



National Toxicology Program
U.S. Department of Health and Human Services

REPORT ON CARCINOGENS

MONOGRAPH ON KAPOSI SARCOMA-ASSOCIATED HERPESVIRUS

RoC MONOGRAPH 10

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Report on Carcinogens Monograph on Kaposi Sarcoma-Associated Herpesvirus

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Foreword

The National Toxicology Program (NTP), established in 1978, is an interagency program within the Public Health Service of the U.S. Department of Health and Human Services. Its activities are executed through a partnership of the National Institute for Occupational Safety and Health (part of the Centers for Disease Control and Prevention), the Food and Drug Administration (primarily at the National Center for Toxicological Research), and the National Institute of Environmental Health Sciences (part of the National Institutes of Health), where the program is administratively located. NTP offers a unique venue for the testing, research, and analysis of agents of concern to identify toxic and biological effects, provide information that strengthens the science base, and inform decisions by health regulatory and research agencies to safeguard public health. NTP also works to develop and apply new and improved methods and approaches that advance toxicology and better assess health effects from environmental exposures.

The Report on Carcinogens Monograph series began in 2012. Report on Carcinogens Monographs present the cancer hazard evaluations of environmental agents, substances, mixtures, or exposure circumstances (collectively referred to as “substances”) under review for the [Report on Carcinogens](#). The Report on Carcinogens is a congressionally mandated, science-based, public health document that provides a cumulative list of substances that pose a cancer hazard for people in the United States. Substances are reviewed for the Report on Carcinogens to (1) be a new listing, (2) reclassify the current listing status, or (3) be removed.

NTP evaluates cancer hazards by following a multistep process and using established criteria to review and integrate the scientific evidence from published human, experimental animal, and mechanistic studies. General instructions for the systematic review and evidence integration methods used in these evaluations are provided in the [Handbook for the Preparation of Report on Carcinogens Monographs](#). The handbook’s instructions are applied to a specific evaluation via a written protocol. The evaluation’s approach as outlined in the protocol is guided by the nature, extent, and complexity of the published scientific information and tailored to address the key scientific issues and questions for determining whether the substance is a potential cancer hazard and should be listed in the Report on Carcinogens. Draft monographs undergo external peer review before they are finalized and published.

The Report on Carcinogens Monographs are available free of charge on the [NTP website](#) and cataloged in [PubMed](#), a free resource developed and maintained by the National Library of Medicine (part of the National Institutes of Health). Data for these evaluations are included in the [Health Assessment and Workspace Collaborative](#). Information about the Report on Carcinogens is also available on the NTP website.

For questions about the monographs, please email [NTP](#) or call 984-287-3211.

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This report has been reformatted to meet new NTP publishing requirements; its content has not changed. The proposed substance profile is no longer part of the document because it is published in the 14th Report on Carcinogens.

About This Report

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Peer Review

Peer review of the Draft RoC Monograph on Kaposi Sarcoma-Associated Herpesvirus (KSHV) was conducted by an ad hoc expert panel at a public meeting held December 17, 2015, in the Rodbell Auditorium at the National Institute of Environmental Health Sciences, David P. Rall Building, Research Triangle Park, NC (see <http://ntp.niehs.nih.gov/go/38854>) for materials, minutes, and panel recommendations from the peer-review meeting). The selection of panel members and conduct of the peer review were performed in accordance with the Federal Advisory Committee Act and federal policies and regulations. The panel members served as independent scientists, not as representatives of any institution, company, or governmental agency.

The charge to the Peer-Review Panel was as follows:

- (1) Comment on the draft cancer evaluation component for KSHV, specifically, whether it was technically correct and clearly stated, whether the NTP has objectively presented and assessed the scientific evidence, and whether the scientific evidence is adequate for applying the RoC listing criteria,
- (2) Comment on the draft substance profile for KSHV, specifically, whether the scientific justification presented in the substance profile supports the NTP's preliminary policy decision on the RoC listing status of the substance (available in the 14th edition of the Report on Carcinogens).

The Panel was asked to vote on the following questions:

- (1) Whether the scientific evidence supports the NTP's preliminary conclusion on the level of evidence for carcinogenicity for the specific types of cancer from cancer studies in humans.
- (2) Whether the scientific evidence supports the NTP's preliminary listing decision for KSHV in the RoC.

This RoC monograph on KSHV has been revised based on NTP's review of the Panel's peer-review comments. The Peer-Review Panel Report, which captures the Panel recommendations for listing status of KSHV in the RoC and their scientific comments, and the NTP Response to the Peer-Review Report are available on the Peer-Review Meeting webpage for Kaposi sarcoma-associated herpesvirus (<http://ntp.niehs.nih.gov/go/38854>).

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Abstract

Introduction: Kaposi sarcoma-associated herpesvirus (KSHV), also known as human herpesvirus 8 (HHV8), is an enveloped double-stranded DNA gamma-2 herpesvirus (rhadinovirus) that was first identified in humans in 1994 in association with acquired immunodeficiency syndrome (AIDS) and cancer. The overall prevalence of KSHV antibodies in the U. S. general population is approximately 7%. KSHV prevalence rates are much higher in certain geographical areas (e.g., 50% in some sub-Saharan African populations). KSHV is thought to be transmitted primarily via saliva, but transmission has also been reported in injection drug users, in transfusion recipients, and from organ-transplant donors to recipients, all of which suggest it can also be spread via blood.

Methods: The National Toxicology Program (NTP) conducted a cancer hazard evaluation of KSHV infection and several types of cancer for possible listing in the Report on Carcinogens. The evaluation included the findings from studies reported in the IARC monograph in Volume 100B and from human cancer studies and mechanistic reviews published after the IARC monograph. For each cancer site, the evidence from human and mechanistic studies was integrated considering the following guidelines: Hill's characteristics of causality, multicausality epidemiology considerations, guidance from the IARC 100B working group, and concepts of direct and indirect carcinogenesis proposed several virus experts.

Results and Discussion: NTP concluded there was sufficient evidence of carcinogenicity for KSHV from studies in humans for the following three types of human cancer:

Kaposi sarcoma: This cancer of the cells that line blood or lymph vessels is associated with KSHV infection based on consistent findings of increased risk (some very high, ranging from 10- to 100-fold) in many prospective cohort and case-control studies in different populations for all four subtypes of Kaposi sarcoma and on the presence of an exposure-response relationship between the degree of viral infection and the cancer. KSHV is found in >90% of Kaposi sarcoma tumors in biopsies from Kaposi sarcoma case series. Many, but not all, patients infected with KSHV who develop Kaposi sarcoma have immune systems compromised either by HIV-1 infection or as a result of drug treatments after organ or tissue transplants. KSHV codes for viral proteins that transform cells into cancer cells, promote tumor growth, and evade and alter the immune system.

Primary effusion lymphoma (PEL): This rare B-cell non-Hodgkin lymphoma is associated with KSHV infection based on its detection in tumors from 95% of 115 KSHV-infected patients (reported in case reports, several small case series, and a case-comparison study), together with molecular studies of the tumors' specific morphological and immunological features. Molecular studies show that PEL tumors are monoclonal for the virus, contain high levels of KSHV DNA, and express proteins similar to Kaposi sarcoma. KSHV infection is a diagnostic criterion.

Multicentric Castleman disease (plasmablastic variant): This is a second type of rare B-cell non-Hodgkin lymphoma linked with KSHV infection based on nine case-series studies and four case-comparison studies supporting an association between KSHV infection and all types of multicentric Castleman disease and molecular studies. The latter found that KSHV DNA was detected in all tumors co-infected with HIV and KSHV and 50% infected with only KSHV. Molecular analysis of tumor tissue confirmed the association between KSHV infection and multicentric Castleman disease and demonstrated that the plasmablastic variant has a unique

molecular profile and produces a distinctive monotypic form of immunoglobulin M that is not found in KSHV-negative multicentric Castleman disease.

NTP Hazard Conclusion and Significance: The conclusion of the cancer hazard evaluation was that KSHV should be listed as *known to be a human carcinogen* in the RoC. The Secretary of Health and Human Services approved the listing of KSHV in the 14th RoC. The rationale for the listing was sufficient evidence from studies in humans (human cancer and mechanistic) for three types of cancer. Globally, KSHV is estimated to be responsible for approximately 44,000 cancers per year.

Introduction and Methods

This is one of a collection of five monographs that provide cancer hazard evaluations for the following human viruses for potential listing in the Report on Carcinogens (RoC): Epstein-Barr virus, Kaposi sarcoma-associated herpesvirus, human immunodeficiency virus type 1, human T-cell lymphotropic virus type 1, and Merkel cell polyomavirus. Viruses currently listed in the RoC include human papillomaviruses: some genital-mucosal types (HPV), hepatitis B virus (HBV), and hepatitis C virus (HCV). Each virus was selected for review for the RoC based on a large database of scientific information (including authoritative reviews), public health concerns for adverse health outcomes, and evidence that a significant number of people are infected with each virus both in the United States and worldwide.

This section provides background information on the preparation of the monographs as well as a discussion of overarching issues related to evaluating the evidence for cancer from human epidemiological studies and evaluating the causation by viruses.

Monograph Contents

The RoC monograph for each virus reviews the relevant scientific information and assesses its quality, applies the RoC listing criteria to the scientific information, and recommends an RoC listing status. Information reviewed in the monographs, with the exception of information on properties and exposure, comes from publicly available and peer-reviewed sources. All sections of the monographs underwent scientific and quality assurance review by independent reviewers.

The monograph provides the following information relevant to a RoC listing recommendation: Properties and Detection (Section 1), Human Exposure (Section 2), Human Cancer Studies (Section 3), Mechanistic and Other Relevant Data (Section 4), and Overall Cancer Hazard Evaluation and Listing Recommendation (Section 5). Because these viruses are primarily species-specific for humans, we are not conducting an evaluation of the level of evidence for carcinogenicity from studies in experimental animals and are including studies in animals that inform the mechanisms of carcinogenicity in the Mechanistic and Other Relevant Data section of the monographs, which is similar to the approach used by IARC. Also, specific details about the strains of the viruses are given only if needed to provide context, such as in the viral Properties and Detection section. The monographs relied on the information and data provided in previous IARC monographs on these five viruses in addition to newer key studies or reviews published since the IARC monographs; it is a peer-review assessment of available data through August 17, 2015. Additional publications published after that date were added to the monograph based on recommendations from the peer-review panel that reviewed this document on December 17, 2015. Literature search strategies to obtain information relevant to the cancer evaluation are in Appendix A of each virus monograph; search terms were developed in collaboration with a reference librarian.

Evaluating the Evidence from Human Epidemiological Studies

The available studies of specific types of cancer for these human viruses present several challenges with respect to the evaluation of methodological strengths and limitations of the body of evidence. Large prospective cohort studies, particularly those that follow individuals for

whom infection status is documented prior to follow-up or cancer diagnosis, have several potential methodological strengths, including evidence that infection precedes cancer diagnosis, adequate statistical power, and, in some studies, have the ability to analyze dose-response relationships. However, there is the potential for misclassification of exposure in studies with a long follow-up period that measure the virus once and have a long follow-up period as new infections might not be identified. For most types of cancer, only cross-sectional or retrospective cohort studies or hospital- or clinic-based case-control studies are available, all of which lack direct evidence of temporality and may lack power or adequate exposure data, e.g., on viral load. However, molecular evidence from human studies and mechanistic data can be used in the evaluation of temporality, distinguishing latent infections caused by the tumor virus and causality. For some (typically rare) outcomes (e.g., cutaneous T-cell lymphoma and human T-cell lymphotropic virus type 1, or lymphoepithelial carcinoma of the salivary gland and Epstein-Barr virus), only case-comparison studies, in which selection of comparison groups may be biased, unmatched, or inadequately described, or case series are available.

For several rare types of cancer, e.g., adult T-cell leukemia/lymphoma and human T-cell lymphotropic virus type 1, or primary effusion lymphoma and Kaposi sarcoma-associated herpesvirus, the presence of the virus in the tumor cells is used as a diagnostic criterion to define the cancer, and thus, evidence of causality relies on cases defined by this criterion and molecular evidence from human studies rather than on epidemiological population-based studies of the association of the virus with a level of cancer risk.

In addition, methodologically adequate studies should include measurement of cofactors and consider potentially confounding factors; however, relatively few studies have measured a panel of other viruses or taken into account other cofactors. Further, while studies comparing cancer risk in treated vs. untreated populations may provide indirect evidence of the role of human immunodeficiency virus type 1, these studies, in particular calendar-period analyses, may not adequately account for changes in risk attributable to improved survival rates or changes in other risk factors.

Evaluating Causality of Viruses

Approximately 12% of all human cancers have been attributed to viral infections. Although the known oncogenic viruses belong to different virus families, they often share several common traits, such as, viral cancers appear in the context of persistent infections, occur many years to decades after acute infection, and the immune system can play a deleterious or a protective role (Mesri et al. 2014). Many viruses generally increase cancer risk in the context of immunosuppression or chronic inflammation (Mesri et al. 2014). Similar to other carcinogenic agents, only a small percentage of infected or exposed individuals develop cancer, often decades after the initial infection, reflecting the complex nature of oncogenesis. Some cofactors produced by other organisms or agents in conjunction with risk modifiers such as virus-host cell interactions, host genetic factors, immune dysfunction, or chronic inflammation often can contribute to malignant transformation. In addition, severe immunosuppression, as seen with congenital immunodeficiency syndromes, chronic human immunodeficiency virus type 1 infection, or as a result of tissue anti-rejection medication, can severely compromise the immune surveillance capabilities of the patient. There are also other challenges that are somewhat unique to the evaluation of the epidemiological studies of viruses and cancer (discussed below) and thus molecular evidence from human tissues is often considered in the evaluation of causality.

In light of these issues, IARC monographs and several other publications have recommended paths to evaluate causality, which are discussed below and incorporated into the NTP approach for evaluating causality of the viruses. What is important for public health in determination of causation of a health effect, such as risk for cancer, is whether the health effect is eliminated or mitigated by removal of the substance (Rothman and Greenland 2005).

A number of attempts have been made to develop criteria or considerations that address causal associations. However, all of them have limitations, especially when applied to infectious agents (Moore and Chang 2010). The following sections identify factors to consider for evaluating causality, some limitations arising from a strict application of the criteria in the context of virally induced cancers, some alternative approaches, and finally, the NTP’s approach for evaluating the role of select viral agents in human cancer.

Hill’s Characteristics of Causality

Hill proposed nine characteristics to consider when evaluating causality, primarily for epidemiological studies, although they have been expanded for evaluating mechanistic and other types of data (Table 1). Several considerations—strength of the association, consistency across studies, evidence of an exposure-response gradient, and temporality of exposure (Hill 1965)—are used to help guide the RoC evaluations of the human epidemiological data (see RoC Handbook, NTP 2015). However, it should be noted that these are not criteria; and, with the exception of temporality, each and every element is not required in order to demonstrate causality (Rothman and Greenland 2005). Hill (1965) avoided discussing the meaning of “causation,” noting that the “cause” of an illness could be immediate and direct or remote and indirect. The primary question addressed by Hill was “whether the frequency of the undesirable event B will be influenced by a change in the environmental feature A.”

Table 1. Hill’s Epidemiological Characteristics for Evaluating Causality

Characteristic	Description
1. Strength of association	A strong association between a virus and a cancer increases the confidence for causality unless confounded by some other exposure. However, a weak association does not give evidence against causality.
2. Consistency	Consistent findings observed among different groups of people, in different places, circumstances, and times.
3. Specificity	A viral exposure is limited only to specific types of cancer; this is considered a weak factor because there are well-established examples in which a virus might cause several types of cancer.
4. Temporality	Exposure to the virus must occur prior to the onset of the cancer, in contrast to a “passenger infection.”
5. Biological gradient	The virus is more likely to be found at the tumor site than at non-tumor sites.
6. Plausibility	This characteristic should be applied with caution because it is limited by current medical knowledge (e.g., a currently implausible mechanism may gain acceptance with increased understanding of the underlying biology).
7. Coherence	A virus-cancer association should not seriously conflict with known facts on the cancer’s natural history and biology.

Characteristic	Description
8. Experiment	Changing either exposure or continued infection in a randomized clinical trial should change the measure of clinical outcome (e.g., vaccination programs for HPV and HBV).
9. Analogy	Are related viruses clearly established to cause cancers in animals or humans?

Source: Moore and Chang (2014).

Evaluating Mechanistic Data from Human Studies

In their evaluation of the evidence for Epstein-Barr virus, the IARC working group noted that the large majority of people are latently infected with Epstein-Barr virus, thus, epidemiological studies may be limited in determining whether the presence of Epstein-Barr virus in tumor tissue is a cause of the cancer or an effect of the tumor. Therefore, in addition to the Hill characteristics, IARC (1997b) considered the following factors in their evaluation of Epstein-Barr virus, which are also applicable to other viruses:

- The proportion of Epstein-Barr virus-positive cases in a given tumor entity.
- The proportion of tumor cells that carry the virus.
- The monoclonality of Epstein-Barr virus in the tumor.
- The expression of Epstein-Barr virus proteins.

zur Hausen (1994; 2001) proposed consideration of the following types of mechanistic or epidemiological evidence for evaluating causality of viruses and cancer:

- The presence and persistence of viral DNA in tumor biopsies and cell lines derived from the same tumor type.
- The growth-promoting activity of specific viral genes or of virus-modified host-cell genes in tissue culture systems or in suitable animal systems.
- The continuous expression of viral oncogenes or the modification of host-cell genes containing viral sequences which maintains the malignant phenotype.
- The epidemiological evidence that the virus infection is a major risk factor.

It is difficult to prove that a virus causes cancer, and such determinations almost always generate considerable controversy and debate (Moore and Chang 2010). Viral cancers employ various mechanisms that involve both direct and indirect modes of interaction (Table 2) (zur Hausen and de Villiers 2014). Understanding and managing viral-induced cancers in humans has been hampered by a lack of suitable animal models, the disparate nature of tumor types, a long latency period between primary infection and cancer development, the different types of oncogenic viruses, and the complex nature of the virus-host cell interactions leading to cancer (Mesri et al. 2014; zur Hausen and de Villiers 2014).

Table 2. Direct and Indirect Modes of Interaction of Viral Infections and Cancers

Type	Description
Direct carcinogenesis	Continued presence and expression of viral oncogenes usually after viral genome integration into host cell DNA. Insertional gene activation or suppression. Continued episomal presence of viral nucleic acid and suppression or activation of cellular genes (e.g., by viral microRNA).
Indirect carcinogenesis	Induction of immunomodulation, activation of latent tumor virus genomes. Induction of oxygen and nitrogen radicals. Amplification of latent tumor virus DNA. Induction of mutations and/or translocations. Prevention of apoptosis.

Source: zur Hausen and de Villiers (2014).

Multicausality Issues

Although thousands of viruses are known to cause infection, only a few have been shown to cause cancer in humans (Moore and Chang 2010). An important consideration regarding causality (not limited to viruses) is “multicausality,” that is, the concept that many determinants act together to cause a disease. Rothman and colleagues (2005) defined a sufficient cause as “complete causal mechanism”—not a single factor but a set of minimal factors (i.e., component causes)—that if present in an individual will cause disease. Most causes are neither necessary nor sufficient in the absence of other factors to produce the disease; however, a cause does not have to be either necessary or sufficient for its removal to result in disease prevention (Rothman and Greenland 2005; zur Hausen and de Villiers 2014).

Application of Causality Criteria and Alternative Approaches

Moore and Chang (2010) investigated the difficulties associated with strict application of the Hill characteristics for two of the most recently discovered oncogenic viruses: Kaposi sarcoma-associated herpesvirus and Merkel cell polyomavirus. Kaposi sarcoma-associated herpesvirus was shown to fulfill Hill’s characteristics for causality of Kaposi sarcoma; however, the application of the characteristics was problematic in the case of Merkel cell polyomavirus and Merkel cell carcinoma (see the monographs for Kaposi sarcoma-associated herpesvirus and Merkel cell polyomavirus). These two examples illustrate the diversity in the patterns of tumor virus epidemiology. Some of the reasons Hill’s characteristics worked for Kaposi sarcoma-associated herpesvirus but not Merkel cell polyomavirus is that all clinical forms of Kaposi sarcoma require infection by Kaposi sarcoma-associated herpesvirus while most studies indicate that not all forms of Merkel cell carcinoma require the presence of Merkel cell polyomavirus. In the case of Merkel cell polyomavirus, additional considerations, as suggested by IARC (1997b) and zur Hausen (1994; 2001), provide molecular evidence of the association between Merkel cell polyomavirus and Merkel cell carcinoma, such as mutation and monoclonal integration of the tumor-causing form of the virus into the cellular genome and requirement of tumor cells for the presence of viral oncoproteins for cell survival and proliferation.

While causal criteria can be helpful, there are flaws and practical limitations that restrict their use in cancer biology (Moore and Chang 2010). Therefore, a more probabilistic approach may be more useful for determining whether or not certain viruses cause human cancers. For example, instead of trying to determine if virus A causes cancer B, the probabilistic approach examines if

cancer B is more probable in the presence of virus A. Although a correlation does not imply causation, it can be argued that correlations that are strong, reproducible, and predictive have a similar value as a causative conclusion. In a similar fashion, zur Hausen and de Villiers (2014) also expressed concern over all attempts to summarize criteria for “causality” of infectious agents in cancer development and proposed replacing “causal factor” with “risk factor” and grading them according to their contribution to an individual’s cancer risk. This will require a greater understanding of the complexity of factors involved and their mechanistic contribution to individual cancers.

RoC Listing Criteria

Known to Be Human Carcinogen:

There is sufficient evidence of carcinogenicity from studies in humans*, which indicates a causal relationship between exposure to the agent, substance, or mixture, and human cancer.

Reasonably Anticipated to Be Human Carcinogen:

There is limited evidence of carcinogenicity from studies in humans*, which indicates that causal interpretation is credible, but that alternative explanations, such as chance, bias, or confounding factors, could not adequately be excluded, OR

there is sufficient evidence of carcinogenicity from studies in experimental animals, which indicates there is an increased incidence of malignant and/or a combination of malignant and benign tumors (1) in multiple species or at multiple tissue sites, or (2) by multiple routes of exposure, or (3) to an unusual degree with regard to incidence, site, or type of tumor, or age at onset, OR

there is less than sufficient evidence of carcinogenicity in humans or laboratory animals; however, the agent, substance, or mixture belongs to a well-defined, structurally related class of substances whose members are listed in a previous Report on Carcinogens as either known to be a human carcinogen or reasonably anticipated to be a human carcinogen, or there is convincing relevant information that the agent acts through mechanisms indicating it would likely cause cancer in humans.

Conclusions regarding carcinogenicity in humans or experimental animals are based on scientific judgment, with consideration given to all relevant information. Relevant information includes, but is not limited to, dose response, route of exposure, chemical structure, metabolism, pharmacokinetics, sensitive sub-populations, genetic effects, or other data relating to mechanism of action or factors that may be unique to a given substance. For example, there may be substances for which there is evidence of carcinogenicity in laboratory animals, but there are compelling data indicating that the agent acts through mechanisms which do not operate in humans and would therefore not reasonably be anticipated to cause cancer in humans.

*This evidence can include traditional cancer epidemiology studies, data from clinical studies, and/or data derived from the study of tissues or cells from humans exposed to the substance in question that can be useful for evaluating whether a relevant cancer mechanism is operating in people.

NTP’s Approach

For each virus, the NTP applied the RoC listing criteria (see text box) to the body of literature to reach the listing recommendation. The level of evidence conclusion from studies in humans considers the evidence from epidemiological studies as well as clinical and molecular studies of tissues from exposed (i.e., infected) individuals. In evaluating the mechanistic data and determining the recommendations for its level of evidence conclusion and overall listing recommendation, the NTP considered the principles outlined by Hill (1965), IARC (1997a), zur Hausen (1994; 2001; 2014), and Rothman and Greenland (2005) in its assessment of causality for the five viruses reviewed. However, these factors were not used as a strict checklist to either

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prove or disprove a causal association but rather as guidance to assess the level of epidemiological or molecular evidence that a virus contributes to a carcinogenic effect.

1. Properties and Detection

This section reviews the biological properties (Section 1.1) and detection methods (Section 1.2) of the Kaposi sarcoma-associated herpesvirus (KSHV). The information in this section is summarized in Section 1.3.

1.1. Biological Properties

1.1.1. Family and Type

KSHV, also designated as human herpesvirus 8 (HHV8), was the first member of the gamma-2 herpesviruses identified in humans in 1994 in association with acquired immunodeficiency syndrome (AIDS) (Chang et al. 1994; Fukumoto et al. 2011; IARC 1997b). Rhadinoviruses also include herpesviruses that infect New World monkeys, macaque Old World monkeys, cattle, and rodents (IARC 1997b).

KSHV consists of linear double-stranded DNA (dsDNA) wrapped around a core protein within a protein capsid, surrounded by a membrane envelope containing glycoproteins (Edelman 2005; Fukumoto et al. 2011; Giffin and Damania 2014; IARC 1997b; 2012) (see Figure 1-1). The capsid is made up of five major capsid proteins forming hexamer and pentamer proteins and a minor capsid protein that binds to the edges of the hexamer and pentamer junctions (Giffin and Damania 2014; IARC 2012). Between the capsid and the membrane envelope are six tegument proteins and 11 viral RNA strands (Fukumoto et al. 2011; Giffin and Damania 2014).

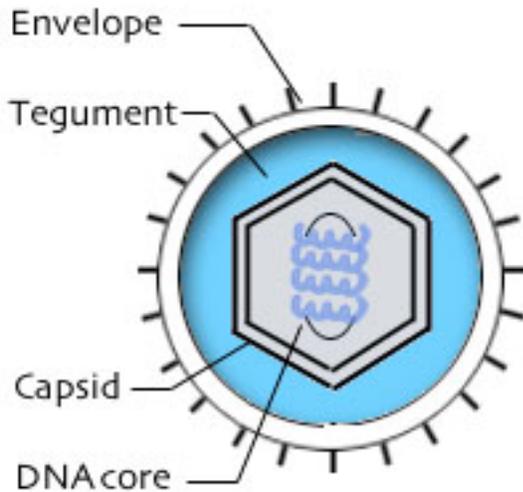


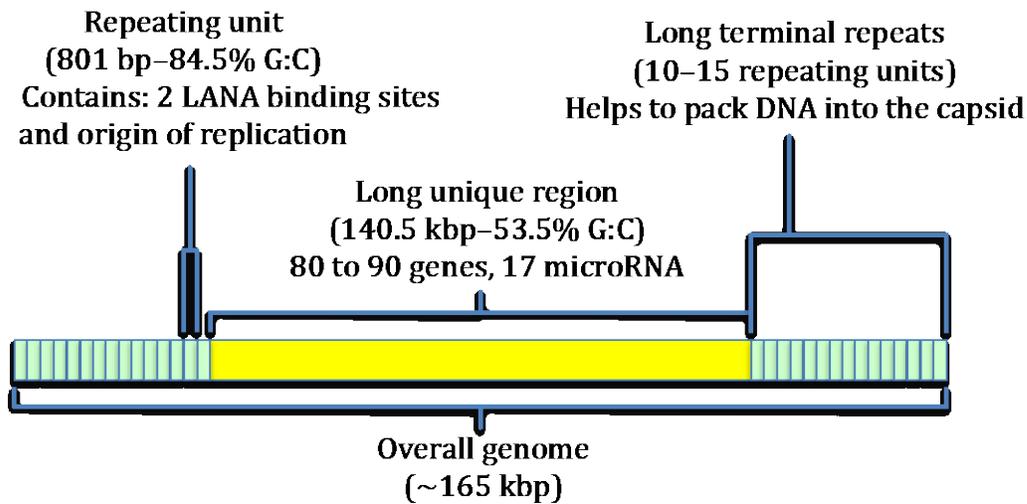
Figure 1-1. Kaposi Sarcoma-Associated Herpes Virus Particle

Source: Los Alamos National Laboratory.

1.1.2. Genome

The KSHV genome, with an overall size of 165 kbp, consists of two main sections, (1) the long unique region, which contains over 80 open reading frames (ORF) for protein and microRNA (miRNA) genes, is 140 kbp long and (2) two flanking terminal repeat regions composed of a variable number of repeating units (see Figure 1-2) (Fukumoto et al. 2011; IARC 1997b; 2012). The terminal repeats do not contain open reading frames, but function by providing the origin of replication, location of genome circularization, and binding sites to tether the viral genome to host chromosomes.

Most of the genes are conserved among herpesviruses and are named after the genes of the closest related virus, *Herpesvirus saimiri*, which infects non-human primates (IARC 1997b; 2012). These genes are designated by the number identifier of their open reading frame, e.g., ORF 16, and are numbered consecutively from left to right across the genome (Giffin and Damania 2014). Other genes originated from host cellular genes during viral evolution and are designated by their cellular homologue, preceded by “v-” denoting a viral origin, e.g., v-Bcl-2 (IARC 1997b; 2012). Some genes are unique to KSHV and are designated by the letter “K” in their open reading frame, e.g., ORF K12. MiRNAs are designated by “miR” and a number identifier, e.g., miR-K5.



Gene categories

Homologues of Herpes virus Saimiri

Homologues of human genes

Unique to KSHV (designated by “K” before the ORF number, ex. ORF K2)

Figure 1-2. Genome Schematic

LANA = latency-associated nuclear antigen.

1.1.3. Infection and Replication

Like other herpesviruses, the KSHV replication cycle includes a latent phase and a lytic phase, which allow the virus to transition between a quiescent infection and active replication (see Figure 1-3). KSHV has been detected in endothelial cells, epithelial cells, B lymphocytes, and

monocytes *in vivo*, while a wider variety of cells can be infected *in vitro* (Giffin and Damania 2014). CD19⁺ B lymphocytes are a long-term latency reservoir for the virus. KSHV glycoproteins on the capsid surface mediate fusion with several target cell receptors, and the replication cycle starts as KSHV enters a cell by a receptor-mediated endocytosis or macropinocytosis process (Campbell et al. 2014a; Giffin and Damania 2014). The viral capsid then enters the nucleus and releases dsDNA. Inside the virus particle, the genome is linear, but within the host cell nucleus it circularizes, joining the terminal repeat ends together and attaching to host cell chromosomes (Campbell et al. 2014a; Fukumoto et al. 2011; IARC 1997b). In the latent phase, the viral episome persists and is replicated by host machinery to daughter cells with each cell division. No infectious virus particles are produced during latency and only a small number of genes located in the latency locus are expressed. Only a low copy number of the viral genome is present in a latently infected cell, while a high copy number is produced during a lytic infection.

Most of the time, KSHV will remain in the latent phase but cell stressors, such as phorbol esters, sodium butyrate, some signaling cytokines, cell differentiation, reactive oxygen species, and innate immune signaling by Toll-like receptors, can initiate the lytic phase (Giffin and Damania 2014). At the start of the lytic phase the viral lytic transactivator protein, RTA, causes the expression of many viral genes, beginning with those involved in controlling viral gene expression. The next viral genes expressed are those involved in DNA replication and immunomodulation. Viral DNA replication occurs at multiple origins within the terminal repeat region of the circular genome to produce linear copies of newly formed genomes. The viral capsid is then enveloped by the lipid bilayer membrane as it buds off of the nuclear membrane into the cytoplasm and progeny virions are released from the cell. See Section 4.1.2 for a detailed description of latent and lytic genes.

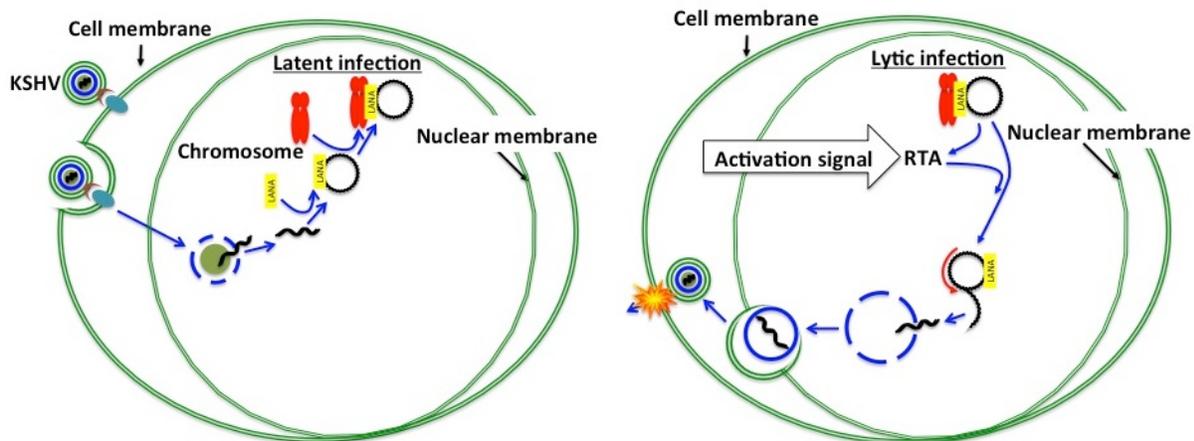


Figure 1-3. KSHV Infection and Replication Cycle

1.2. Detection Methods

KSHV infections can be detected by measuring viral protein antigens or viral DNA in tissues and antibodies against the virus in blood (see Table 1-1). The level of KSHV antibodies in the blood only suggests that a viral infection has occurred, as both the specificity and sensitivity of the test methods are low (Fukumoto et al. 2011; IARC 2012; Xu et al. 2015). KSHV DNA or antibodies against KSHV-specific antigens in the blood can be used to measure viral load. The nature of the

antigens recognized by the antibodies, i.e., either latent or lytic, can help to determine the predominant nature of the infection, but this test alone is not conclusive because of variations in development of antibody responses among individuals (IARC 2012). Both latent and lytic viral infections are associated with carcinogenesis (IARC 2012). In cases of Kaposi sarcoma or primary effusion lymphoma, KSHV latently infects almost all tumor cells while lytic infection is frequently seen in the plasmablastic variant of multicentric Castleman disease (see Mechanisms and Other Relevant Data, Section 4) (Damania 2010; Dupin et al. 2000). Antibodies against two main viral proteins have been measured in humans to detect KSHV, though other protein-specific antibodies can be detected as well (see Mechanisms and Other Relevant Data, Section 4) (Fukumoto et al. 2011; IARC 1997b; 2012). These include the latent phase protein, latency-associated nuclear antigen (LANA), (ORF 73), and the lytic phase protein, K8.1.

1.2.1. Detection in Fluids

Antibodies

The level of antibody response varies depending on the phase of the infection (IARC 2012). Antibody responses are low in latently infected individuals and higher in patients with lytic infections or in patients with Kaposi sarcoma (IARC 2012). Latently infected cell lines can be used to immunohistochemically detect anti-KSHV antibodies, which stain in the nucleus only. Infected cell lines can be stimulated with phorbol esters or sodium butyrate to increase the number of cells in the lytic phase and to detect antibodies against lytic antigens, which stain the cytoplasm as well as the nucleus (Fukumoto et al. 2011; IARC 1997b). Recombinant viral proteins and peptides have also been used in ELISA tests for KSHV antibodies (IARC 2012). Polymerase chain reaction (PCR) techniques can detect viral DNA in saliva and to a lesser extent in vaginal secretions and semen (Campbell et al. 2014a); however, these techniques are not used clinically.

1.2.2. Detection in Cells

Antigens

KSHV can infect many different cell types including B cells, dendritic cells, monocytes, prostate cells, keratinocytes, fibroblasts, endothelial cells, and epithelial cells, as detected by immunohistochemical staining for KSHV antigens (Campbell et al. 2014a; Fukumoto et al. 2011; Giffin and Damania 2014; IARC 1997b; 2012). KSHV encodes a viral homolog of interleukin-6 (vIL-6), which can be detected in the affected cells and blood of patients with multicentric Castleman disease, primary effusion lymphoma, and Kaposi sarcoma (Aoki et al. 2001; Bhutani et al. 2015; Fukumoto et al. 2011; Mesri et al. 2010; Parravicini et al. 2000; Parravicini et al. 1997). vIL-6 is thought to play a role in multicentric Castleman disease pathogenesis by stimulating the proliferation of plasma cells.

DNA

Viral DNA detected in tissues by PCR can indicate KSHV infections in those tissues (Fukumoto et al. 2011; IARC 1997b; 2012). KSHV DNA can be detected in peripheral blood mononuclear cells, but not all KSHV-infected patients will give positive results (Campbell et al. 2014a; Fukumoto et al. 2011; IARC 1997b). KSHV infection can occur without Kaposi sarcoma or multicentric Castleman disease, so detecting KSHV DNA in peripheral blood mononuclear cells does not necessarily indicate the presence of these diseases. However, those with Kaposi

sarcoma or multicentric Castleman disease tend to have higher viral loads in peripheral blood mononuclear cells.

Table 1-1. Detection Methods

Analyte	Method	Lytic Marker	Latent Marker
Fluids			
Antibodies	Immunohistochemistry – infected primary effusion lymphoma cells	Nuclear and cytoplasmic staining ^a	Only nuclear staining
	ELISA	High levels – Suggestive	Low levels – Suggestive
DNA	PCR	Genome detection - Not phase specific	–
Cells			
Antigen	Immunohistochemistry – tissue	Nuclear and cytoplasm staining	Only nuclear staining
DNA	PCR	Genome detection - Not phase specific	–

^aPhorbol esters are used to induce the lytic phase in primary effusion lymphoma cells.

1.3. Summary

Kaposi sarcoma-associated herpesvirus (KSHV) is an enveloped DNA virus found in Kaposi sarcomas, primary effusion lymphoma, and some cases of multicentric Castleman disease. The genome circularizes and attaches to the host chromosome but does not integrate into the host genome. There are over 80 genes and 17 mRNAs, which include some genes that originated from host cell genes during the evolution of KSHV. The virus can reproduce lytically or can remain latent, tethered to the host chromosome. The lytic phase can be initiated by innate immune signaling, cytokine signaling, or cell differentiation or by exposure to phorbol esters, sodium butyrate, or reactive oxygen. KSHV can be detected by anti-KSHV antibodies, intracellular viral antigens, and DNA.

2. Human Exposure

This section describes prevalence and transmission (Section 2.1), and non-cancer diseases, prevention, and treatment of Kaposi sarcoma-associated herpesvirus (KSHV) (Section 2.2). The material presented in Sections 2.1 and 2.2 is summarized in Section 2.3.

2.1. Prevalence and Transmission

Serological tests for detecting the multiple antigens encoded by KSHV vary in sensitivity and specificity and are poorly standardized, resulting in uncertainty in prevalence estimates and complicating comparison of KSHV in different populations (IARC 2012). Considering this caveat, KSHV prevalence rates appear to vary widely in different populations; high-level endemic areas (adult general public seroprevalences between 30% and 70%) are found in many parts of Africa (Martin 2007); intermediate-level endemic areas (general public seroprevalences between 10% and 25%) are found primarily in the Mediterranean area (Whitby et al. 1998); and non-endemic areas (general public seroprevalences <10%) include North America, Central America, South America, northern Europe, and Asia. However, in non-endemic areas, certain population groups exhibit seroprevalences comparable to those in high- and intermediate-level endemic areas (e.g., between 30% and 60% of human immunodeficiency virus type 1-infected men who have sex with men and between 20% and 30% of human immunodeficiency virus type 1-uninfected men who have sex with men are infected with KSHV (Martin et al. 1998; O'Brien et al. 1999).

The first systematic evaluation of KSHV epidemiology in the general public in the United States (based on enzyme immunoassays conducted on serum samples from National Health and Nutrition Examination Survey [NHANES] III data collection) reported that overall KSHV seroprevalence is approximately 7% and is similar among men and women (Engels et al. 2007a). These seroprevalence data indicate that a significant number of people in the United States are exposed to KSHV. A previous study of 1,000 U.S. blood donors (collected in 1994 and 1995) tested by six independent laboratories, using various serological tests ranging from single immunofluorescence assays to decision trees based on results of several individual assays, reported KSHV seropositivity estimates ranging from 0.5% to 5% (IARC 2012; Pellett et al. 2003). KSHV seropositivity has been found to be lower among human immunodeficiency virus type 1-infected women than in human immunodeficiency virus type 1-infected men who have sex with men, including bisexual men (Kedes et al. 1997). Global KSHV seroprevalence has been shown to mirror the geographical distribution of classic or endemic (i.e., non-human immunodeficiency virus type 1-associated) forms of classic Kaposi sarcoma, e.g., high (15% to 60%) in African and southern Mediterranean regions, and low (1% to 5%) in the United States and northern Europe (Ganem 2010; Minhas and Wood 2014).

Transmission of KSHV appears to be primarily via saliva (IARC 2012). The presence of KSHV in peripheral blood suggests that transmission via blood is also possible, and transmission among some intravenous drug users, transfusion recipients, and from transplant donor to transplant recipient has been reported (Barozzi et al. 2003; IARC 2012). In populations with high endemic KSHV prevalence, both horizontal and vertical transmission appear to occur, primarily in childhood between the ages of 6 and 10 years (particularly if the mother is infected) and infection rates increase with age.

Risk factors for infection may include contact with, e.g., infected family members, sources of water, and, in particular, human immunodeficiency virus type 1 infection (IARC 2012), so factors that increase the risk of human immunodeficiency virus type 1 infection (e.g., number of sexual partners) also increase the risk of infection with KSHV. Further, higher KSHV infection rates in human immunodeficiency virus type 1-positive cohorts other than those acquiring human immunodeficiency virus type 1 via parenteral infection were found to reflect sexual activity, for which human immunodeficiency virus type 1 seropositivity serves as a marker (Kedes et al. 1996). Men who have sex with men may have a higher risk of KSHV transmission than heterosexual sex partners even in the absence of human immunodeficiency virus type 1 infection (Giuliani et al. 2007), and orogenital sex has been shown to be significantly correlated with KSHV seroconversion in men who have sex with men (Dukers et al. 2000). The possibility of insect bites facilitating the transmission of KSHV via human saliva (i.e., application of virus-carrying saliva at the bite site to relieve itching and reduce scratching (Amodio et al. 2011b; Coluzzi et al. 2003) has also been reported.

KSHV is generally not associated with sexual risk factors in heterosexuals (Engels et al. 2007a; IARC 2012; Smith et al. 1999). However, there is some evidence for spouse-to spouse transmission among heterosexual couples, which appears to be more efficient for female-to-male than for male-to-female transmission (Dupuy et al. 2009). This is based on a study that found higher KSHV seroprevalence among heterosexual spouses of Kaposi sarcoma patients than among spouses of controls without cancer. Overall, KSHV prevalence was higher among male spouses than female spouses.

2.2. Diseases, Prevention, and Treatment

Most individuals who are otherwise healthy and infected with KSHV are asymptomatic (ACS 2014; DHHS 2013; NCI 2014). There are very few reports of primary infection with KSHV, but reported symptoms associated with initial KSHV infection include a febrile maculopapular skin rash (as observed in immunocompetent children in Egypt) (Andreoni et al. 2002), as well as diarrhea, fatigue, localized rash, and lymphadenopathy (in men who have sex with men without human immunodeficiency virus type 1 infection) (Wang et al. 2001). Other symptoms include fever, splenomegaly, cytopenia, and bone marrow failure with plasmacytosis (in renal transplant recipients) (Luppi et al. 2000a). Active KSHV infection may be associated with fever, cutaneous rash, and hepatitis in autologous peripheral blood stem cell infusion recipients (Luppi et al. 2000b).

A limited number of studies have suggested associations between KSHV infection and some non-cancer endpoints, including proliferative and nonproliferative skin diseases such as pemphigus vulgaris and pemphigus foliaceus, and actinic keratosis, but other studies have failed to confirm these associations (Ablashi et al. 2002). In addition, KSHV has been found in inflammatory cells in isolated cases of interstitial pneumonitis, in sarcoid tissue, and in histocytic necrotic lymphadenitis, indicating lymph node infiltration, but an etiologic role of KSHV in these diseases has not been established (Ablashi et al. 2002).

Because KSHV transmission is associated with KSHV shedding in saliva and occasional shedding in genital secretions, avoiding salivary exposure and following safe sex practices should theoretically prevent transmission (Chang-Moore 2009; DHHS 2013; 2014)

Some drugs have been reported to reduce or inhibit KSHV shedding (e.g., see Casper et al. 2008; Cattamanchi et al. 2011); however, currently there are no FDA-approved drugs for treatment of KSHV infection. Currently, there is no vaccine against KSHV; however, limited efforts to develop a vaccine are ongoing (ACS 2014; Wu et al. 2012).

2.3. Summary

U.S. seroprevalence study data indicate that a significant number of people living in the United States are exposed to KSHV. Most individuals who are otherwise healthy and infected with KSHV are asymptomatic. Transmission appears to be primarily via saliva. Transmission via blood is also possible, and transmission among some intravenous drug users, transfusion recipients and from transplant donor to transplant recipient has been reported. Both horizontal and vertical transmission appears to occur, primarily in childhood (between the ages of 6 and 10 years, with infection rates increasing with age) in populations with high endemic KSHV prevalence, particularly if the mother is infected. Risk factors for infection may include contact with infected family members, sources of water, and particularly human immunodeficiency virus type 1 infection, so factors that increase the risk of human immunodeficiency virus type 1 infection also increase the risk of infection with KSHV. Men who have sex with men may have a higher risk of KSHV transmission than heterosexual sex partners even in the absence of human immunodeficiency virus type 1 infection. A limited number of studies have suggested associations between infection with KSHV and some non-cancer endpoints (e.g., pemphigus vulgaris, pemphigus foliaceus, and actinic keratosis), but other studies have failed to confirm these associations. There is currently no vaccine against KSHV, although limited vaccine development efforts are ongoing.

3. Human Cancer Studies

3.1. Introduction

The majority of human epidemiological studies for KSHV have focused on Kaposi sarcoma, which was first described by Dr. Mori Kaposi in 1872 (IARC 1997b), prior to the discovery of the virus in 1994 (Chang et al. 1994). Since 1994, a number of other cancer endpoints have been evaluated, the major ones are certain B-cell non-Hodgkin lymphomas, in particular rare forms of primary effusion lymphoma, multicentric Castleman disease, multiple myeloma, and other lymphohematopoietic cancers. The evidence for these endpoints, which were identified by IARC (1997b; 2012), is assessed in this section. A limited number of studies of solid tumor endpoints (including prostate, bladder, head and neck, angiosarcoma, skin, hepatocellular, and vulvar cancers, and childhood inflammatory myofibroblastoma) have also been conducted, but only in single or small studies for most endpoints, and thus are only reviewed briefly.

One of the key issues in the cancer hazard evaluation is the extent to which observed associations between KSHV and specific cancer endpoints can be explained by cofactors, including host genetic factors, co-infection with other viruses, or other environmental and/or other risk factors, as distinct from confounding factors. However, while a substantial number of studies have investigated KSHV cancer risk in association with human immunodeficiency virus type 1 infection, relatively few studies have clearly identified other cofactors, in particular the presence of other oncoviruses (e.g., Epstein-Barr virus) and non-viral cofactors.

In the majority of studies, KSHV exposure is detected based on DNA in the peripheral blood mononuclear cells, tumor, normal tissue, semen, saliva, and other biological samples or via serological measures usually measuring antibodies to lytic or latent viral antigens. Earlier studies included in this evaluation primarily used serological measurements, while later studies generally used more sensitive and specific seroprevalence measures or detected KSHV DNA.

This evaluation of the human cancer hazard associated with KSHV is divided into three major parts. First, a summary of the approach for selection of the studies is provided (Section 3.2). Next, the cancer evaluation for each endpoint is presented (Sections 3.3 to 3.5), and lastly, a summary of the evaluation across cancer endpoints is provided (Section 3.6). The level of evidence from cancer studies in humans also considers molecular studies of tissues from humans in addition to epidemiological studies and is provided in Section 5.

The NTP used the body of knowledge published in the IARC (1997b; 2012) monographs on KSHV as the resource for studies conducted up to and including 2008. The key human studies identified in these monographs, together with new human studies identified from 2008 to 2015, are considered in the RoC monograph and used to evaluate the scientific evidence for specific cancer endpoints independently of IARC's conclusions. Where available, IARC data tables of the effect estimates have informed the cancer hazard assessment.

3.2. Selection of the Literature

A literature search of major databases, citations, and other authoritative sources for literature from 2008 to August 2015 was conducted. The literature search strategy (including the databases and search terms, and other sources for identifying literature), procedures for selecting the

literature (systematic screening procedures and inclusion/exclusion criteria), and the results of the literature search are described in Appendix A. Cross-sectional or prospective cohort studies, and case-control studies, which may range from broadly defined, non-matched hospital or population case-comparison designs to formal age-, sex-, and race-matched case-control designs, as well as summaries of multiple case reports or case-series studies are included in the review.

3.3. Cancer Evaluation: Kaposi Sarcoma

3.3.1. Background Information

Studies of Kaposi sarcoma incidence or prevalence have been conducted among four main epidemiological types. Although Kaposi sarcoma is histologically indistinguishable in these four types, the age at diagnosis, clinical features, and progression of the disease vary considerably by type.

- “Epidemic” or “human immunodeficiency virus type 1/AIDS-related” Kaposi sarcoma occurs among human immunodeficiency virus type 1-positive, typically immunocompromised individuals;
- “Iatrogenic,” “transplant,” or “immunosuppressive” Kaposi sarcoma occurs primarily among organ recipients, mostly renal and liver transplant patients, generally in the presence of immune suppression, and also among other patients with immune suppression (e.g., hemodialysis patients (Jalilvand et al. 2011));
- “Classic,” “sporadic,” or “indolent” Kaposi sarcoma is rare, less aggressive in its course than human immunodeficiency virus type 1-related Kaposi sarcoma (Hiatt et al. 2008), predominantly affects the lower extremities, and occurs mostly among older males 50 to 70 years of age in specific populations, e.g., in some Mediterranean countries such as southern Italy, or among East Europeans of Jewish descent with higher (e.g., 10% to 20%) KSHV prevalence rates (IARC 1997b; 2012);
- “Endemic” Kaposi sarcoma also occurs mostly among men, but among younger groups than classic Kaposi sarcoma, including children, in regions of sub-Saharan Africa with relatively high KSHV seroprevalence rates, e.g., of 25% to over 50% (IARC 2012). The course of Kaposi sarcoma in children tends to be much more aggressive than that observed in adults (Senba et al. 2011). Since the advent of the human immunodeficiency virus type 1 epidemic, the ratio of Kaposi sarcoma in men to women has decreased from 7:1 to 2:1 in South Africa (Sitas and Newton 2001), despite little evidence that the male to female ratio of KSHV infection differs or has changed over the past two decades (Dedicoat and Newton 2003).

Kaposi sarcoma appears to be rare in immunocompetent individuals among populations with the epidemic type of the cancer, and the expression and course of the cancer may also be affected by compromised immune status in populations with classic or endemic types of Kaposi sarcoma. In the United States, Kaposi sarcoma occurred in <1 per 100,000 individuals prior to the human immunodeficiency virus type 1/AIDS epidemic starting in the early 1980s, peaking at approximately 5 to 6 per 100,000 in the U.S. population by the early 1990s, prior to the advent of highly active antiretroviral therapy (HAART) (NCI 2014).

Approximately 12,000 patients were diagnosed with Kaposi sarcoma between 1975 and 2005, according to SEER registry statistics (Armstrong et al. 2013). In Europe, the Surveillance of Rare Cancers in Europe (RARECARE) project (Stiller et al. 2014) reported 2,667 incident cases of Kaposi sarcoma between 1995 and 2002, an age-standardized rate of 0.3 per 100,000 across the entire European Union. In the subgroup of southern European countries, where predominantly classic cases have been identified, the average incidence was 0.8 per 100,000; the incidence rates for other areas in Europe ranged from 0.02 to 0.25. The Kaposi sarcoma incidence rate among U.S. men (approximately 3.3/100,000) (Rouhani et al. 2008) is higher than that among European men (0.5/10,000) but comparable among women in the United States and Europe (approximately 0.1/100,000; see Stiller et al. (2014)).

3.3.2. Descriptive Epidemiological Studies

A number of case series, descriptive epidemiological, or surveillance studies of Kaposi sarcoma from multiple countries, conducted from 2008 to 2015, were identified (Hiatt et al. 2008 [United States]; Jalilvand et al. 2011 [Iran]; Jalilvand et al. 2012 [Iran]; Kanno et al. 2010 [Japan]; Koski et al. 2014 [Tanzania]; Lanternier et al. 2008 [Tanzania]; Magri et al. 2009 [Brazil]; Mousavi et al. 2014 [immigrants to Sweden]; Mwakigonja et al. 2008 [Tanzania]; Nsubuga et al. 2008 [Uganda]; Ogoina et al. 2011 [Nigeria]; Senba et al. 2011 [Kenya]; Stiller et al. 2014 [European cancer surveillance registry]; Tiussi et al. 2012 [Brazil]). As supported by studies reviewed by IARC (2012), descriptive studies that report KSHV seroprevalence (typically LANA) or KSHV-DNA among cases of Kaposi sarcoma indicate ranges from approximately 88% to 98%, irrespective of whether these are human immunodeficiency virus type 1 positive, human immunodeficiency virus type 1 negative, endemic, or classic Kaposi sarcoma cases (Hiatt et al. 2008; IARC 2012; Kanno et al. 2010; Lanternier et al. 2008; Magri et al. 2009; Mwakigonja et al. 2008; Nsubuga et al. 2008; Ogoina et al. 2011). However, relatively few case studies of KSHV seroprevalence have been reported among human immunodeficiency virus type 1-negative populations in regions with endemic or classic Kaposi sarcoma.

3.3.3. Cohort and Nested Case-control Studies

Table 3-1 summarizes findings from 13 cohort or nested case-control studies conducted prior to 2009 and reviewed by IARC (2012) and from two prospective cohort and one nested case-control studies identified since the IARC review (Labo et al. 2015; Nawar et al. 2008; Wakeham et al. 2015) that reported risk estimates for KSHV seroprevalence or DNA and Kaposi sarcoma. Most of the cohort studies were of immunosuppressed populations either human immunodeficiency virus type 1-positive or transplant recipients and were conducted among U.S., Canadian, or European-based populations; two cohorts were of southern Mediterranean populations who have a high prevalence of classic Kaposi sarcoma (Parravicini et al. 1997; Rezza et al. 1999) and the nested case-control study was in Uganda, a country with a high prevalence of endemic Kaposi sarcoma (Labo et al. 2015).

Among the studies reviewed by IARC (2012), all of the relative risks were statistically significant, ranging from 2.5 to 75; elevated risks were observed in both human immunodeficiency virus type 1-positive and organ transplant populations, which provide support for KSHV causing Kaposi sarcoma independently of human immunodeficiency virus type 1 infection. Moreover, Newton et al. (2006) found that risk of Kaposi sarcoma increased with increasing anti-KSHV titers. The two prospective cohort studies conducted in the United States

(Labo et al. 2015; Nawar et al. 2008), and the small nested case-control study conducted in Uganda (Wakeham et al. 2015), published after the IARC review, are consistent with these findings and reported risk estimates ranging between 1.8 to 9.5. One cohort study, the multi-city U.S. cohort study of 1,354 men who have sex with men (Nawar et al. 2008), found that acquiring human immunodeficiency virus type 1 infection prior to KSHV infection was associated with an increase in Kaposi sarcoma risk vs. co-prevalent infection (hazard ratio [HR] = 1.81, 95% CI = 1.32 to 2.48), whereas acquiring KSHV infection prior to human immunodeficiency virus type 1 did not increase risk in comparison with co-prevalent infection (HR = 1.05, 95% CI = 0.59 to 1.87). The nested case-control study calculated risks for both lytic and latent antigens; relative risks were somewhat higher for antibody titers to K8.1 lytic antigen (RR = 4.14, 95% CI = 3.34 to 4.94) than latent antigen (LANA) (RR = 2.2, 95% CI = 1.16 to 3.25) (Wakeham et al. 2015). It is not possible to draw conclusions as to whether risk varies among different countries due to the limited number of studies (and few studies reported in detail on the racial or ethnic composition of their cohorts).

IARC (2012) also reported on seven cohort studies of human immunodeficiency virus type 1-positive populations or organ transplant recipients (Chatlynne et al. 1998; Frances et al. 1999; Frances et al. 2000; Garcia-Astudillo and Leyva-Cobian 2006; Marcelin et al. 2004; Melbye et al. 1998; Regamey et al. 1998) that did not calculate risk estimates, primarily due to small numbers; three of these publications reported that KSHV infection was significantly higher in Kaposi sarcoma cases than controls with P-values ranging from <0.001 (Frances et al. 2000; Garcia-Astudillo and Leyva-Cobian 2006) to <0.0001 (Frances et al. 1999).

Table 3-1. Summary of Cohort and Nested Case-control Studies of Risk of Kaposi Sarcoma among KSHV-Seropositive vs. KSHV-Negative Participants

Reference	Detection Methods	Cohort (Comparison Group) and Cases and Controls	RR
HIV-1-positive/AIDS populations			
Cohort studies			
Grulich et al. (1999) (USA)	Latent and lytic antigens	AIDS+ MSM	4.4*
O'Brien et al. (1999) (USA)	Latent nuclear antigen	HIV-1+ MSM	3.6*
Jacobson et al. (2000) (USA) ^a	Lytic antigens	HIV-1+ MSM (seroconversion to KSHV after HIV-1 infection vs. before HIV-1 infection)	2.6*
Rezza et al. (1999) (Italy)	Latent nuclear antigen	HIV-1+ (various exposures)	29.6*
Nawar et al. (2008) (USA)	Lytic antigens	KSHV and HIV-1 concurrent infections; MSM KSHV infection prior to HIV-1 infection; MSM	1.8* 1.1 (NS)
Labo et al. (2015) (USA, Puerto Rico)	Latent and lytic antigens	HIV-1+ men and women	9.5*

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Reference	Detection Methods	Cohort (Comparison Group) and Cases and Controls	RR
Range			1.8–29.6
Nested case-control studies			
Moore et al. (1996) Parry and Moore (1997) (USA)	PCR	KS cases: AIDS+ MSM Controls: HIV-1+ MSM	11.6*
Gao et al. (1996) (USA)	Latent nuclear antigen	KS cases: AIDS+ MSM Controls: HIV-1+ MSM	[16.3]*
Engels et al. (2003) (USA)	Lytic antigens PBMC DNA	KS cases: HIV-1+ MSM Controls: HIV-1+ MSM	11.7*
Quinlivan et al. (2001) ^b (Switzerland)	Latent nuclear antigen	KS cases: HIV-1+ M or F Controls: HIV-1+ M or F	3.0
Newton et al. (2006) (UK)	Latent and lytic antigens	KS cases: HIV-1+ M or F Controls: HIV-1+ M or F	4.4*
		Titer (latent antigens) -	
		Min	3.5*
		Med	4.1*
		Max	8.7*
		P _{trend}	<0.001
Whitby et al. (1995) (UK)	PCR	KS cases: AIDS+ M or F Controls: HIV-1+ M or F	12.7*
Wakeham et al. (2015) (Uganda)	Latent and lytic antigens	KS cases: HIV-1+ M or F Controls: HIV-1+ M or F	
		K8.1	4.1*
		LANA	2.2*
Range			2.2–16.3
Organ transplant recipients			
Cohort study			
Cattani et al. (2001) (Italy)	Latent and lytic antigens	Transplant recipients tested for KSHV before transplant, follow-up 10 years	34.4*
Nested case-control studies			
Parravicini et al. (1997) (Italy)	Latent and lytic antigens	Transplant recipients tested for KSHV before transplant	75.0*
Rabkin et al. (1999) (Canada)	Latent antigens, whole virus assay	Transplant recipients tested for KSHV before transplant	2.5 (NS)

*Lower 95% confidence interval (CI) > 1.0.

Source: IARC (2012) (with reported or calculated risk estimate), Table 2.2, Nawar et al. (2008), Labo et al. (2015), Wakeham et al. (2015). IARC also described seven other nested case-control or cohort studies that reported the number of KSHV-positive or -negative Kaposi sarcoma, but did not report or provide enough information to calculate a risk estimate

[] = RR or OR calculated by NTP

AIDS = acquired immunodeficiency syndrome; HIV-1 = human immunodeficiency virus type 1; KS = Kaposi sarcoma; KSHV = Kaposi sarcoma-associated herpesvirus; LANA = latent antinuclear antigen; MSM = men who have sex with men; PBMC = peripheral blood mononuclear cells; PCR = polymerase chain reaction; RR = relative risk; NS = lower 95% confidence interval (CI) < 1.0.

^aKSHV- and HIV-1-positive MSM with detectable KSHV viral load 1 year prior to diagnosis vs. KSHV- and HIV-1-positive MSM with no detectable viral load.

^bNote that membrane antigen RR = 1.7 (95% CI = 0.5 to 6.7) and lytic antigen RR = 0.9 (95% CI = 0.2 to 6.8).

3.3.4. Case-control Studies

IARC (2012) reviewed 80 case-control studies of Kaposi sarcoma; 68 studies included AIDS cases, 7 included human immunodeficiency virus type 1-positive or “non-AIDS” cases, and 10 studies included human immunodeficiency virus type 1-negative cases (plus 4 studies in which human immunodeficiency virus type 1 status was unclear or not specified); 27 included classic cases, 14 included endemic cases, and 9 included transplant cases (some studies had more than one group). Table 3-2 summarizes data from 39 case-control studies in which risk estimates for KSHV were reported. One new case-control study of classic cases in a Sicilian population [Amodio et al. (2011b); based on an earlier study by Goedert et al. 2002] was identified after the IARC (2012) review. (Further studies among KSHV-positive patients in this population were conducted by Pelser et al. (2010) and Anderson et al. (2008) and are discussed under cofactors in Section 3.3.5, below.) Cases that fall into more than one category of Kaposi sarcoma were sometimes combined by study authors for analysis. Comparison groups may be human immunodeficiency virus type 1-positive or AIDS patients, or blood donors, oncology patients, or patients with other skin diseases or other non-cancer conditions, or combinations of such comparison groups from which a single risk estimate was calculated by authors or IARC working groups.

Among the studies of patients with human immunodeficiency virus type 1 (some of which had AIDS), odds ratios (ORs), almost all statistically significant, ranged from 1.0 to 1,683 (Table 3-2). The two studies of human immunodeficiency virus type 1-negative cases and controls, both conducted in African populations with, as noted above, high endemic KSHV prevalence rates, reported ORs of 1.5 to 12.0, depending on the level of KSHV titer (Newton et al. 2003a; Sitas et al. 1999). The studies designated as grouped populations consist of combinations of human immunodeficiency virus type 1-positive, human immunodeficiency virus type 1-negative or undetermined, endemic, classic, or transplant-related Kaposi sarcoma patients in comparison with similar Kaposi sarcoma-negative groups, as noted in Table 3-2, and for which only single risk estimates were reported, ORs ranging from 3.8 to 924 were observed. ORs could also be calculated for some constituent groups within these studies, although in some instances, only a single combined control group was used and/or no formal matching of controls was conducted, so that such risk estimates must be interpreted with caution. Nevertheless, for both classic and endemic Kaposi sarcoma, KSHV was observed in >80% to 100% of cases (Table 3-2). Among the few studies that included transplant patients with Kaposi sarcoma, KSHV was observed in approximately 66% to 100% of cases.

Three studies reviewed by IARC (2012) reported on dose-response relationships between titers of KSHV exposure and risk for Kaposi sarcoma. Sitas et al. (1999) and Newton et al. (2003a) observed statistically significant trends ($P < 0.001$) among both human immunodeficiency virus type 1-positive and human immunodeficiency virus type 1-negative groups with a higher prevalence of endemic Kaposi sarcoma in Africa; Albrecht et al. (2004) reported a similar trend among human immunodeficiency virus type 1-positive AIDS patients in Germany.

Table 3-2. Summary of Case-control Studies of Kaposi Sarcoma and Kaposi Sarcoma-Associated Herpesvirus (KSHV)

Reference	Detection Method	OR ^a	Comments
HIV-1-positive/AIDS populations			
Chang et al. (1994) (USA)	PCR	68.8	—
Whitby et al. (1995) (UK)	PCR	29.0	—
Monini et al. (1996a); Monini et al. (1996b) (Italy)	PCR	1.7 ^a	—
Parry and Moore (1997) (USA)	PCR	7.3 MSM 21.8 hemophiliacs	—
Humphrey et al. (1996) (USA)	PCR	2.3	—
Decker et al. (1996) (USA)	PCR	1.1 ^b	—
Gao et al. (1996) (USA)	LANA, WB	18.9	—
Lefrere et al. (1996) (France)	PCR	285.0	—
Miller et al. (1996) (USA)	WB, IFA	13.4 (WB)/12.2 (IFA)	—
Noel (1995) (Belgium)	PCR	42.2	—
Howard et al. (1997) (UK)	PCR	10.1	—
Sitas et al. (1999) (South Africa)	LANA, IFA	10.8–1,683	Sig. ↑ inc. KSHV titer
Min and Katzenstein (1999) (USA)	PCR	16.3	—
Boivin et al. (1999) (Canada)	PCR	6.7	—
Greenblatt et al. (2001) (USA)	PCR	148.0	—
Keller et al. (2001) (Brazil)	PCR	7.4–17.0	—
Cannon et al. (2003) (USA)	PCR	8.6	—
Newton et al. (2003a) (Uganda)	LANA, IFA	4.1–0.8	Sig. ↑ inc. KSHV titer
Alagiozoglou et al. (2003) (South Africa)	LANA, IFA, PCR	15.4–25.1	—
Albrecht et al. (2004) (Germany)	IFA	1.04–23.2	Sig. ↑ inc. KSHV titer
Szalai et al. (2005) (Hungary)	LANA, IFA, ELISA	2.3 ^b –23.1	—
van der Kuyl et al. (2005) (Netherlands)	PCR	6.3	—
Martro et al. (2007) (Spain)	IFA	4.8	—
Widmer et al. (2006) (Switzerland)	PCR	1.2 ^b	—
Laney et al. (2007) (USA)	PCR	1.6 ^b –3.4	—
Zago et al. (2000) (Brazil)	PCR	23.4–104.8	—
HIV-1-negative populations			
Sitas et al. (1999) (South Africa)	LANA, IFA	1.5–12.0	Endemic—sign. trend with ↑ KSHV titer
Newton et al. (2003a); Newton et al. (2003b) (Uganda)	LANA, IFA	2.3–7.1	Endemic—sign. trend with ↑ KSHV titer

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Reference	Detection Method	OR ^a	Comments
Cattani et al. (2001) (Italy)	IFA	34.4	Transplant patients
Amodio et al. (2011a) (Sicily)	LANA, lytic (K8.1)	5.13 ^b	Classic
Grouped populations			Case groups
Moore and Chang (1995) (USA)	PCR	400 (19–17,300) [210 (12–3,712)] [∞] [∞]	Total (HIV-1+ men, HIV-1-neg. MSM, Classic HIV-1+ HIV-1-neg. MSM Classic)
Chang et al. (1996) (USA)	PCR	49.4 (9.0–328.0) [66 (5.1–857.7)] [36 (5.3–253.6)]	HIV-1+, endemic HIV-1+ Endemic
Luppi et al. (1996) (Italy)	PCR	41.6 (7.0–327.1) [∞] [∞]	HIV-1+, classic HIV-1+ Classic
Albini et al. (1996) (Italy)	PCR	924.3 (125–10,194) [∞] [∞] [∞] [198 (10.8–3,617)]	Total: HIV-1+, endemic, classic, transplant AIDS vs. HIV-1+ Endemic vs. HIV-1+ Classic vs. HIV-1+ Transplant vs. HIV-1 neg.
Herman et al. (1998) (USA)	PCR	336 (14.9–47,561)	HIV-1+, classic (vs. HIV-1+ and HIV-1 neg. controls combined)
Cattani et al. (1998) (Italy)	PCR	7.4 (2.4–23.8) [5.9 (1.8–19.2)] [20.0 (1.7–238.6)]	Classic, transplant Classic Transplant
Kazakov et al. (2002) (Switzerland)	PCR	543 (52–14,041) [600 (34.2–10,541.2)] [150 (11.1–2,025)] 1,275 (75.9–21,420)]	Total: HIV-1+, transplant, classic HIV-1+ Transplant Classic
Lager et al. (2003) (South Africa)	PCR	572 (26–79,693)	HIV-1 status unknown
Massambu et al. (2003) (Tanzania)	PCR	3.8 (0.3–60.9)	HIV-1+, endemic

Source: IARC (2012), Table 2.1, Amodio et al. (2011a).

[] = OR calculated by NTP

CI = 95% confidence interval; ELISA = enzyme-linked immunosorbent assay; HIV-1 = human immunodeficiency virus type 1; IFA = immunofluorescence assay; KS = Kaposi sarcoma; KSHV = Kaposi sarcoma-associated herpesvirus; LANA = latent antinuclear antigen; MSM = men who have sex with men; OR = odds ratio; PCR = polymerase chain reaction; WB = Western blot assay.

^aLower 95% CI = 0.0.

^bLower 95% CI < 1.0.

3.3.5. Cofactors for Kaposi Sarcoma

KSHV has been identified in over 90% (including all four types) of Kaposi sarcoma lesions (Dedicoat and Newton 2003; IARC 2012; Mesri et al. 2010; Moore and Chang 1998). The

principal cofactor identified for Kaposi sarcoma in the presence of KSHV infection is human immunodeficiency virus type 1 infection via immune suppression, among populations in both the United States and Europe (“epidemic” Kaposi sarcoma) and those with an increased prevalence of “classic” or “endemic” Kaposi sarcoma (Table 3-1 and Table 3-2). Prospective studies, largely among men who have sex with men and infrequently among human immunodeficiency virus type 1-positive intravenous drug users or women, suggest that human immunodeficiency virus type 1 infection significantly increases the risk of Kaposi sarcoma development in the presence of KSHV in a range of geographical populations, particularly among AIDS patients. There is additional evidence that infection with human immunodeficiency virus type 1 prior to infection with KSHV may increase the risk of Kaposi sarcoma by up to 2.6-fold compared with those infected with KSHV before human immunodeficiency virus type 1, and increasing duration of human immunodeficiency virus type 1 infection, and decreasing CD4 counts are associated with a more rapid course of development of the cancer (Jacobson et al. 2000; Nawar et al. 2008; Renwick et al. 1998). (See also accompanying human immunodeficiency virus type 1 monograph.)

Immune suppression among organ recipients, primarily renal and liver transplant patients, has also been identified as a major cofactor among patients who were KSHV positive prior to transplantation or who acquired KSHV during organ transplantation (see Table 3-1). In a review of 38 case-series studies by Hosseini-Moghaddam et al. (2012), approximately 13% of previously KSHV-seropositive patients reportedly developed Kaposi sarcoma after renal transplantation; approximately 5% of the patients developed the cancer as a result of primary KSHV (donor KSHV positive, recipient KSHV negative) infection.

Few studies have investigated the role of recreational drugs with immunomodulatory properties. In one prospective study, prior use of marijuana, amyl nitrate “poppers,” cocaine, or amphetamines was weakly associated with Kaposi sarcoma risk among co-KSHV and human immunodeficiency virus type 1-infected men who have sex with men, although a clear dose-response relationship was lacking (Chao et al. 2009).

The role of co-factors is less clear for the endemic and classic forms of Kaposi sarcoma. Never smoking, diabetes, and the use of oral corticosteroids have all been identified as potential risk factors for classic Kaposi sarcoma among KSHV-positive individuals in the absence of human immunodeficiency virus type 1 infection or iatrogenic or other causes of immune suppression in a well-conducted case-control study of a population in Sicily (Amodio et al. 2011a; Anderson et al. 2008; Goedert et al. 2002). While this study provides limited evidence that these factors increase the risk of Kaposi sarcoma among KSHV-positive individuals, few other data in other populations include examination of these risk factors and no firm conclusions can be drawn about their role, or that of other risk factors.

With respect to co-infection with other viruses, the role of Epstein-Barr virus is uncertain. It appears that the prevalence of Epstein-Barr virus infection is similar in Kaposi sarcoma and non-Kaposi sarcoma patients and does not appear to play a direct role in the development of the sarcoma, at least according to one well-conducted case-control study among classic cases of Kaposi sarcoma (Table 3-3) (Pelser et al. 2010). Other viruses, such as herpes simplex type 2, human cytomegalovirus, human herpesvirus-6 and 7, and human papillomavirus have also been implicated in the activating lytic replication of KSHV and thus in Kaposi sarcoma pathogenesis (reviewed by Purushothaman et al. 2015). However, no cohort or case-control studies

specifically addressing the risk of Kaposi sarcoma in the presence of these viruses as cofactors among KSHV-positive populations have been identified to date.

Among populations with high rates of endemic Kaposi sarcoma, particularly prior to the global human immunodeficiency virus type 1 epidemic, other potential cofactors, including malaria (see e.g., Nalwoga et al. 2015), other parasitic infections, soil types causing immunosuppression, or oncogenic plants have been suggested as increasing the risk of KSHV infection and/or reactivation (Dedicoat and Newton 2003; IARC 2012). Tuberculosis has been reported as exacerbating the severity of endemic cases (e.g., in Tanzania, (Koski et al. 2014)) but it is not clear if it is a risk factor for the initial development of the sarcoma. Finally, prior to the human immunodeficiency virus type 1 epidemic, Kaposi sarcoma was more prevalent among men than women in, e.g., populations with endemic cases, despite similar KSHV seroprevalence in both sexes, suggesting that cofactors not yet clearly established might play a role in the development of the cancer (Dedicoat and Newton 2003).

Table 3-3. Case-control Study of Co-factors for the Development of Classic Kaposi Sarcoma among a KSHV-positive Population in Sicily

Reference	Cofactor	# KS Cases//KSHV+Controls	OR (95% CI) for KS
Anderson et al. (2008)	Diabetes	Cases (45/142) Controls (15/123)	4.02 (1.73–9.37)
	Never smoking	Cases (23/142) Controls (12/123)	2.66 (1.06–6.64)
	Oral corticosteroid use	Cases (53/142) Controls (26/123)	2.25 (1.16–4.38)
Pelser et al. (2010)	EBV	Cases (low EBNA-1) (43/119) Controls (low EBNA-1) (34/105)	0.97 (0.52–1.82) ^a
		Cases (high EBV VCA) (45/119) Controls (high EBV VCA) (45/105)	0.87 (0.45–1.69) ^a

CI = confidence interval; EBNA = Epstein-Barr virus nuclear antigen; EBV = Epstein-Barr virus; EBV VCA = EBV viral capsid antigen; KS = Kaposi sarcoma; KSHV = Kaposi sarcoma-associated herpesvirus; OR = odds ratio.

^aAdjusted for age, sex, smoking, diabetes, and oral corticosteroid use.

3.3.6. Integration across Studies of Kaposi Sarcoma

At least 25 cohort or nested case-control studies and 81 case-control studies conducted in populations differing by race or ethnicity and in various geographical locations have demonstrated that KSHV infection causes Kaposi sarcoma. KSHV has been identified in over 80% of cases by serology and in virtually all Kaposi sarcoma tumors and is considered to be the diagnostic prerequisite for a diagnosis of Kaposi sarcoma. The histopathology of all four epidemiological types of Kaposi sarcoma (epidemic, iatrogenic, classic, and endemic) is identical. Case-control studies conducted among populations exhibiting the different types showed statistically significant increased risks for Kaposi sarcoma generally exceeding 10 and up to 300 or more (using serology and/or DNA in the tumor to identify KSHV infection). Most cohort studies report risks from approximately 2 to 16 although a few studies, primarily among transplant patients, have reported risks up to 75. In addition, statistically significant dose-response relationships for measures of KSHV infection and Kaposi sarcoma risk among both

human immunodeficiency virus type 1-positive and/or human immunodeficiency virus type 1-negative populations have been reported (Albrecht et al. 2004; Newton et al. 2006; Newton et al. 2003a; Newton et al. 2003b; Sitas et al. 1999).

The heterogeneity in risk observed particularly in case-control studies may be at least partly due to methodological limitations. A majority of the case-control or case-comparison studies have small numbers of cases and lack formal methods of selection or matching of controls or have inadequate reporting. In addition, temporality (evidence that KSHV infection preceded the development of Kaposi sarcoma) cannot generally be clearly established in these studies. The majority of cohort or nested case-control studies have somewhat limited statistical power, and the sensitivity and specificity of KSHV detection methods in earlier studies is generally more limited than in later studies. However, several prospective cohort studies and nested case-control studies (e.g., Gao et al. 1996; Labo et al. 2015; Moore et al. 1996; Nawar et al. 2008; Wakeham et al. 2015; Whitby et al. 1995) provide evidence of temporality. Overall, confounding by other factors can be ruled out with confidence because of the findings of highly statistically significant increased risks across studies with different designs and conducted in different populations, and evidence of dose-response relationships.

With respect to cofactors, immune suppression—primarily resulting from human immunodeficiency virus type 1 infection or iatrogenically in, for example, transplant cases—is the principal cofactor. human immunodeficiency virus type 1 infection prior to KSHV infection may increase the risk of epidemic Kaposi sarcoma between 50% and 100% compared with human immunodeficiency virus type 1 infection during or after KSHV infection. While a recent, well-conducted case-control study in Sicily (Anderson et al. 2008) provides limited evidence that diabetes, corticosteroid use, and never smoking increase the risk of Kaposi sarcoma among KSHV-positive individuals, few other data in other populations have included examination of these risk factors and no firm conclusions can be drawn. Clear evidence for a modulatory role of other specific cofactors, such as genetic factors, malaria, hypoxic stress, or environmental and dietary factors, particularly among endemic and classic cases, is lacking. Co-infection with other viruses, such as Epstein-Barr virus, cannot be completely ruled out as cofactors in the development of Kaposi sarcoma in KSHV-infected individuals; although one case-control study (Pelser et al. 2010) suggests no association with co-infection with Epstein-Barr virus, there are few other data to evaluate the role of this or other viruses.

3.4. Lymphohematopoietic Cancers

3.4.1. Primary Effusion Lymphoma

Background Information

Primary effusion lymphoma, a monoclonal lymphoproliferative disorder also called body cavity-based B-cell lymphoma, is a rare type of B-cell non-Hodgkin lymphoma that presents primarily as pleural, peritoneal, or pericardial lymphomatous effusions and makes up approximately 2% to 4% of human immunodeficiency virus type 1-related non-Hodgkin lymphomas (Simonelli et al. 2003; Sullivan et al. 2008). In addition to lymphomatous effusions, diagnosis of primary effusion lymphoma includes KSHV infection; large-cell immunoblastic or anaplastic large-cell lymphomas; expression of CD45, clonal immunoglobulin gene rearrangements; and lack of *c-myc*, *bcl-2*, *ras*, and *p53* gene alterations (Ablashi et al. 2002; Nador et al. 1996). Primary

effusion lymphomas are thought to arise from post-germinal center B cells because they have mutations in their immunoglobulin genes. Because a large number of cases of primary effusion lymphoma identified in association with KSHV have distinctive morphological, immunophenotypical, and molecular genetic characteristics, they have been grouped as a single distinct pathological entity (IARC 1997b; 2012). Such entities should be distinguished from other large body cavity-based B-cell lymphomas or lymphoproliferative disorders observed in KSHV-negative patients and may also have a different prognosis (see e.g., Chen et al. 2009; Kishimoto et al. 2009; Xiao et al. 2013).

Epidemiological Studies

Epidemiological evidence of an association between primary effusion lymphoma and KSHV relies primarily on a large number of case reports, case-series, and case-comparison studies rather than formal case-control or cohort studies, due to the rarity of the condition, and the fact that the presence of KSHV is a diagnostic criterion for the specific pathological entity that constitutes primary effusion lymphoma. KSHV-positive cases of primary effusion lymphoma have been identified in both human immunodeficiency virus type 1-positive and human immunodeficiency virus type 1-negative individuals; approximately half of the cases have Kaposi sarcoma. Primary effusion lymphoma among human immunodeficiency virus type 1-positive patients exhibits a rapid progression with short survival times, whereas in human immunodeficiency virus type 1-negative and immunocompetent patients, progression appears to be much slower (IARC 1997b). The large majority of primary effusion lymphoma cases occur among men, irrespective of human immunodeficiency virus type 1 or Kaposi sarcoma status, presumably reflecting a higher prevalence of KSHV infection among men (IARC 2012).

IARC ((2012), Table 2.5) reviewed 97 individual cases reported in the literature to be primary effusion lymphoma; 44 cases were reported as both KSHV and human immunodeficiency virus type 1 positive, 31 cases were KSHV positive but human immunodeficiency virus type 1 negative, and three case were uncertain as to KSHV (N = 2) or human immunodeficiency virus type 1 status (N = 1). The remaining 19 cases were KSHV-negative and human immunodeficiency virus type 1-negative and associated with genetic or other pre-existing conditions and/or observed among patients 67 years of age or older; however, IARC noted that the KSHV-negative cases probably represented another form of non-Hodgkin lymphoma because they do not meet the diagnostic criteria for primary effusion lymphoma. Several small case-series studies (Aoki et al. 2001; Judde et al. 2000; Oksenhendler et al. 2002; Parravicini et al. 2000) were identified that reported a total of 12 additional (i.e., not included in the 97 cases reviewed by IARC) KSHV-positive cases of primary effusion lymphoma, 10 of which were from human immunodeficiency virus type 1-positive/AIDS patients.

KSHV-positive, human immunodeficiency virus type 1-negative cases (11 of the 31 cases reported by IARC and one additional case) have been observed among organ transplant patients (Boulanger et al. 2008; Dotti et al. 1999; IARC 2012; Testa et al. 2010) and among populations (including approximately 14 reviewed by IARC and 8 additional cases) that are known to have a high risk of endemic or classic epidemiological Kaposi sarcoma, leading to the proposition that a “classic” form of primary effusion lymphoma can be identified (Yiakoumis et al. (2010), reviewed by Ascoli et al. (2002)).

Among 47 KSHV-positive cases of primary effusion lymphoma with known human immunodeficiency virus type 1 status (reported by IARC), approximately half of the cases in

both human immunodeficiency virus type 1-positive (14/30) and human immunodeficiency virus type 1-negative patients (8/17) also had Kaposi sarcoma; some also presented with multicentric Castleman disease (reviewed below).

In a large case-comparison study of 191 patients with a range of lymphoproliferative disorders (Asou et al. 2000), 21 patients were identified with primary effusion lymphoma, all of whom were KSHV DNA positive, in contrast to 1 of 170 patients with AIDS-related non-Hodgkin lymphoma or with non-AIDS-related lymphomas (Castleman disease, reactive lymphadenopathy, mucosa-associated lymphoid tissue lymphoma, and non-AIDS non-Hodgkin lymphoma). (In this study, the human immunodeficiency virus type 1 status of primary effusion lymphoma cases is unclear.) No additional cohort or case-control studies have been identified (see review by Zhang et al. 2010).

Cofactors for Primary Effusion Lymphoma

Immune suppression resulting from human immunodeficiency virus type 1 infection is a cofactor for primary effusion lymphoma development among KSHV-positive cases. Due in part to its rarity, there are few data on primary effusion lymphoma cases among other immunosuppressed groups although one study reviewed by IARC (2012), Kapelushnik et al. (2001), reported a case in a KSHV-positive renal transplant patient. However, no other case studies were identified for the current review. A substantial proportion (50%) of KSHV-related primary effusion lymphoma cases also have evidence of Epstein-Barr virus infection (IARC 1997b; 2012), which has also been postulated as a cofactor (Boulanger et al. 2005; Bryant-Greenwood et al. 2003; Gloghini et al. 2013).

3.4.2. Multicentric Castleman Disease

Background and Epidemiological Evidence

Multicentric Castleman disease is a subset (20%) (Talat and Schulte 2011) of Castleman disease, first identified by Castleman et al. (1956) and characterized inflammatory symptoms, plasmacytic lymphadenopathy, splenomegaly, and cytopenia with polyclonal hyperimmunoglobulinemia and high serum levels of IL-6 (Fukumoto et al. 2011; Oksenhendler et al. 2013), and has an aggressive course and poor prognosis (IARC 1997b).

Evidence of a positive association between multicentric Castleman disease and KSHV has been reported in several early case reports and case series (Barozzi et al. 1996; Corbellino et al. 1996; Gessain et al. 1996; Soulier et al. 1995); and in four case-comparison studies (63 cases of multicentric Castleman disease and 213 controls) (Asou et al. 2000; Belec et al. 1999; Parravicini et al. 1997; Soulier et al. 1995) reviewed by IARC (2012). These studies reported a higher frequency of KSHV, primarily in human immunodeficiency virus type 1-positive but infrequently in human immunodeficiency virus type 1-negative groups, in comparison with controls (Table 3-4). Several histological variants of multicentric Castleman disease exist (hyaline vascular, plasma cell, mixed, and plasmablastic) but KSHV in individuals with and without human immunodeficiency virus type 1 infection, is almost always associated with the plasmablastic variant and rarely in the hyaline vascular form of the disease (Ascoli et al. 1999; Damania 2010; Dupin et al. 2000; Dupin et al. 1999; Fukumoto et al. 2011; Parravicini et al. 2000). Dupin et al. (2000) reported that KSHV was specifically associated with a plasmablastic variant of multicentric Castleman disease in which KSHV-positive plasmablasts showing γ

light-chain restriction localized in the mantle zone of B-cell follicles (Dupin et al. 2000). In some cases, these plasmablasts coalesce to form foci of microlymphoma. These plasmablasts are not present in KSHV-negative multicentric Castleman disease (see Section 3.5 for a discussion of the two different forms of multicentric Castleman disease). Findings described in Table 3-4 illustrate the preponderance of plasmablastic types.

Table 3-4. Summary of Case-series and Case-control/Comparison Studies of KSHV and Multicentric Castleman Disease

Reference	KSHV Detection Method	HIV-1 Status of MCD Cases/Controls	KSHV-exposed Cases/Total Cases or OR (95% CI) ^a Exposed Cases vs. Exposed Controls/
Case reports and case series			
Corbellino et al. (1996)	PCR, Southern blot	HIV-1 negative	4/6 (4/4 with plasma cell type)
Barozzi et al. (1996)	PCR	HIV-1 negative	1/16 (1/1 is hyaline vascular type)
Gessain et al. (1996)	PCR	HIV-1 positive HIV-1 negative	3/4 (mixed cell type) ^c 1/6 (plasma cell type)
Soulier et al. (1995)	PCR, Southern blot	HIV-1 positive HIV-1 negative	14/14 (6/14 plasma type) 7/17 (3/7 plasma type)
Ascoli et al. (1999)	PCR	HIV-1 positive HIV-1 negative	1/1 (type not mentioned) 1/1 (type not mentioned)
Gopal et al. (2014)	LANA/viral load	HIV-1 positive	1/1 (plasmablastic variant)
Parravicini et al. (2000)	Immuno-histochemistry	HIV-1 positive HIV-1 negative	4/4 (plasma cell type) 6/6 (plasma cell type)
Dupin et al. (1999)	Immuno-histochemistry	HIV-1 positive HIV-1 negative	5/5 (plasmablastic) 0/1 ^b
Dupin et al. (2000)	PCR	HIV-1 positive HIV-1 negative	8/8 (plasmablastic) 2/2 (plasmablastic)
Case-comparison studies			
Belec et al. (1999) (France)	IFA antibodies	8 cases, 15 controls	[∞ (6/8 vs. 0/15)] ^b
Parravicini et al. (1997) (Italy)	PCR	All HIV-1 negative	[∞ (6/14 vs. 0/25)] ^c
Soulier et al. (1995) (France)	PCR	HIV-1 positive HIV-1 negative Total	14/14 vs. 1/34 7/17 [30.2.(3.8–237.9)][23.0 (2.9–181.5) (21/31 vs. 1/34) ^{c,d}
Asou et al. (2000) (Japan)	PCR	Unclear	[∞ (1/10 vs. 0/139)] ^b

Source: IARC (2012), Table 2.6 and Table 2.7.

CI = confidence interval; IFA = immunofluorescence assay; HIV-1 = human immunodeficiency virus type 1; OR = odds ratio; PCR = polymerase chain reaction.

^a[] ORs calculated by NTP.

^bCell type not specified.

^cPlasma cell or mixed type.

^dRoC calculation based on 2×2 table.

While rare, the incidence and prevalence of KSHV-multicentric Castleman disease across populations are uncertain, as it is not tracked in cancer registries and is likely to be under-diagnosed due to its irregular course. Among 32 cases of MCD followed at the NIH Clinical Center in Bethesda, MD, five were in recent African immigrants (Uldrick et al. 2012); Gopal et al. (2014) reported a single KSHV-multicentric Castleman disease case in Malawi.

Cofactors for Multicentric Castleman Disease

Human immunodeficiency virus type 1 co-infection substantially increases the risk of multicentric Castleman disease among KSHV-positive patients (Table 3-5; also see Section 4), and KSHV appears to be found in almost all cases of human immunodeficiency virus type 1-related multicentric Castleman disease and approximately half of human immunodeficiency virus type 1-negative cases (Oksenhendler et al. 2002; Oksenhendler et al. 2013; Parravicini et al. 1997).

Based on 24 cases of human immunodeficiency virus type 1-associated MCD, Powles et al. (2009) measured the incidence of MCD as 4.3 per 10,000 patient-years (95% CI = 2.7 to 6.4). The incidence increased significantly from 2.3 (95% CI = 0.02 to 4.2) in the pre-HAART era to 8.3 (95% CI = 4.6 to 12.6) in the post-HAART era. A nadir CD4 count $>200/\text{mm}^3$ increased age, no previous HAART exposure and non-Caucasian ethnicity were all associated with an increased risk of multicentric Castleman disease. In a U.K. study of 41 human immunodeficiency virus type 1-positive patients with KSHV-related Kaposi sarcoma or multicentric Castleman disease, Westrop et al. (2012) reported that KSHV-infected human immunodeficiency virus type 1-positive people of African ancestry were significantly more likely to develop multicentric Castleman disease than their European counterparts (relative risk [RR] = 2.42, 95% CI = 1.28 to 4.55). An analysis of the frequency of A299G, a toll-like receptor 4 (TLR4) single nucleotide polymorphism associated with increased multicentric Castleman disease incidence, showed the polymorphism to be three-fold higher in patients of native African descent compared to those of European descent. Finally, the role of Epstein-Barr virus in KSHV-associated multicentric Castleman disease has not been extensively investigated, but the mantle zone plasmablastic cells predominantly infected with KSHV do not appear to be co-infected with Epstein-Barr virus (Dupin et al. 2000; Oksenhendler et al. 2002).

3.4.3. Multiple Myeloma

Multiple myeloma is a comparatively rare type of lymphohematopoietic cancer, making up $<2\%$ of incident cancers in the United States. The annual (2008 to 2011) U.S. incidence and death rate has been stable at approximately 6.3 per 100,000 in men and 3.3 per 100,000 in women with an approximately 47% 5-year survival rate (SEER 2015).

Twenty hospital-based case-control/comparison studies and two nested case-control studies of the association between multiple myeloma and KSHV were reviewed by IARC (2012). One large case-control study, including 254 cases of multiple myeloma, has been identified since 2008 (Benavente et al. 2011), together with two case series of multiple myeloma patients that reported a higher frequency of KSHV in bone marrow tissue (Ismail et al. 2011; Sadeghian et al. 2008) than among healthy controls. Excluding five studies using a case-control or case-comparison design (Benavente et al. 2011; Schonrich et al. 1998; Sitas et al. 1999) or nested case-control design (Tedeschi et al. 2001; Tedeschi et al. 2005) with age-matched controls (see Table 3-5), the majority of studies were clinic based and did not report methods for the selection

of cases and controls or comparison groups and few appear to have controlled for age, sex, or other variables. Among these lower quality studies, a total of 118 cases of multiple myeloma were associated with KSHV (22%) compared with 233 of 1,524 patients without multiple myeloma (23%) in 17 of 18 studies where rates among controls were reported. The five case-control or nested case-control studies also do not support a positive association between KSHV infection and multiple myeloma risk (Table 3-5). In the nested case-control studies (Tedeschi et al. 2001; Tedeschi et al. 2005), increased risks were observed for KSHV detected by latent antibodies; however, IARC (2012) reported that after stratifying by detection method, no statistically significant differences in KSHV positivity between cases and controls were observed by the Working Group.

Table 3-5. Summary of Five Case-control/Comparison and Nested Case-control Studies of KSHV and Multiple Myeloma^a

Reference Study Type	KSHV Detection Method	HIV-1 Status	OR or RR (95% CI) (KSHV-exposed Cases vs. Exposed Controls)
Schonrich et al. (1998) (Germany) Case-comparison	IFA lytic KS-1	HIV-1 negative	[1.39 (0.15–13.3)] (4/99 cases vs. 1/34 healthy controls ^b)
Sitas et al. (1999) (S. Africa) Combined 2 case-control studies	IFA latent Titer 1:100 1:>20,000	Not specified	Adjusted prevalence rate ^c (108 cases and 108 controls) 24% cases vs. 32% blood-donor controls 1.5% cases vs. 3% blood-donor controls
Tedeschi et al. (2001) (Finland) Nested case-control study	IFA lytic Latent (LANA) Western blot (ORF 65, 73, or K8.1A)	Not specified	2.02 (0.94–4.33) (13/47 cases vs. 36/224 controls) 10.0 (0.91–110.3) (2/47 cases vs. 1/224 controls) 0.89 (0.25–3.25) (3/47 cases vs. 16/224 controls)
Tedeschi et al. (2005) (Scandinavia) 5 cohorts, nested case-control studies	IFA lytic IFA latent	Not specified	1.08 (0.5–1.1) (39/329 cases vs. 238/1,393 controls ^d) 0.6 (0.1–2.7) (2/329 cases vs. 16/1,615 controls ^d)
Benavente et al. (2011) (Europe) EpiLymph multisite case-control study	Latent (ORF 73 antigen) Lytic (K8.1)	Not specified	0.31 (0.11–0.85) (4/254 cases; NR controls ^e) 0.43 (0.15–1.2) (4 cases; NR controls ^e)

Source: IARC (2012), Table 2.8 and Table 2.9) except for Benavente et al. (2011).

[] = OR calculated by NTP

CI = confidence interval; IFA = immunofluorescence assay; LANA = latent nuclear antigen; KS = Kaposi sarcoma; KSHV = Kaposi sarcoma-associated herpesvirus; MM = multiple myeloma; NR = not reported; OR = odds ratio; RR = relative risk.

^aStudies with unclear selection of cases or controls or no adjustment for age or other variables were excluded.

^bAge- and sex-matched controls.

^cAdjusted for age, sex, and education and sex partner.

^dAge-, sex-, and area-matched controls; OR adjusted for age.

^eAge-, sex-, sampling date-, length of follow-up- and area-matched controls.

3.4.4. Other Lymphohematopoietic Cancers

Several case-series and case-control studies have been conducted of other lymphohematopoietic cancers, including other lymphomas. An increased incidence of non-Hodgkin lymphoma has been reported in association with KSHV-related multicentric Castleman disease or primary effusion lymphoma in some patients (Oksenhendler et al. 2002; Oksenhendler et al. 2013). Pan et al. (2012) recently described a rare KSHV-associated large B-cell lymphoma in lymph nodes or extranodal sites that do not exhibit lymphomatous effusions and appear to have a different immunological profile, but which may form a continuum with classic primary effusion lymphoma. Deloose et al. (2005) also reported that 38% of human immunodeficiency virus type 1-positive cases of solid immunoblastic/non-Hodgkin lymphoma were KSHV positive among 99 cases of non-Hodgkin lymphoma without evidence of primary effusion lymphoma or multicentric Castleman disease. Burbelo et al. (2012) also reported a higher frequency of KSHV among a small series of human immunodeficiency virus type 1-positive non-Hodgkin lymphoma cases than among healthy controls, but no differences in KSHV frequency were reported in a series of human immunodeficiency virus type 1-positive non-Hodgkin lymphoma cases compared according to duration of human immunodeficiency virus type 1 immunosuppression (Gerard et al. 2009).

A nested case-control study of 155 incident cases of non-Hodgkin lymphoma among human immunodeficiency virus type 1-positive men who have sex with men vs. 155 non-cancer controls (Beachler et al. 2011) did not detect a difference in serum KSHV after adjustment for age and CD4 status. The multisite EpiLymph study in Europe (Benavente et al. 2011), comprising 2,083 cases of lymphoma and 2,048 age-, sex-, and country-matched controls with KSHV serotyping, also reported no associations between KSHV seropositivity and B-cell lymphoma, T-cell lymphoma or Hodgkin lymphoma. Positive associations for splenic marginal zone lymphoma (OR = 4.1, 95% CI = 1.57 to 10.83; 6 cases, using the lytic K8.1 antigen) and mantle-cell lymphoma (OR = 2.63, 95% CI = 0.88 to 7.86; 4 cases, using lytic K8.1 antigen). Although this was a large study, exposure prevalence was low resulting in few exposed cases for some subtypes of B-cell lymphomas, T-cell lymphoma, and Hodgkin lymphoma. KSHV-related non-Hodgkin lymphoma is uncommon in sub-Saharan African populations despite a high prevalence of endemic KSHV (Engels et al. 2007b).

3.4.5. Integration across Studies

Over 115 KSHV-positive cases of primary effusion lymphoma have been reported in the literature, primarily in case reports or case series, and have demonstrated a form of KSHV-related primary effusion lymphoma with distinguishing clinical, morphological, and immunophenotypic features that are uniquely associated with KSHV infection; cases occur in both human immunodeficiency virus type 1-positive and human immunodeficiency virus type 1 negative patients (IARC 2012). KSHV has also been associated with the plasmablastic variant of multicentric Castleman disease (see also Section 4). A majority of KSHV-related cases occur in human immunodeficiency virus type 1-positive patients (IARC 2012). To date, it is unclear if other viruses, including Epstein-Barr virus, or other cofactors, play a role in the development of these conditions, although their rarity has precluded large-scale studies of these factors. No association of multiple myeloma with KSHV infection was found in several studies. Data are insufficient to evaluate other lymphomas.

3.5. Other Tumor Sites

Few studies have been conducted on other tumor sites, with the partial exception of prostate cancer. Case-control or nested case-control studies of prostate cancer identified since 2008 have reported no or small increases in risk in association with KSHV (Huang et al. 2008; McDonald et al. 2011; Sutcliffe et al. 2015). In the most recent nested case-control study within a prospective clinical cancer prevention trial, Sutcliffe et al. (2015) reported no difference in KSHV-positive serostatus (11.6% in cases, 11.1% in controls, $P = 0.81$). These findings are consistent with those reported in earlier studies and reviewed by IARC (2012). IARC (1997b) reviewed six case-series studies of angiosarcoma, four of which were reported as showing no association with KSHV; five case studies of skin cancer were reviewed, four of which showed no association with KSHV (IARC 1997b). In addition, IARC (1997b) reviewed approximately 28 case-series and small case-control studies comparing KSHV DNA in skin and other tissue samples from patients with Kaposi sarcoma lesions with patients with other skin tumors or tissue lesions resembling Kaposi sarcoma and found, overall, only 3% of non-Kaposi sarcoma tissues contained KSHV DNA.

Since 2008, single studies have been identified for KSHV and hepatocellular (Su et al. 2014), vulvar (Simbiri et al. 2014), bladder cancers (Panagiotakis et al. 2013), laryngeal cancer (Guvenc et al. 2008; Mohamadian Roshan et al. 2014), head and neck squamous-cell carcinoma (McLemore et al. 2010), and childhood inflammatory myofibroblastoma (Alaggio et al. 2010). The number of studies on specific solid tumors is insufficient to evaluate these endpoints, with the possible exception of prostate cancer, for which no associations with KSHV serostatus have been reported to date.

3.6. Synthesis across Cancer Endpoints

A summary of the evidence for KSHV infection and the different cancer endpoints from epidemiological studies is provided in Table 3-6. The level of evidence from cancer studies in human also considers studies of tissues from humans in addition to epidemiological studies and is provided in Section 5.

Table 3-6. Summary of KSHV Cancer Endpoints and Strength of the Epidemiological Evidence

Cancer Endpoint	Strength of Evidence
Kaposi sarcoma	<ul style="list-style-type: none"> • Consistent evidence of highly increased, statistically significant risk in many prospective cohort and case-control studies. • KSHV found in >90% of Kaposi sarcoma tumors in biopsies from Kaposi sarcoma case series. • Dose-response relationships observed in several studies.
Primary effusion lymphoma	<ul style="list-style-type: none"> • Consistent evidence of KSHV seropositivity or KSHV DNA in over 115 cases (individual case reports, case-series, case-comparison studies; morphologically and immunophenotypically distinct primary effusion lymphoma)
Multicentric Castleman disease	<ul style="list-style-type: none"> • Consistent evidence of KSHV seropositivity in MCD. KSHV is found in more than 99% of the plasmablastic variant of MCD. Molecular studies support the association with this specific form. • Most cases observed in HIV-1-positive individuals.

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Cancer Endpoint	Strength of Evidence
Multiple myeloma	<ul style="list-style-type: none">• Inconsistent evidence, the majority with no or non-significant modest positive associations, from several case-control or case-comparison studies.
Other lymphohematopoietic cancers and solid tumor sites	<ul style="list-style-type: none">• Inconsistent evidence for prostate cancer risk based on few studies.• Inadequate number of epidemiological studies to evaluate other endpoints.

KSHV = Kaposi sarcoma-associated herpesvirus; MCD = multicentric Castleman disease.

4. Mechanistic and Other Relevant Data

KSHV-associated oncogenesis is a complex process that involves interactions among various viral, host, and environmental cofactors (Fukumoto et al. 2011; Mesri et al. 2014). Although many of the mechanisms by which KSHV is able to establish and maintain infection are known, and many KSHV-encoded proteins and their functions have been characterized in vitro, some aspects of infection and transformation are still not well understood (Fukumoto et al. 2011; Giffin and Damania 2014). This section reviews the characteristics of KSHV-associated neoplasms and risk factors (Section 4.1), evaluates the mode of action and evidence that KSHV is an oncogenic virus (Section 4.2), and provides a synthesis of the information (Section 4.3).

As discussed in Section 3, three neoplasms have been associated with KSHV in humans, although the level of evidence for each endpoint varies: (1) Kaposi sarcoma, (2) primary effusion lymphoma, and (3) a plasmablastic variant of multicentric Castleman disease. These cancers occur most frequently in the context of immunosuppression and are the focus of this section (Giffin and Damania 2014; Mesri et al. 2014). Although other lymphohematopoietic neoplasms and several solid tumor sites (see Section 3) have been investigated, the available data were insufficient to establish a causal relationship with KSHV and are not discussed in this section.

4.1. Characteristics and Risk Factors

Some basic characteristics of the neoplasms associated with KSHV are shown in Table 4-1. The epidemiological data reviewed in Section 3 indicated that human immunodeficiency virus type 1 infection and immunosuppression are important host-related cofactors that increase the risk of developing KSHV-associated neoplasms. However, it is also clear that not all host and environmental cofactors have been identified. Further, KSHV latent and lytic transcripts include genes and non-coding RNAs that promote acquisition of various cancer hallmarks (e.g., insensitivity to antigrowth signals, avoiding cell-cycle arrest, immune evasion, genetic instability, cell proliferation, resisting apoptosis, and angiogenesis) (Mesri et al. 2014). This section reviews the role of immunosuppression, viral proteins, and non-coding RNAs, and other possible cofactors in KSHV-induced neoplasms.

Table 4-1. Characteristics of KSHV-associated Neoplasms

Neoplasm	Presentation	Lineage and Primary Tumor Cell	Clonality	KSHV Genomes
KS	Highly angiogenic lesions found on skin, visceral organs, or mucosal surfaces; leaky vasculature	Endothelial cell origin; tumor cells are spindle cells with mixed blood and lymphatic endothelial cell markers	Oligoclonal or monoclonal	>99% of tumor cells contain single copy of KSHV genome
PEL	Non-Hodgkin lymphoma; B-cell expansion (usually serous effusion without detectable tumor masses) in body cavity	B cells; CD20 ⁻ ; markers resemble partially differentiated plasma cells	Monoclonal	Tumor cells contain 50 to 100 copies of KSHV genome

Neoplasm	Presentation	Lineage and Primary Tumor Cell	Clonality	KSHV Genomes
MCD	Plasmablastic variant; disseminated lymphadenopathy	B cell; IgM γ -restricted plasmablasts	Typically polyclonal	Unknown, detected in most HIV-1+ MCD cases

Source: Adapted from Giffin and Damania (2014).

KS = Kaposi sarcoma; MCD = multicentric Castleman disease; PEL = primary effusion lymphoma.

4.1.1. Human Immunodeficiency Virus Type 1 and Immunosuppression

Although KSHV encodes oncogenic genes that could potentially induce all Kaposi sarcoma phenotypes, the risk of malignancy is greatly enhanced in the presence of cofactors, particularly immunosuppression by human immunodeficiency virus type 1 or iatrogenically during organ transplantation (Mesri et al. 2010). The importance of human immunodeficiency virus type 1 infection as a potent cofactor for KSHV oncogenesis is demonstrated by the dramatic increase in Kaposi sarcoma incidence in human immunodeficiency virus type 1-infected individuals (see Section 3). The risk for developing Kaposi sarcoma is strongly associated with defects in both cellular and humoral immunity. Decreasing CD4 cell counts are associated with an increasing risk of Kaposi sarcoma in both AIDS-associated and classic Kaposi sarcoma cases; however, human immunodeficiency virus type 1-infected individuals with higher CD4 counts are also developing Kaposi sarcoma as they age (Krown et al. 2008). Decreased CD19 cell counts are also associated with an increased risk of Kaposi sarcoma in human immunodeficiency virus type 1-positive and human immunodeficiency virus type 1-negative individuals (Uldrick and Whitby 2011). Iatrogenic immunosuppression also is associated with an increased risk (primarily in kidney allograft patients), but it is not nearly as great as that seen with human immunodeficiency virus type 1 infection (Mesri et al. 2010). This also may reflect differences in KSHV infection rates rather than human immunodeficiency virus type 1-specific causes, or differences in immune dysfunction. Further, human immunodeficiency virus type 1 infection causes changes in cytokine profiles and produces several viral proteins (human immunodeficiency virus type 1 transactivating protein [tat], human immunodeficiency virus type 1 negative factor protein [Nef]) that may be potent cofactors that can activate KSHV lytic replication and influence pathogenesis (Mesri et al. 2014; Purushothaman et al. 2015; Zhu et al. 2014). The biological basis for the role of immunosuppression in KSHV oncogenesis also involves the interactions of latent and lytic infection and is discussed in the following sections.

4.1.2. KSHV Transcripts

The KSHV genome contains 87 open reading frames including many genes found in other herpesviruses, several unique open reading frames (designated K1 to K15) not found in other herpesviruses, and at least 14 viral genes that are homologues of human cellular genes (Mesri et al. 2010; Wen and Damania 2010). Viral transcripts dysregulate several cellular signaling pathways including those involved in cell-cycle progression (e.g., vCyclin, LANA), angiogenesis (e.g., LANA, K1, vCCL, vGPCR, vIL6), apoptosis (e.g., LANA, K1, vFLIP, vBCL-2), immune modulation/evasion (e.g., vFLIP, K3, K5, vIRFs), signal transduction (e.g., K1, K15), and antiviral responses (IARC 2012; Mesri et al. 2010; Wen and Damania 2010). While latent infection is dominant in KSHV-infected cells in vivo and in vitro, both latent and lytic genes contribute to the malignant phenotype (Fukumoto et al. 2011; Mesri et al. 2010). Viral

transcription profiling identified significant differences in the degree of KSHV transcription in human immunodeficiency virus type 1-infected Kaposi sarcoma patients that had not received antiviral treatment and/or chemotherapy (Hosseinipour et al. 2014). Two primary subtypes of Kaposi sarcoma transcriptional signatures were identified: (1) lesions that displayed only a latent transcription pattern (i.e., LANA, vCyclin, vFLIP, miRNAs), and (2) lesions that exhibited extended but incomplete viral RNA transcription (e.g., vIRFs, K1, K15, Orf21/thymidine kinase, Orf36/protein kinase, and others). Only one sample exhibited a complete lytic transcription profile. The data demonstrate multiple subtypes of Kaposi sarcoma lesions and is consistent with other studies reporting similar “extended” KSHV transcripts under conditions of incomplete or abortive replication (discussed below).

A large portion of the KSHV genome is devoted toward evading the innate immune response of the host (e.g., interferon production, interferon regulatory factor activation, NK cell activity, complement activation, inflammasome activation, and chemokine activity), thus facilitating life-long infection (Fukumoto et al. 2011; Giffin and Damania 2014). In addition, KSHV evades adaptive immune responses by repressing viral antigen presentation, T-cell activation, BCR-mediated B-cell activation and B-cell differentiation (Giffin and Damania 2014). Professional antigen-presenting cells, including B cells, dendritic cells, and macrophages, are primary targets for KSHV infection (Campbell et al. 2014a; Knowlton et al. 2013). Cytokine profiles, surface expression of major histocompatibility complex (MHC) molecules, and T-cell activation are altered in infected antigen-presenting cells. This likely explains why T-cell responses to KSHV antigens are not very robust. Both complete and abortive virus replication cycles in antigen-presenting cells (APCs) can affect viral pathogenesis and progression to Kaposi sarcoma and B-cell cancers. Host cell transformation and oncogenesis are thought to result inadvertently from the survival mechanisms used by KSHV and other oncogenic viruses (Wen and Damania 2010).

In an immune-compromised host, lytic infected cells escape immunosurveillance and are able to express the full oncogenic repertoire, including genes that induce angiogenesis and inflammation (Cavallin et al. 2014; Mesri et al. 2014). In addition, some latently infected cells also express some of the early lytic genes but do not complete the lytic cycle. These cells may become progressively transformed and acquire oncogenic alterations that allow them to switch back to a less immunogenic latent form. Latent proteins and miRNAs play an important role in KSHV-associated neoplasms through inhibition of apoptosis and maintenance of latency while KSHV lytic proteins mimic or disrupt host cytokine signals, resulting in microenvironments that promote tumor growth through mechanisms called “paracrine neoplasia” (Cavallin et al. 2014; Fukumoto et al. 2011; Mesri et al. 2010). This section briefly reviews the role of latent proteins, lytic proteins, non-coding RNAs, and their interactions in KSHV pathogenesis.

Latent Proteins

Latent KSHV infection is characterized by a circularized, extra-chromosomal viral genome (episome) that is tethered to the host chromosomes by latency-associated nuclear antigen (LANA) (Giffin and Damania 2014). All KSHV-infected cells express LANA, and antibody-based detection methods are the most powerful tool for diagnosis of pathological samples of KSHV infection (Fukumoto et al. 2011). Only a small portion of the viral genome is actively transcribed during latency and no functional or infectious viral particles are produced (Giffin and Damania 2014). LANA is the most consistently detected viral protein in KSHV-associated tumor cells and is necessary for replicating the episomal viral DNA (IARC 2012). In addition to

LANA, latent transcripts include vCyclin, viral FLICE-inhibitory protein (vFLIP), kaposin A and B, viral interferon regulatory factor 3 (vIRF-3, also known as LANA-2) (expressed in primary effusion lymphoma and multicentric Castleman disease cells but not in Kaposi sarcoma) and viral miRNAs. Although the primary function of LANA is to maintain the viral episome, it also interferes with several anti-tumorigenic pathways, including p53 and anti-proliferative transforming growth factor- β (TGF β), and might contribute to angiogenesis by stabilizing hypoxia-inducible factor-1 α (HIF-1 α) and by targeting von Hippel Lindau for degradation (Mesri et al. 2010). Recent evidence also suggests that caspase cleavage sites in LANA have an important role in delaying apoptosis and blunting the caspase-1-mediated inflammasome, thus inhibiting key cellular defense mechanisms (Davis et al. 2015). vCyclin is a constitutive activator of cyclin-dependent kinase 6 (CDK6), a gene that is overexpressed in lymphomas and leukemias, induces cytokinesis defects and polyploidy, and promotes viral replication (Kollmann et al. 2013; Mesri et al. 2010). vFLIP and kaposin A and B contribute to the inflammatory microenvironment. Thus, these transcripts are associated with growth and proliferative signals, evasion of apoptosis, angiogenic and inflammatory signals, and a limitless replicative potential that support tumor growth and progression (Mesri et al. 2010). Transgenic mice expressing some or all of the KSHV latency genes develop phenotypes characteristic of KSHV malignancies (e.g., B-cell hyperplasia and lymphoma) (Fakhari et al. 2006; Sin and Dittmer 2013). Some biochemical and biological properties, including their role in carcinogenesis, of KSHV latent proteins are shown in Table 4-2.

Table 4-2. Biochemical and Biological Properties of Latent KSHV Proteins

KSHV Gene/Protein	Function in Viral Life Cycle	Homology to Human Protein	Biochemical Properties	Role in Carcinogenesis
ORF 73/LANA	Replication and maintenance of latent viral episome; partition of episomes to daughter cells	None	Interacts with histones, pRB, BET proteins, GSK-3 β and others; inactivates p53-dependent transcriptional activation; induces S-phase entry and activates hTERT transcription; recruits origin-binding proteins	Anti-apoptotic activity, cell survival, deregulation of cell cycle, enhances ras-mediated transforming properties in vitro, tumorigenic in transgenic mice
ORF 71, K13/vFLIP	Viral persistence; spindle cell formation and lymphomagenesis; inhibition of lytic viral replication	FLICE (caspase-8)-inhibitory proteins	Activates NF- κ B; inhibits CD95/Fas-induced apoptosis, anoikis, superoxide-induced cell death; modulates MHC-1 expression	Anti-apoptotic activity, cell survival, immune evasion
ORF 72/vCYC	Viral cyclin; strongly activates CDK6 protein kinase activity	D-type cyclin	Phosphorylates H1, pRB, BCL-2, p27 ^{KIP1} in tandem with CDK6	Deregulation of cell cycle
K12/Kaposin A ^a , Kaposin B ^a	Modulation of cytokine mRNAs regulated by the p38 pathway	None	Interacts with cytohesin-1 Modulates p38/MK2	Transforming properties in cultured cells
K10.5/vIRF3, LANA-2 ^b	Modulates viral interferon response	Interferon regulatory factor	Modulates p53 function; activates IRF-3, IRF-7, c-myc; inhibits IRF-5	Anti-apoptotic activity, immune evasion, cell survival
K15/K15 protein ^b	Recruits endothelial cells to infected cells	None	Activates NF- κ B, MEK/Erk; induces inflammatory cytokines; interacts with proteins involved in signal transduction, with members of src family of PTK, and with an apoptotic regulatory protein HAX-1	Possible anti-apoptotic and angiogenic activity

Source: IARC (2012).

BET = bromodomain and extra-terminal; CDK6 = cyclin-dependent kinase 6; FLICE = FADD-like interleukin-1 beta-converting enzyme; HAX-1 = HS1-associated protein X1; hTERT = human telomerase reverse transcriptase; IRF = interferon regulatory factor; LANA = latency associated nuclear antigen; MHC = major histocompatibility complex; NF- κ B = nuclear factor kappa-light-chain-enhancer of activated B cells; pRB = retinoblastoma protein; PTK = protein tyrosine kinase; vCYC = viral cyclin; vIRF3 = viral interferon regulatory factor-3.

^aExpression increases after activation of the lytic cycle.

^bLytic in endothelial cells; latent in B cells.

Lytic KSHV Proteins

The lytic cycle is characterized by expression of all viral transcripts in an orchestrated temporal order, replication of the viral genome, viral assembly, and viral egress (Wen and Damania 2010). Lytic reactivation requires expression of the replication and transcription activator (RTA) protein and is under epigenetic control (Giffin and Damania 2014; Li et al. 2014; Pantry and Medveczky 2009). RTA plays an important role as both an initiator and controller of KSHV lytic DNA replication (Purushothaman et al. 2015). Many of the lytic viral proteins, including K1, viral interferon response factors (vIRFs), vIL-6, viral-encoded chemokines (vCCLs), viral G protein-coupled receptor (vGPCR) and K15 contribute to the angiogenic and inflammatory phenotype of oncogenic lesions (Purushothaman et al. 2015; Sodhi et al. 2000). However, lytic infection generally results in cellular lysis and is unlikely to have a direct role in endothelial cell growth, transformation, or immortalization (Mesri et al. 2010). Two hypotheses (paracrine oncogenesis and abortive lytic replication) have been proposed to explain how the interactions between latent and lytic KSHV-infected cells contribute to a malignant phenotype (Bais et al. 2003; Cavallin et al. 2014; Mesri et al. 2010).

The paracrine hypothesis recognizes that host and viral growth factors can enhance latent genes and cytokines supplied by a minority of lytically infected cells or latently infected cells expressing early lytic genes (Cavallin et al. 2014; Mesri et al. 2010). Lytic genes induce a number of paracrine-acting factors such as vascular endothelial growth factor (VEGF), platelet-derived growth factor (PDGF), IL-6, angiopoietin 2 (ANGP2), and others that could drive latently infected cell proliferation, angiogenesis, and inflammation and support immune escape and survival. Experimental evidence supporting the role of lytic infection in oncogenesis include the following: (1) lytic viral proteins are expressed and virions are present in a minority of cells within Kaposi sarcoma lesions, (2) immunosuppression increases KSHV re-activation and lytic replication, (3) interruption of lytic replication by immune reconstitution or anti-lytic herpes anti-virals inhibits or prevents tumor development, (4) lytic infection is necessary to support viral episomal maintenance by recruitment of new cells to latency, and (5) endothelial cells expressing latent genes were tumorigenic in nude mice when co-injected with a few vGPCR-expressing cells (at a ratio that approximated the proportion of vGPCR-expressing and latent gene-expressing tumor cells found in human Kaposi sarcoma) but lost their tumorigenic potential in the absence of paracrine secretions from vGPCR-expressing cells (Mesri et al. 2010; Montaner et al. 2006). In addition, controlling KSHV lytic infection decreases the risk of developing Kaposi sarcoma in patients with AIDS (Uldrick and Whitby 2011) and transgenic mice expressing vGPCR develop angiogenic lesions that resemble Kaposi sarcoma (Guo et al. 2003; Yang et al. 2000).

The abortive lytic hypothesis recognizes that not all cells undergoing lytic reactivation complete the lytic cycle (i.e., abortive lytic replication). Such cells express only the oncogenic early lytic genes and can be transformed by genetic or epigenetic alterations, including vGPCR-mediated immortalization, and switch back to a less immunogenic latent status (Bais et al. 2003; Cavallin et al. 2014). Lytically infected cells can stimulate these cells through paracrine mechanisms.

Biochemical and biological properties of some KSHV lytic proteins are shown in Table 4-3.

Table 4-3. Lytic KSHV Proteins and Their Role in Carcinogenesis

KSHV Gene/Protein	Function in Viral Lifecycle	Homology to Human Protein	Biochemical Properties	Role in Carcinogenesis
K1/VIP	May increase/decrease viral reactivation	None	Activates intracellular signaling cascades; induces angiogenic cytokines; blocks intracellular transport of BCR-complexes to cell surface	Transforming properties, angiogenesis, anti-apoptotic activity
ORF 74/vGPCR	Stimulates cellular proliferation	G-protein-coupled receptor	Activates Akt, MEK/Erk, JNK, p38; induces secretion of proinflammatory cytokines and angiogenic growth factors	Transforming properties in cells, tumorigenicity in mice, angiogenesis, anti-apoptotic activity
K2/vIL6	Viral IL6	Interleukin-6	Induces proliferation of PEL cell lines; induces VEGF and STAT3 phosphorylation	Tumor cell survival, angiogenesis, hematopoiesis
K3/miR-1, ZMP-B	Down modulates HLA, ICAM-1, B7-2	None	E3 ubiquitin ligase	Immune evasion
K5/miR-2	Down modulates HLA-A, HLA-B, ICAM-1, CD86, CD1d	Part of a family of membrane-bound-E3-ubiquitin ligases	E3 ubiquitin ligase	Immune evasion
K6/vCCL-1, vMIP-I	Viral chemokine	Chemokine homologue related to MIP-1 α	CCR8 agonist; induces monocyte chemotaxis (VEGF production)	Angiogenic properties, anti-apoptotic activity
K4/vCCL-2, vMIP-II	Viral chemokine	Chemokine homologue related to macrophage inflammatory protein (MIP)-1 α	CCR3, CCR5, CCR8 agonist; induces monocyte chemotaxis	Angiogenic properties
K4.1/vCCL-3, vMIP-III	Viral chemokine	Some homology to chemokines TARC and eotaxin	CCR4, XCR1 agonist	Angiogenic properties
K7/vIAP	Apoptosis inhibitor	Structurally related to a splice variant of survivin	Binds to and inhibits several proteins involved in apoptosis; induces degradation of I κ B, p53, vGCR	Anti-apoptotic activity
ORF 16/vBCL-2	Viral Bcl-2	Bcl-2	Heterodimerizes with human Bcl-2	Anti-apoptotic activity

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KSHV Gene/Protein	Function in Viral Lifecycle	Homology to Human Protein	Biochemical Properties	Role in Carcinogenesis
ORF 45/ORF 45	Virion protein important for lytic replication; inhibits virus-mediated induction of type 1 interferon	None	Binds to and inhibits phosphorylation of IRF-7	Virion infectivity, immune evasion
ORF 50/K-RTA	Immediate-early transactivator; ubiquitin E3 ligase	None	Binds to and activates several lytic viral promoters directly or by interacting with RBPJk; promotes ubiquitination and degradation of IRF-7; represses p53	Reactivation of lytic viral replication from latency, immune evasion, anti-apoptotic activity
K8/K-bZIP	Modulates cell cycle and lytic reactivation	None	EBV Zta homologue; binds to lytic replication origin; binds to, antagonizes, and recruits p53 to ND10/PML bodies; inhibits G1/S transition; co-regulator of K-RTA	Deregulation of cell cycle
K9/vIRF-1	Modulates viral interferon responses	Interferon regulatory factor	Prevents IRF-3-mediated transcription; inhibits p53-transcriptional activity and prevents p53-dependent apoptosis	Transformation of rodent fibroblasts, immune evasion, anti-apoptotic activity
K11/vIRF-2	Modulates viral interferon responses	Interferon regulatory factor	Inhibits interferon induction; inhibits induction of CD95L	Immune evasion, anti-apoptotic activity
K10.5/vIRF3, LANA-2 ^a	Modulates viral interferon responses	Interferon regulatory factor	Modulates p53 function; activates IRF-3, IRF-7, c-myc; inhibits IRF-5	Anti-apoptotic activity, immune evasion, cell survival
K15/K15 protein ^a	Recruits endothelial cells to infected cells	None	Activates NF-κB, MEK/Erk; induces inflammatory cytokines; interacts with proteins involved in signal transduction, with members of src family of protein tyrosine kinases, and with an apoptotic regulatory protein HAX-1	Possible anti-apoptotic and angiogenic activity

Sources: IARC (2012); Purushothaman et al. (2015).

^aLytic in endothelial cells; latent in B cells.

Non-coding RNAs

KSHV-encoded miRNAs are expressed in latently infected cells and are involved with suppressing lytic reactivation by activating NF- κ B, endothelial cell differentiation, and angiogenesis (Mesri et al. 2010; Moody et al. 2013). KSHV infection also induces cellular miRNAs, particularly miR-132. miR-132 inhibits anti-viral innate immune responses and induces abnormal endothelial cell proliferation, thus, linking viral immune escape with angiogenesis, two important features of Kaposi sarcoma. Moody et al. (2013) demonstrated that KSHV miRNAs mediated cellular transformation and tumorigenesis using a KSHV-induced cellular transformation system of primary rat mesenchymal precursor cells. A mutant virus with a cluster of precursor miRNAs deleted failed to transform primary cells and caused cell-cycle arrest and apoptosis. The oncogenicity of the mutant virus was restored by complementation with the miRNA cluster or several individual precursor miRNAs. Qin et al. (2010) also demonstrated that KSHV miRNAs induce IL-6 and IL-10 secretion in murine macrophages and human myelomonocytic cells and support a role in programming macrophage cytokine responses that favor KSHV-associated tumor progression. Transgenic mice expressing KSHV miRNAs as well as multiple viral latent proteins (e.g., LANA, vFLIP, vCYC) recapitulated the precancerous latent state of KSHV infection (i.e., chronic activation of mature B cells, increased plasma cell frequency, marginal zone B-cell hyperplasia, and hyperglobulinemia) (Sin and Dittmer 2013). A subsequent study that crossed these KSHV latency locus transgenic mice with Myc transgenic mice demonstrated that the KSHV latency locus cooperates with the deregulated Myc pathways to induce lymphoma at a higher rate than in single latency or Myc transgenic mice (Sin et al. 2015).

In addition to the miRNAs, KSHV also encodes a long, non-coding RNA known as polyadenylated nuclear (PAN) RNA during the early lytic stage (Campbell et al. 2014b). PAN RNA has been implicated in KSHV gene expression, replication, and immune modulation and is required for optimal expression of all KSHV lytic genes. It also facilitates LANA-episomal dissociation during lytic replication.

4.1.3. Other Possible Cofactors

It is likely that other cofactors are involved in KSHV-associated neoplasms as evidenced by the geographic variation in incidence before the human immunodeficiency virus type 1 epidemic (see Section 3.3.1). Co-infection with other human herpesviruses (e.g., Epstein-Barr virus; see monograph on Epstein-Barr virus), or human cytomegalovirus can activate KSHV lytic replication and influence its pathogenesis (Purushothaman et al. 2015). While other cofactors have been proposed (see Section 3), their mode of action and role as risk factors for specific cancers have not been established.

4.2. Mode of Action and Evidence for Cancer Causation

As discussed in the Overview and Introduction Section, it is often difficult to apply stringent criteria, such as Koch's postulates or Hill's considerations, for determining that a human tumor virus is oncogenic (Moore and Chang 2010; zur Hausen 2001). Therefore, in addition to the usual criteria used by epidemiologists to determine causality, other factors should be considered as proposed by IARC (1997b) and zur Hausen (1994; 2001). Unlike other oncogenic viruses, Hill's epidemiological considerations for causality are met for KSHV and Kaposi sarcoma (Moore and Chang 2010). Thus, application of various criteria applicable to oncogenic viruses

and mechanistic data provide strong evidence that KSHV is oncogenic in humans and are briefly reviewed below by tumor type.

4.2.1. Kaposi Sarcoma

Chang et al. (1994) was the first to report KSHV in Kaposi sarcoma tissues obtained from AIDS patients. There is now substantial evidence that KSHV is the etiological agent of Kaposi sarcoma. KSHV is present in the vast majority of Kaposi sarcoma tumor cells, thus meeting Hill's consideration for strength and consistency (each cell contains one copy of the KSHV genome and its seroprevalence was correlated with the global incidence of the disease) (Fukumoto et al. 2011; Mesri et al. 2010). In addition, the most difficult of the Hill considerations, experimental epidemiological evidence in a randomized clinical trial, was fulfilled when AIDS patients who were treated with an antiherpesvirus drug were protected from new occurrences of Kaposi sarcoma but not against established tumors (Moore and Chang 2010). Other lines of evidence linking KSHV and Kaposi sarcoma include the following (Cavallin et al. 2014):

- KSHV is associated with all four clinical forms of the disease,
- KSHV is found in spindle cells,
- KSHV infection precedes the onset of Kaposi sarcoma,
- KSHV seroprevalence is highest in areas of high Kaposi sarcoma incidence,
- KSHV encodes many viral oncogenes, and
- KSHV transforms and induces tumorigenesis in endothelial cells.
- Monoclonal expansion of KSHV tumors supports an etiologic role for the virus (Duprez et al. 2007; Judde et al. 2000).

In addition, *in vitro* models and animal models have been developed that accurately reproduce many features observed in KSHV-associated neoplasms (An et al. 2006; Ashlock et al. 2014; Dittmer et al. 2015; Mesri and Cesarman 2011; Mutlu et al. 2007).

4.2.2. Primary Effusion Lymphoma

Primary effusion lymphoma is rare. It occurs most frequently in human immunodeficiency virus type 1-infected homosexual males; however, it has been described in association with post-transplant immunosuppression, and in human immunodeficiency virus type 1-negative elderly patients of Eastern European/Mediterranean and Jewish descent (two populations with high seropositivity for KSHV and elevated incidence of classic Kaposi sarcoma) (Dourmishev et al. 2003; Fukumoto et al. 2011; IARC 2012). Because of inadequate pathology and public health infrastructures, the rates of primary effusion lymphoma in the areas of highest KSHV prevalence (i.e., sub-Saharan Africa) are currently unknown.

KSHV DNA sequences were first identified in eight body-cavity-based lymphomas (later identified as primary effusion lymphoma) taken from patients with AIDS, but they were not detected in 185 other lymphomas examined from patients with or without AIDS (Cesarman et al. 1995). Asou et al. (2000) reported similar findings—KSHV was present in 21 of 21 primary effusion lymphoma patients but was not detected in 139 patients with other AIDS- and non-AIDS-related lymphomas. KSHV infection in primary effusion lymphoma cells is predominantly

latent with only a small subpopulation of cells that stain for markers of lytic reactivation (Fukumoto et al. 2011). vIL-6 is the most frequently detected lytic protein and induces VEGF expression and cytokine signals in a broad range of cell types (Aoki et al. 2001; Fukumoto et al. 2011). Further evidence that supports KSHV infection as a causal agent in primary effusion lymphoma is as follows:

- Primary effusion lymphoma neoplasms always carry KSHV and are commonly co-infected with Epstein-Barr virus (Cesarman et al. 1995; Fukumoto et al. 2011);
- KSHV has been incorporated as a diagnostic criterion for primary effusion lymphoma (IARC 2012);
- About half of primary effusion lymphoma patients also have Kaposi sarcoma, and a previous Kaposi sarcoma diagnosis confers an increased risk of primary effusion lymphoma relative to all other AIDS-associated non-Hodgkin lymphomas (Dourmishev et al. 2003; Fukumoto et al. 2011);
- Primary effusion lymphoma cells contain 50 to 100 copies per cell of KSHV DNA, and the expression pattern of KSHV-encoded proteins is almost identical in primary effusion lymphoma and Kaposi sarcoma (Fukumoto et al. 2011; Giffin and Damania 2014; IARC 2012);
- Several KSHV-infected cell lines have been established from primary effusion lymphoma cells that retain a stable latent viral genome including a KSHV+/EBV– cell line established from KSHV+ and Epstein-Barr virus+ primary effusion lymphoma cases, suggesting that KSHV plays an essential role in primary effusion lymphoma pathogenesis (Fukumoto et al. 2011; Katano et al. 1999); and
- Expression of several KSHV viral genes was required for survival of primary effusion lymphoma cells in culture (IARC 2012).

4.2.3. Multicentric Castleman Disease

Castleman disease is an uncommon lymphoproliferative disorder with several histological variants (hyaline vascular, plasma cell, mixed, and plasmablastic types) and two clinical forms; unicentric (or localized) and multicentric (Al-Maghrabi 2011; Bonekamp et al. 2011; El-Osta and Kurzrock 2011; Fajgenbaum et al. 2014). The plasmablastic form of multicentric Castleman disease has been specifically associated with KSHV in both human immunodeficiency virus type 1-positive and human immunodeficiency virus type 1-negative cases (Dupin et al. 2000). Thus, KSHV-associated multicentric Castleman disease is now recognized as a distinct entity from other forms of multicentric Castleman disease and is classified by WHO as “large B-cell lymphoma arising in HHV8-associated multicentric Castleman disease” (IARC 2008). This plasmablastic variant of diffuse large B cell lymphoma has KSHV expression of lytic antigens, cytoplasmic IgM with light chain restriction, and viral interleukin 6 expression and is characterized by severe inflammatory symptoms (attributed primarily to elevated levels of IL-6), an aggressive course, and a poor prognosis (Bonekamp et al. 2011; Fajgenbaum et al. 2014; Polizzotto et al. 2012; Venkataraman et al. 2013). Dysregulated IL-6 levels are thought to contribute to multicentric Castleman disease development (Cai et al. 2010). Fewer studies have investigated the association of multicentric Castleman disease and KSHV compared to Kaposi sarcoma or primary effusion lymphoma; however, additional supporting evidence is as follows:

- Several case-control, case-comparison or case series studies have reported an association between KSHV and multicentric Castleman disease (see Section 3 and Table 3-4);
- Cases of Kaposi sarcoma and multicentric Castleman disease frequently occur together in the human immunodeficiency virus type 1-positive population (Cronin and Warnke 2009; Reddy and Mitsuyasu 2011);
- The level of KSHV in peripheral blood monocytes or plasma corresponds with symptoms during multicentric Castleman disease flares in human immunodeficiency virus type 1-positive individuals (Reddy and Mitsuyasu 2011);
- KSHV-positive multicentric Castleman disease cases are associated with KSHV lytic infection, and high levels of vIL-6 have been detected in infected B cells and sera and likely are associated with B-cell proliferation seen in multicentric Castleman disease (Aoki et al. 2001; Fukumoto et al. 2011; IARC 2012);
- vIL-6, a frequently detected lytic protein, enhances cytokine signaling, increases human IL-6 and induces VEGF expression, and likely exacerbates inflammation and disease progression and may be a mechanism leading to multicentric Castleman disease (Al-Maghrabi 2011; Fukumoto et al. 2011; Giffin and Damania 2014); and
- Treatment of multicentric Castleman disease cases with an inhibitor of KSHV infection has shown some success (Casper et al. 2004).

4.3. Synthesis

Human viral oncogenesis is a complex process that involves interactions among many viral, host, and environmental factors. Immunosuppression is an important cofactor based on the dramatic increase in Kaposi sarcoma incidence among human immunodeficiency virus type 1-infected individuals. KSHV infection has been clearly linked with all clinical forms of Kaposi sarcoma, as well as primary effusion lymphoma and a plasmablastic variant of multicentric Castleman disease, and biologically plausible modes-of-action have been described. One or more KSHV transcripts are expressed in all KSHV-associated tumors and are required for survival of tumor cells in culture. Latent transcripts drive viral persistence and replication, promote host cell proliferation, and prevent apoptosis while lytic transcripts dysregulate cell signaling pathways that contribute to the angiogenic and inflammatory phenotype of oncogenic lesions via paracrine mechanisms.

5. Overall Cancer Hazard Evaluation and Listing Recommendation

Kaposi sarcoma-associated virus (KSHV) is known to be a human carcinogen based on sufficient evidence from studies in humans. This conclusion is based on epidemiological and molecular studies showing that it causes Kaposi sarcoma (Table 5-1) primary effusion lymphoma (Table 5-2), and a plasmablastic variant of multicentric Castleman disease (Table 5-3) in humans, together with supporting evidence from mechanistic studies demonstrating the biological plausibility of its carcinogenicity in humans.

Data are inadequate to evaluate the association between KSHV and multiple myeloma, which has inconsistent evidence from epidemiological studies and no available evidence from mechanistic studies.

The following tables provide the level of evidence recommendations for the carcinogenicity of KSHV for each endpoint from studies in humans, including the key data from both epidemiological and molecular studies in humans.

Table 5-1. Summary of the evidence for KSHV and Kaposi sarcoma from human studies

Types of Studies	Kaposi Sarcoma
Epidemiological	
Positive associations	39/39 ^a case-control studies (all ORs > 1.0) and all 16 ^a cohort/nested case-control studies; ORs/RRs for all studies are mostly statistically significant and some very high (10 to >100-fold) Elevated RR in both HIV-1-negative and HIV-1-positive populations and in all types of Kaposi sarcoma Dose response in several studies
Molecular (human tissue)	
Clonality	Mono- or oligoclonal
% KSHV-infected tumors	>99% (~1 copy/cell)
KSHV protein expression ^b	
Latent	LANA, vCyclin, vFLIP, kaposin A and B
Lytic	RTA, K1, vIRFs, vIL-6, vGPCR, vCCLs, K15
Level of evidence	Sufficient

HIV-1 = human immunodeficiency virus type 1; K1 = unique KSHV protein 1; K15 = unique KSHV protein 15; KSHV = Kaposi sarcoma-associated herpes virus; LANA = latency-associated nuclear antigen; OR = odds ratio; RR = risk ratio;

RTA = replication and transactivation protein; vCCLs = viral-encoded chemokines; vFLIP = viral FLICE-inhibitory protein; vGPCR = viral G protein-coupled receptor; vIL-6 = viral homolog of interleukin-6; vIRF = viral interferon regulatory factors.

^aThe number of studies is based on those reporting risk estimates.

^bSee Section 4.1.2 for more details.

Table 5-2. Summary of the Evidence for KSHV and Primary Effusion Lymphoma from Human Studies

Types of Studies	Primary Effusion Lymphoma (PEL)
Epidemiological	
Positive associations	Found in over 115 cases; at least 95 individual case reports and case-series studies and 21 cases in one comparison study PEL is a single distinct pathological entity Found in both HIV-1-negative and -positive cases and in transplant patients Approximately 50% cases also have Kaposi sarcoma; some PEL cases found in geographical regions associated with endemic or classic Kaposi sarcoma
Molecular (human tissue)	
Clonality	Monoclonal
% KSHV-infected tumors	100% (high copy number); cell lines established from PEL tumors retain a stable latent viral genome
KSHV protein expression	Similar to Kaposi sarcoma
Other	KSHV is part of diagnostic criteria Expression of KSHV viral genes was required for survival of PEL cells in culture
Level of evidence	Sufficient
HIV-1 = human immunodeficiency virus type 1; KSHV = Kaposi sarcoma-associated herpesvirus; PEL = primary effusion lymphoma.	

Table 5-3. Summary of the Evidence for KSHV and Multicentric Castleman Disease from Human Studies

Types of Studies	Multicentric Castleman Disease (MCD)
Epidemiological	
Positive associations	Found in most cases of MCD (plasmablastic variant) in several case series studies; 4/4 case comparison studies; very high ORs or no cases of KSHV among controls
Molecular (human tissue)	
Clonality	Typically polyclonal ^b
% KSHV-infected tumors	100% of cancerous lymph nodes KSHV+ with HIV-1+ and 50% KSHV+ with HIV-1-
KSHV protein expression ^a	LANA, vIL-6
Level of evidence	Sufficient (plasmablastic variant)
HIV-1 = human immunodeficiency virus type 1; KSHV = Kaposi sarcoma-associated herpesvirus; LANA = latency-associated nuclear antigen; OR = odds ratio; vIL-6 = viral homolog of interleukin-6.	
^a Multicentric Castleman disease is associated with lytic infection.	
^b Monoclonal B-cell expansion have been reported.	

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Glossary

Case report: Detailed descriptions of a few patients or clinical cases (frequently, just one sick person) with an unusual disease or complication, uncommon combinations of diseases, an unusual or misleading semiology, cause, or outcome (maybe a surprising recovery). They often are preliminary observations that are later refuted. They cannot estimate disease frequency or risk (e.g., for lack of a valid denominator).

Case series: A collection of subjects (usually, patients) with common characteristics used to describe some clinical, pathophysiological, or operational aspect of a disease, treatment, exposure, or diagnostic procedure. A case series does not include a comparison group and is often based on prevalent cases and on a sample of convenience. Common selection biases and confounding severely limit their power to make causal inferences.

Case-comparison study (case-control study, case referent study): The observational epidemiological study of persons with the disease (or another outcome variable) of interest and a suitable control group of persons without the disease (comparison group, reference group). The potential relationship of a suspected risk factor or an attribute to the disease is examined by comparing the diseased and non-diseased subjects with regard to how frequently the factor or attribute is present (or, if quantitative, the levels of the attribute) in each of the groups (diseased and non-diseased).

Cellular immunity: Immunity independent of antibody but dependent on the recognition of antigen by T cells and their subsequent destruction of cells bearing the antigen or on the secretion by T cells of lymphokines that enhance the ability of phagocytes to eliminate the antigen.

Cofactor: A factor that activates or enhances the action of another entity such as a disease-causing agent. Cofactors may influence the progression of a disease or the likelihood of becoming ill.

Diagnostic criteria: The specific combination of signs, symptoms, and test results that a clinician uses to identify a person as representing a case of a particular disease or condition.

Enzyme immunoassay: An assay that uses an enzyme-bound antibody to detect antigen. The enzyme catalyzes a color reaction when exposed to substrate.

Highly active antiretroviral therapy: Treatment regimens that stop or slow the HIV virus from reproducing and keep HIV disease from progressing. The usual HAART regimen combines 3 or more HIV drugs from at least 2 different classes.

Horizontal transmission: The spread of an infectious agent from one individual to another, usually through contact with bodily excretions or fluids, such as sputum or blood, which contains the agent.

Humoral immunity: The component of the immune system involving antibodies that are secreted by B-cells and circulate as soluble proteins in blood.

Immunohistochemical staining: A method to detect specific antigens in cells based on an antigen-antibody reaction, which can be recognized at the light microscopic level.

Latent phase: A phase of the virus life cycle during which the virus is not replicating.

Lytic phase: A phase of the virus life cycle during which the virus replicates within the host cell, releasing a new generation of viruses when the infected cell lyses.

Lytic reactivation: The biological events beginning with emergence of a virus from latency and ending with lysis of the host cell and release of progeny virions.

microRNA: Small, non-coding RNA molecules approximately 22 nucleotides in length that act post translationally in a regulatory role to target messenger RNAs for cleavage or translational expression.

Monoclonal: Pertaining to or designating a group of identical cells or organisms derived from a single cell or organism.

Non-coding RNAs: Functional RNA molecules that are transcribed from DNA but are not translated into proteins.

Oligoclonal: A few different clones, or the product of a few different clones.

Paracrine neoplasia: A process whereby KSHV-infected cells induce neighboring uninfected cells to produce cytokines and growth factors that are necessary as autocrine and paracrine factors for driving tumor production.

Parenteral: By some other means than through the gastrointestinal tract; the parenteral route of infection involves breaks in the skin such as cuts and scrapes, puncture wounds, bites, and burns.

Peripheral blood monocytes: Circulating precursors of macrophages and dendritic cells that migrate from the blood stream across vascular endothelium for immunological surveillance, as well as respond to inflammation.

Polyclonal: Pertaining to or designating a group of cells or organisms derived from several cells.

Polymerase chain reaction: A laboratory technique used to produce large amounts of specific DNA fragments. Polymerase chain reaction is used for genetic testing and to diagnose disease.

Professional antigen-presenting cells (APCs): Specialized white blood cells that express MHC class II and are able to activate a helper T-cell that has never encountered its antigen before. The three main types of professional APCs are macrophages, dendritic cells, and B cells.

Titer: A laboratory measurement of the concentration of a substance in a solution (e.g., an antibody titer measures the presence and amount of antibodies in the blood).

Toll-like receptors: A family of pattern recognition receptors involved in the detection of structures associated with pathogens or damaged host tissues.

Vertical transmission: The transmission of infection from one generation to the next (e.g., from mother to infant prenatally, during delivery, or in the postnatal period via breast milk).

Abbreviations

AIDS:	Acquired Immune Deficiency Syndrome
ANGP2:	angiopoietin 2
APC:	antigen-presenting cell
BET:	bromodomain and extra-terminal
CDC:	Centers for Disease Control and Prevention
CDK6:	cyclin-dependent kinase 6
CI:	confidence interval
DNA:	deoxyribonucleic acid
DOT:	Department of Transportation
dsDNA:	double-stranded DNA
EBNA:	Epstein-Barr virus nuclear antigen
EBV:	Epstein-Barr virus
EBV VCA:	EBV viral capsid antigen
ELISA:	enzyme-linked immunosorbent assays
F:	female
FDA:	Food and Drug Administration
FLICE:	FADD-like interleukin-1 beta-converting enzyme
HAART:	highly active antiretroviral therapy
HAX-1:	HS1-associated protein X1
HHV8:	human herpesvirus 8
HIF-1 α :	hypoxia-inducible factor-1 α
HIV:	human immunodeficiency virus
HR:	hazard ratio
hTERT:	human telomerase reverse transcriptase
IARC:	International Agency for Research on Cancer
IFA:	immunofluorescence assay
HHV8:	human herpesvirus 8
IFA:	immunofluorescence assay
K1:	unique KSHV protein 1
K15:	unique KSHV protein 15
KS:	Kaposi sarcoma

KSHV:	Kaposi sarcoma-associated herpesvirus
LANA:	latency-associated nuclear antigen
MHC:	major histocompatibility complex
miRNA:	microRNA
M:	male
Max:	maximum
MCD:	multicentric Castleman disease
Med:	median
Min:	minimum
MM:	multiple myeloma
MSM:	men who have sex with men
Nef:	negative factor protein
NF- κ B:	nuclear factor kappa-light-chain enhancer of activated B cells
NHANES:	National Health and Nutrition Examination Survey
NR:	not reported
NS:	not significant
NTP:	National Toxicology Program
OR:	odds ratio
ORF:	open reading frames
OSHA:	Occupational Safety and Health Administration
PAN:	polyadenylated nuclear
PBMC:	peripheral blood mononuclear cells
PCR:	polymerase chain reaction
PDGF:	platelet-derived growth factor
PEL:	primary effusion lymphoma
pRB:	retinoblastoma protein
PTK:	protein tyrosine kinase
RARECARE:	Surveillance of Rare Cancers in Europe
RNA:	ribonucleic acid
RR:	relative risk
RTA:	replication and transcription activator
SEER:	Surveillance, Epidemiology, and End Results Program
TGFBeta:	transforming growth factor- β

TLR4	toll-like receptor 4
U.K.:	United Kingdom
U.S.:	United States
U.S.A.:	United States of America
vCCL:	viral-encoded chemokines
VEGF:	vascular endothelial growth factor
vFLIP:	viral FLICE-inhibitory protein
vGPCR:	viral G protein-coupled receptor
vIL-6:	interleukin-6
vIRF:	viral interferon regulatory factors
WB:	western blot assay

Appendix A. Literature Search Strategy

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The objective of the literature search approach is to identify published literature that is relevant for evaluating the potential carcinogenicity of the Kaposi sarcoma-associated herpes virus (KSHV). As discussed in the Viruses Concept Document (https://ntp.niehs.nih.gov/ntp/roc/concept_docs/2014/virusesconcept_508.pdf), the monograph relies on the IARC monograph and studies published since the monograph (new studies). The literature search strategy was used to identify new human cancer studies and recent reviews of mechanistic data.

A.1. General Approach

Database searching encompasses selecting databases and search terms and conducting the searches. Searches of several citation databases are generally conducted using search terms for the individual viruses of interest, combined with search terms for cancer and/or specific topics, including epidemiological and mechanistic studies. A critical step in the process involves consultation with an information specialist to develop relevant search terms. These terms are used to search bibliographic databases. IARC used literature found by searching PubMed for KSHV through 12/2008, so PubMed, Web of Science and Scopus were searched for new information about HTLV from >2008 to August 2015. Table A-1 highlights the general concepts searched with selected example terms. To review all the terms used, please refer to the full search strings below.

Table A-1. Major Topics Searched

Topics	Example Terms
Kaposi’s sarcoma-associated herpes virus	Herpesvirus 8, human (Mesh), Kaposi’s sarcoma-associated herpesvirus, human herpesvirus 8, KSHV, HHV8

The literature for KSHV was searched without using narrowing terms within the bibliographic databases. The results were then processed in EndNote to remove duplicates before being transferred to DistillerSR for screening.

The bibliographic database search results (3,314) were processed in Endnote then imported into DistillerSR for first and second tier screening. Relevant studies found through the citations of review articles and other secondary searched were also included. Tagging in DistillerSR categorized the useful articles into Human Epidemiologic literature (212) or Mechanistic literature (704).

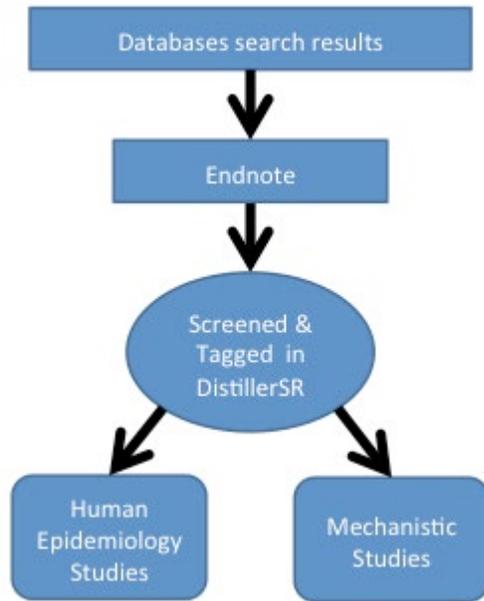


Figure A-1. Literature Processing Flow

A.2. Search Strings for KSHV Searches

PubMed: 2008–2015

"Herpesvirus 8, human"[mh] OR "Kaposi's sarcoma-associated herpes virus"[tiab] OR "Kaposi's sarcoma-associated herpesvirus"[tiab] OR "Kaposi sarcoma-associated herpes virus"[tiab] OR "Kaposi sarcoma-associated herpesvirus"[tiab] OR KSHV[tiab] OR "human herpesvirus 8"[tiab] OR "human herpes virus 8"[tiab] OR HHV8[tiab] OR "HHV-8"[tiab]

Web of Science and Scopus: 2008–2015

"Kaposi's sarcoma-associated herpes virus" OR "Kaposi's sarcoma-associated herpesvirus" OR KSHV OR "human herpesvirus 8" OR "human herpes virus 8" OR HHV8



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