KSHV interacts with other pathogens is poorly understood *in vivo* but several *in vitro* studies have attempted to delineate these events. HIV Tat alone can induce RTA expression and enhance KSHV entry into endothelial cells [161, 162, 163]. Coinfection of PEL cells with EBV favors viral persistence of both viruses [164, 165]. KSHV RTA, EBV ZTA, and EBV LMP1 prevent reactivation of both viruses. Additionally, HCMV, HHV-6, HSV-1, HSV-2, and HHV-7 can induce KSHV reactivation [166, 167, 168, 169, 170, 171]. Bacterial metabolic products such as LPS, short-chain fatty acids, and lipoteichoic acid enhance infectivity and reactivation [172, 173, 174].

Hypoxia plays a critical role in reactivation [175]. Binding of HIF-1 $\alpha$  to hypoxia-responsive elements (HRE) in the promoters of KSHV lytic genes enhances their expression and lytic replication [175, 176, 177]. Furthermore, LANA cooperates with HIF-1 $\alpha$  at the HRE to enhance RTA expression [178, 179]. Another hypoxia-inducible gene, XBP-1, binds to the RTA promoter to enhance reactivation [180, 181]. Cross talk between hypoxia and epigenetics could occur through KAP1, which is recruited to the KSHV genome through LANA, and decreased levels of KAP1 during hypoxia enhance lytic gene expression [182, 183].

Moreover, oxidative stress also contributes to KSHV reactivation. In fact, hydrogen peroxide (H<sub>2</sub>O<sub>2</sub>) is necessary and sufficient for inducing KSHV reactivation [184]. Since KS is a highly inflammatory tumor, the abundant infiltrating immune cells and inflammatory cytokines in KS tumors could secrete or induce H<sub>2</sub>O<sub>2</sub>, respectively, leading to KSHV reactivation [184, 185]. H<sub>2</sub>O<sub>2</sub> activates MAPK leading to phosphorylation of ERK1, JNK, p38, and c-Jun, which is sufficient for KSHV reactivation and this can be reversed by the antioxidant N-acetyl-cysteine (NAC) [184, 185]. Furthermore, ROS induced by anticancer drugs such as cisplatin and arsenic trioxide reactivate KSHV and cause cell death in PEL cells [185].



## 2.4. KSHV and Immunity

While the immune system is dedicated to protecting the host from invading pathogens such as viruses, KSHV has evolved various strategies to counteract both the innate and adaptive immune responses, which are essential for viral replication and persistent infection.

### 2.4.1. KSHV and Innate Immunity

Several KSHV-encoded proteins interfere with both type I (IFN- $\alpha$  and IFN- $\beta$ ) and type II (IFN- $\gamma$ ) interferon responses. KSHV was the first virus found to encode viral homologs of cellular interferon regulatory factors (vIRFs) [186]. Each of the four vIRFs blocks the IRF-mediated transcription of type I IFN by a distinct mechanism [186, 187, 188]. Moreover, ORF45 and RTA inhibit IRF7-dependent type I IFN response [189, 190] while K8 inhibits IRF3-mediated IFN- $\beta$  transcription [191]. ORF-K3 and ORF-K5, which are viral E3 ligases, repress the IFN- $\gamma$ -mediated JAK/STAT signaling pathway by inducing the degradation of IFN- $\gamma$  [192,193].

The pattern recognition receptors (PRRs) sense various pathogen-associated molecular patterns (PAMPs) and trigger the type I IFN signaling and production of inflammatory cytokines during pathogen infection. KSHV stimulates TLR3 expression at the early stages of de novo infection; however, the expression of vIRFs inhibits TLR3-mediated immune responses at later time points [194, 195, 196]. RTA, ORF21, and ORF31 inhibit both TLR2 and TLR4 signaling [194, 197]. In addition to modulating the TLR signaling pathway, KSHV ORF63 blocks the cellular NOD-like receptor (NLR)-mediated pathway whereas ORF64 inhibits the activation of retinoic acid-inducible gene-I (RIG-I) [198]. KSHV DNA is sensed by IFI16 and cGAS-STING pathways leading to the activation of inflammasome [199, 200, 201, 202]. To ensure efficient viral lytic replication, KSHV encodes numerous proteins including vIRF1, ORF52, and LANA to inhibit the cGAS-STING pathway [199, 200, 201], while KSHV lytic replication leads to the degradation of IFI16 though the mechanism remains unclear [203].

To facilitate viral evasion of cytotoxic reaction, KSHV induces a Th2-polarized rather than a Th1-polarized response. Three KSHV-encoded CC-chemokine ligands (vCCL), the homologs of cellular chemokines, compete with cellular chemokines to prevent activation of chemokine receptors [188]. KSHV complement control protein (KCP/ORF4) is a functional homolog of the complement regulatory protein which inhibits the activation of the complement system [204]. This mechanism is likely to protect both KSHV-infected cells and free virions from complement-mediated neutralization during acute viral infection. In contrast, KSHV activates the alternative complement system by downregulating the complement regulatory proteins CD55 and CD59 during latency, which is essential for cell survival and persistent infection [205].

KSHV has evolved strategies to evade the natural killer (NK) cells. ORF-K5 decreases cell surface expression of NK-activating ligands including MICA, MICB, and AICL as well as the costimulatory molecules ICAM and B7.2 [188, 206]. Similarly, miR-K12-7 targets MICB mRNA [207] while ORF54 decreases the expression of another NK ligand, NKp44L [208].

### 2.4.2. KSHV and Adaptive Immunity

Both KS patients and asymptomatic individuals develop T cell responses against several KSHV lytic and latent proteins [209]. Importantly, reconstitution of the immune system through antiretroviral therapy can lead to KS tumor regression [210], suggesting an important role of the KSHV-specific T cell response, particularly the CD8<sup>+</sup> T cell response, in the development of KSHV-associated malignancies [209]. KSHV also induces strong humoral responses as antibodies against various viral antigens are present in KS and KSHV-infected patients [72, 73, 74, 211, 212].

B cell activation and differentiation into antibody-producing plasma cells or memory B cells are critical aspects of the adaptive immune response. Several studies suggest that KSHV targets both aspects of the B cell biology to evade the humoral immune response. ORF-K1 reduces the expression of bone marrow stromal antigen 2 (BST-2), which is constitutively expressed in mature B cells [192], and downregulates B cell receptor on the cell surface [213] while ORF-K15 blocks BCR transduction signal, contributing to decreased B cell activation [213].

Evading the cell-mediated immune response is an important strategy for KSHV persistent infection. ORF-K3 and -K5 enhance the internalization and lysosomal degradation of MHC-I molecules through ubiquitination of the cytosolic tails [214, 215, 216, 217]. vIRF1 and vFLIP mediate MHC-I downregulation [218]. LANA evades immune surveillance by inhibiting MHC class I peptide presentation [76]. KSHV induces cellular suppressor of cytokine signaling 3 (SOCS3), and together with vIRF3, interferes with MHC class II antigen presentation to evade KSHV-specific CD4<sup>+</sup> T helper cell immune response [219, 220]. Besides impairing antigen presentation, KSHV interferes with the function of antigen presenting cells by inhibiting differentiation of monocytes into dendritic cells [221] and downregulating costimulatory molecules required for efficient activation of CD8<sup>+</sup> T cells [214, 222].

## 2.5. KSHV and Tumorigenesis

In KS tumors, most of the tumor cells are latently infected by KSHV, suggesting the importance of latent infection and latent genes in the development of KS tumors [65]. A small number of tumor cells undergo spontaneous lytic replication in early stage of tumors, which is essential for the spread and progression of this stage of tumors. However, there is no lytic cell in late stage of KS tumors [65]. Spontaneous lytic replication is also present in small number of cells in PEL and MCD [65]. Numerous KSHV latent and lytic genes have been shown to have oncogenic and tumor-promoting functions [188]. The recent development of a model of KSHV-induced cellular transformation and tumorigenesis of primary cells has allowed the delineation of the cellular pathways and viral genes that promote tumorigenesis in the context of viral infection [14].

### 2.5.1. Models of KSHV-Induced Cellular Transformation and Tumorigenesis

The origin of KS tumor cells remains controversial. KSHV infects both vascular and lymphatic endothelial cells and reprograms them to acquire KS-like cell surface markers

[223, 224]. KSHV efficiently infects endothelial cells and prolongs their life span but cellular transformation remains elusive [225, 226]. Transfection of mouse bone marrow endothelial-lineage cells with recombinant KSHV BAC36 genomes results in immortalization of a subset of cells, which induces tumors in nude mice [227]. However, the exact target cells are unclear and the efficiency is low. In contrast, KSHV efficiently infects and transforms primary rat embryonic metanephric mesenchymal precursor (MM) cells [14]. KSHV-transformed MM cells (KMM) lose contact inhibition and form colonies in soft agar. KMM cells efficiently induce tumors in nude mice with virological and pathological features reminiscent of KS [14]. While KSHV can also infect and transform human mesenchymal stem cells of diverse origins, the efficiency of cellular transformation is much lower [228]. KSHV infection of rat and human mesenchymal stem cells reprograms them to acquire KS-like phenotypes including cell surface markers, and enhances their angiogenic, invasive, and transforming phenotypes [14, 228, 229].

### 2.5.2. KSHV Viral Genes and Tumorigenesis

The roles of the KSHV latent genes LANA, vFLIP and vCyclin, and miRNAs in tumorigenesis have been extensively studied. LANA promotes cell proliferation and survival by inhibiting tumor suppressor genes p53, p73, pRb, and TGF- $\beta$  signaling [230, 231, 232, 233], and activating c-Myc, emmprin, and survivin [234, 235, 236, 237]. LANA promotes tumorigenesis by upregulating BMP-p-Smad1-Id1 pathway in KMM cells [238]. LANA upregulates Par3, SNAIL, and MMP9 while downregulates E-cadherin to promote cell proliferation in B cells [239]. KSHV-encoded miRNAs and vFLIP activate the NF- $\kappa$ B pathway and are essential for KSHV-induced cellular transformation and tumorigenesis by regulating cell proliferation, survival, homeostasis, and metabolic pathways [240, 241, 242]. vCyclin alone can interact with numerous CDKs to promote cell cycle progression and tumorigenesis, and antagonizes the senescence/G1 arrest response triggered by NF- $\kappa$ B hyperactivation [243, 244, 245, 246]. In the context of KSHV infection, vCyclin only promotes cellular transformation and tumorigenesis by overriding cell contact inhibition [247].

Numerous KSHV lytic genes possess cellular transforming and growth-promoting activities. vIRF1 is the first KSHV oncogene identified [186]. It targets interferon, p53, and TGF- $\beta$  pathways [186, 248, 249]. vGPCR is unique in that it is constitutive active without the need of a ligand. It has robust oncogenic activity [250]. vGPCR transgenic mice develop KS-like lesions [251]. Mechanistically, vGPCR activates Akt and mTOR pathways, and promotes genomic instability through miR-34a [252, 253, 254]. Unlike human IL-6, vIL6 only signals through gp130 to activate several downstream pathways, such as JAK/STAT, MAPK, and Akt, driving cellular proliferation, inflammation, and apoptosis inhibition [255, 256]. Of interest, vIL6 can induce intracellular signaling and interacts with splice variant 2 of vitamin K epoxide reductase complex subunit 1 (VKORC1) to promote PEL cell proliferation and survival [257, 258]. ORF-K1 also possesses oncogenic activity [259]. It activates Akt and AMPK pathway to promote cell proliferation and survival [260, 261]. Whether KSHV lytic genes contribute to KSHV-induced tumorigenesis remains to be tested in the context of viral infection.

### 2.5.3. Cellular Genes/Pathways in KSHV-Associated Malignancies

Extensive studies have identified cellular genes/pathways required for KSHV-associated malignancies. Transcriptional factors, such as c-Myc and STAT3, are required for cell survival, and the inhibition of c-Myc and STAT3 induced apoptosis in PEL cells [262, 263]. Epigenetic factors, including class I and II HDACs, as well as class III HDAC SIRT1 are essential for cell proliferation and survival in PEL cells, and their inhibitors SAHA and tennovin-6 significantly induced cell cycle arrest and apoptosis in vitro and in vivo [264, 265, 266]. In addition to the NF- $\kappa$ B and BMP-Smad1-Id pathways that are essential for cell proliferation and cellular transformation [238, 240, 241, 242], Akt and mTOR are also essential for cell proliferation in KS cells [267] while hepatocyte growth factor (HGF)/c-MET pathway is essential for cell cycle progression and cell survival in PEL cells [268, 269].

## 2.6. KSHV and Inflammation

### 2.6.1. Kaposi's Sarcoma: A Tumor Associated with Inflammation

Inflammation can have a double role in the development of cancer. Acute inflammatory response is considered as a physiological process required for the control of microbial infections and tumor growth. However, by stimulating cell proliferation and inhibiting apoptosis, chronic inflammation becomes a pathologic process participating in the modifications of the microenvironment, enhancing uncontrolled tissue regeneration, angiogenesis, and tumorigenesis [270]. It is estimated that more than 25% of cancers are associated with inflammation [271].

Chronic inflammation, a hallmark of KSHV-associated malignancies, participates KS progression through the complex interplay between viral and cellular factors. By interfering with the intracellular signaling pathways during lytic and latent phases of infection, KSHV induces an inflammatory neoplastic network in the tumor microenvironment, which is mainly associated with the abnormal lympho-endothelial proliferations and the recruitment of activated myeloid and lymphoid immune cells [272]. Indeed, at the early stage of tumors, the KS microenvironment has a high level of pro- and anti-inflammatory cytokines (IL-6, TNF- $\alpha$ , and IL-10, respectively), chemokines (CXCL12, CXCR4, CXCR7), interferon (IFN- $\gamma$ ), as well as growth factors (VEGF) [273, 274, 275]. These cytokines can be released by different cell types including monocytes, endothelial cells, and KS tumors. During tumor growth, these mediators stimulate resting and non-proliferative lympho-endothelial cells to enhance inflammation, and therefore promote angiogenesis [276, 277].

### 2.6.2. Latent Viral Factors Involved in Inflammation

LANA upregulates emmprin expression, which induces the secretion of IL-6, VEGF, and MMPs, and enhances inflammation and angiogenesis [236, 278]. By stabilizing the Notch effector Hey-1, LANA also represses the expression of Prox-1 to modulate the differentiation of lymphatic endothelial cells [279]. Moreover, LANA activation of the Notch pathway enhances the invasiveness of KS tumors by activating PDGFR $\beta$  [280]. As stated in the previous section, LANA participates in the suppression of specific T cells immune response by inhibiting MHC-I antigen presentation through its acidic central repeat

domain [281], and by downregulating MHC-II gene expression on APCs through the interaction with RFX proteins to inhibit the recruitment of CIITA to the MHC-II promoter [282].

vFLIP activates the classical and alternative NF- $\kappa$ B signaling pathways and participates in the upregulation of pro-inflammatory cytokines [283, 284]. Particularly, vFLIP promotes tumorigenesis through the induction of COX-2 and its inflammatory metabolite PGE2 in an NF- $\kappa$ B-dependent manner [283, 285].

Most of the KSHV-encoded miRNAs are expressed during latency and play significant roles in tumor growth, inflammation, and angiogenesis. Numerous KSHV miRNAs induce inflammation by activating the NF- $\kappa$ B pathway [112, 242]. Ectopic expression of the miRNA cluster in endothelial cells induces the expression of pro-inflammatory and pro-angiogenic cytokines MMP1, MMP13, and VEGFA [286]. VEGF is important for the recruitment of stem cells and macrophages at the site of infection, and therefore participates in the inflammatory microenvironment of KS tumors [287]. By inducing CXCR2 and activating Akt signaling pathway through targeting GRK2 stimulation, miR-K3 promotes angiogenesis, migration, and invasion of endothelial cells [288, 289]. The miRNAs derived from miR-K6, miR-K6-3p, and miR-K6-5p promote cell migration, invasion, and angiogenesis by targeting SH3BGR to activate the STAT3 pathway and CD8 to activate the c-Met pathway, respectively [290, 291]. miR-K12 promotes cell survival and proliferation by targeting the angiogenesis inhibitor THBS1 and SMAD5 to downregulate TGF- $\beta$  signaling [292, 293].

In the context of inflammation, Kaposin B participates in the lymphatic reprogramming of vascular endothelial cells [294]. Kaposin B activates the p38/MK2 pathway leading to the stabilization of targeted gene transcripts including pro-inflammatory cytokines IL-6 and GM-CSF, as well as the lympho-endothelial differentiation factor PROX1 [294, 295]. By cooperating with c-Myc, Kaposin B triggers angiogenesis by mediating the expression of cellular miRNAs in endothelial cells [296].

In the latent phase, KSHV also expresses vIRF3 (LANA-2) in PEL cells [71]. vIRF3 plays a major role in PEL pathogenesis by promoting viral latency and inhibiting the host innate responses. By stabilizing HIF-1 $\alpha$ , vIRF3 induces its accumulation and activation in the nucleus contributing to the uncontrolled expression of VEGF in KSHV-infected cells [297].

### 2.6.3. Viral Lytic Genes Involved in Inflammation

ORF-K15, predominantly expressed during the lytic cycle, mediates inflammation by activating MAPK, JNK, and NF- $\kappa$ B pathways as well as NFAT/AP1 activities [298, 299]. These signaling pathways induce the expression of cytokines and chemokines such as IL-6, IL-1 $\beta$ , IL-8, CCL20, CXCL3, and COX-2. Depletion of ORF-K15 dramatically impairs KSHV-induced angiogenesis mediated by the recruitment of PLC $\gamma$ 1 and the activation of NFAT1-dependant RCAN1 expression in endothelial cells [300].

As stated earlier, ORF-K1 participates in KSHV-induced tumorigenesis by performing multiple functions. Among them, ORF-K1 induces the secretion of VEGF, IL-6, GM-CSF,

IL-1 $\beta$ , IL-8, and IL-10 in endothelial cells [301], and stimulates the expression of MMP-9, a matrix metalloproteinase involved in the angiogenic switch during tumor progression [302, 303]. In AIDS-related KS, ORF-K1 can synergize with HIV-1 proteins such as Tat to promote inflammation by activating NF- $\kappa$ B signaling [304] and NEF to promote cellular proliferation, vascular tube formation, and angiogenesis by regulating the PTEN/AKT/mTOR pathway [305]. In addition to inhibition of innate and adaptive immune responses, ORF-K5 enhances angiogenesis by disrupting VE-cadherin/ $\beta$ -catenin signaling, promoting the remodeling of cellular tight junctions [306]. vIL6 promotes angiogenesis and hematopoiesis by stimulating the secretion of VEGF [307]. By inducing several signaling pathways such as PKC, MAPK, mTOR, NF- $\kappa$ B, AP1, HIF-1 $\alpha$ , and NFAT, vGPCR mediates the upregulation of pro-inflammatory and pro-angiogenic mediators (IL-2, IL-4, IL-6, IL-8, TNF- $\alpha$ , and VEGF) [308, 309]. vGPCR activation of NF- $\kappa$ B induces the expression of RANTES, IL-8, and GM-CSF as well as adhesion molecules VCAM-1, ICAM-1 and E-selectin [310].

KSHV encodes three homologues of cellular chemokines: vCCL1, vCCL2, and vCCL3. These viral chemokines activate their respective G-coupled protein receptors CCR8, CCR3 and CCR4 expressed on Th2 lymphocytes [311]. These viral chemokines inhibit T cells immune response by inducing Th2 polarization and attracting Th2 lymphocytes to the site of infection, and promoting angiogenesis by inducing the expression of VEGF [312, 313]. Moreover, vCCL2 antagonize CCR1 and CCR5 to inhibit host immune responses of Th1 lymphocytes [314].

## 2.7. KSHV and Metabolism

During latent infection and cellular transformation, KSHV reprograms cellular metabolic pathways to provide biosynthetic and bioenergetic precursors to support the fast anabolic cellular proliferation. During viral lytic replication, KSHV also reprograms specific metabolic pathways to support the production of infectious virions.

### 2.7.1. KSHV Reprograms Glucose Metabolism

A hallmark of tumorigenesis involves the switch of energy metabolism from oxidative phosphorylation to aerobic glycolysis. In untransformed telomerase-immortalized microvascular endothelial cells (TIME cells) and primary dermal microvascular endothelial cells (DMVECs), KSHV infection increases aerobic glycolysis by upregulating hexokinase 2 (HK2) and glucose transporter 3 (GLUT3) [315]. Thus, oxygen consumption and oxidative phosphorylation are decreased, and lactate production is increased. Inhibition of glycolysis leads to apoptosis in KSHV-infected TIME cells but not in uninfected cells, demonstrating the critical role of the aerobic glycolysis on cell survival in untransformed KSHV-infected cells [315]. A similar study in KSHV-infected primary dermal microvascular lymphatic endothelial cells (KLEC) also demonstrated increased aerobic glycolysis [316]. Mechanistically, KSHV miRNAs stabilize HIF-1 $\alpha$  and inhibit mitochondrial biogenesis by downregulating EGLN2 and HSPA9. Moreover, HIF-1 $\alpha$  is stabilized in KSHV-infected telomerase-immortalized HUVEC (TIVE) cells, which results in the upregulation of

glycolytic effector-isoform 2 of pyruvate kinase (PKM2) and increased aerobic glycolysis [316].

However, KSHV-induced glycolysis does not occur in HFF cells [315], which implies cell type specificity in KSHV-induced metabolic reprogramming. In contrast to untransformed KSHV-infected cells, KSHV-transformed KMM cells have reduced glucose and oxygen consumption, lactate production, and intracellular ATP [240]. Mechanistically, vFLIP and the miRNA cluster inhibit the aerobic glycolysis in KMM cells by downregulating glucose transporters GLUT1 and GLUT3 through NF- $\kappa$ B activation. The decreased glycolytic flux confers a survival advantage to KMM cells in a nutrient deficient tumor microenvironment [240].

### 2.7.2. KSHV Reprogramming of Glutamine Metabolism for Host Cell Proliferation and Survival

Glutamine is required for cancer cell proliferation and survival [317, 318]. KSHV infection increases both the intracellular glutamine levels and glutamine uptake in TIME cells. KSHV-infected TIME cells rely on glutamine for their survival and glutamine deprivation-induced apoptosis in KSHV-infected TIME cells with a lesser effect on TIME cells [319].

Suppressing glutaminolytic enzymes in the presence of glutamine causes cell death at the similar levels to those deprived of glutamine in KSHV-infected TIME cells with little effect on TIME cells. The sensitivity to the absence of glutamine can be restored by the addition of TCA cycle intermediates, indicating that in untransformed cells, glutaminolysis is required for cell survivals by feeding the TCA cycle through anaplerosis [319].

KSHV-transformed KMM cells also rely on glutamine for their proliferation and transformation. The expression of glutaminolytic enzymes is upregulated in KMM cells compared to MM cells, and inhibition of any of those enzymes reduces KMM cell proliferation, implying glutaminolysis is required for KMM cell survival [320]. Interestingly, the addition of carbon sources, such as TCA intermediates, only partially rescues the proliferation of KMM cells following glutamine depletion. In contrast, nonessential amino acid asparagine fully rescues the effects of glutamine deprivation, indicating that glutamine and asparagine provide not only carbon source but also nitrogen source [320]. Specifically, glutamine provides the  $\gamma$ -nitrogen for nucleotide synthesis in KSHV-transformed cells. Overall, KSHV reprograms glutaminolysis to supply the building blocks for synthesizing nucleotides, nonessential amino acids, and TCA cycle intermediates to support KSHV-infected cell proliferation and transformation [320].

### 2.7.3. KSHV Infection Induces Lipogenesis

KSHV infection of TIME cells induces lipogenesis with an increase of metabolites involved in de novo fatty acid synthesis (FAS) and formation of lipid droplets [321]. Inhibitors of FAS induce a dose-dependent cell death in KSHV-infected TIME, which can be partially rescued by supplying cells with fatty acid precursors, indicating FAS is necessary for the survival of untransformed KSHV-infected TIME cells [321]. A separate study shows that KSHV infection increases peroxisomes in TIME cells [322]. A major function of peroxisomes is to break down the long-chain fatty acids through  $\beta$ -oxidation. Inhibition of enzymes involved

in the peroxisomal  $\beta$ -oxidation leads to increased cell death in KSHV-infected TIME cells. Together, these observations suggest that KSHV-induced FAS and peroxisomal lipid metabolism are required for KSHV-infected TIME cell survival [322]. Additionally, PEL cells also have highly upregulated FAS compared to primary B cells and are sensitive to FAS inhibitors [323].

#### 2.7.4. KSHV Depends on Glycolysis, Glutaminolysis, and FAS for Lytic Replication

Reprogramming of metabolic pathways is expected to be important for supporting KSHV lytic replication. However, there is so far limited work on metabolic rewiring during KSHV primary infection and reactivation. Inhibitors of glycolysis, glutaminolysis, and FAS significantly reduce the production of virions in both endothelial and SLK cells [324]. Inhibition of glycolysis and glutaminolysis suppresses KSHV replication by stalling early gene transcription and translation, respectively [324]. While inhibition of FAS decreases the production of extracellular virions, it does not affect intracellular viral genome levels, suggesting that FAS is required for virion assembly and maturation [324]. However, some of these inhibitors are not entirely specific and the mechanisms underlying the support of viral lytic replication by glycolysis and glutaminolysis remain unclear. Nevertheless, these results indicate that different stages of viral lytic replication might require different metabolites within the host cells.

## 2.8. Conclusion and Perspectives

Rapid progresses have been made in the KSHV field in the last decade, providing insights into the biology of virus and the scientific basis for developing novel therapeutic approaches for its associated malignancies. KSHV has evolved to hijack cellular machinery for completing its life cycle, which often results in the dysregulation of cellular functions. It is now clear that KSHV-induced uncontrolled cellular proliferation, cell survival, abnormal immune responses, and reprogrammed metabolism promote malignant tumor growth, angiogenesis, and inflammation, which are the hallmarks of KS.

The standard KS chemotherapy with liposomal doxorubicin, daunorubicin, or taxol is highly toxic and ineffective despite effective antiretroviral therapy in some cases [325]. Both PEL and MCD also do not any have effective therapy [326]. Therefore, alternative treatments and new therapeutic targets, particularly those targeting malignant proliferation, angiogenesis, inflammation, and dysregulated immune responses, are needed for KSHV-associated malignancies. Laboratory studies have so far identified numerous new targets and agents. These include sirtuin inhibitors (Tenovin-6 and nicotinamide), HDACs inhibitor, AMPK inhibitor, mTOR inhibitor Rapamycin (sirolimus), and p53 activator Nutlin-3 [264, 265, 266, 327, 328, 329, 330, 331]. Numerous potential therapeutic targets, particularly those targeting KSHV-specific epigenetics and metabolism, are attractive. Nevertheless, rigorous clinical trials are required to evaluate the efficacies of the inhibitors before their extensive usages in the patients. In fact, new drugs bevacizumab and imatinib for KS, and siltuximab for KSHV-MCD have been examined in clinical trials [332, 333, 334]. Ongoing clinical trials are testing the efficacies of Tocilizumab (NCT01441063) for MCD, and lenalidomide (NCT01057121) and pomalidomide (NCT02659930) for KS [335]. Because cellular



pathways often interact with one another, it would be interesting to evaluate interaction effects of multiple pathways and inhibitors. For example, while Rapamycin inhibits the mTOR pathway, it also activates the Akt pathway. Hence, the combination of inhibitors of both pathways would be predicted to be favorable, which has been demonstrated for both KS and PEL cells [267, 336].

Since KSHV is not a ubiquitous herpesvirus and immunosuppression is required for the development of the KSHV-associated malignancies, it would be essential to develop effective strategies to prevent its person-to-person transmission and manage immunosuppression in the affected populations. Development of KSHV vaccines should be one of the focuses of future research.

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