

REVIEW ARTICLE

Gieri Cathomas

Human herpes virus 8: a new virus discloses its face

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Abstract The human herpes virus 8 (HHV8) or Kaposi's sarcoma-associated herpes virus (KSHV) is present in all Kaposi's sarcoma, and the detection of the virus using polymerase chain reaction or in situ hybridization is a highly sensitive and specific diagnostic test for the diagnosis of this neoplasm. HHV8 is furthermore invariably present in primary effusion lymphoma (PEL) and has also been detected in patients with acquired immunodeficiency syndrome (AIDS)-associated multicentric Castleman's disease (MCD) as well as, to a lesser extent, in non-AIDS MCD. In contrast to Kaposi's sarcoma, in which the tumor cells show primarily latent HHV8 infection, a higher rate of lytically infected cells can be observed in MCD. Epidemiological surveys indicate that the seroprevalence for HHV8 parallels the risk of developing Kaposi's sarcoma – 5–10% in the general population of the Western world but ranging up to 20–70% in homosexual human immunodeficiency virus (HIV)-infected patients, and the infection precedes the development of Kaposi's sarcoma. Finally, HHV8 has been reported in a number of other diseases, especially in multiple myeloma. However, the highly controversial role of HHV8 in these lesions has to be clarified. Based on the data available today, HHV8 can be assigned as a new human virus, associated with tumors.

Key words Herpes virus · HHV8 · Kaposi's sarcoma · Castleman's disease · Non-Hodgkin's lymphoma · Review

Introduction

Based on the epidemiology and the clinical course of disease, Kaposi's sarcoma has long been suspected to be either caused by or closely related to an infectious agent, and a variety of viruses and bacteria have been implicated, including cytomegalovirus, hepatitis B, the human immunodeficiency virus (HIV) and mycoplasma [13, 14, 42, 118, 135, 137]. In 1994, Chang and co-workers reported the presence of herpes-virus-like DNA in tumor tissue of patients with Kaposi's sarcoma [33]. Subsequent work confirmed these findings and the detection of a new human herpes virus referred to as Kaposi's sarcoma-associated herpes virus (KSHV) or human herpes virus 8 (HHV8) [88]. In recent years, an increasing body of information has been generated confirming the link between HHV8 and Kaposi's sarcoma as well as with two lymphoproliferative diseases, the primary effusion lymphoma (PEL) and the multicentric Castleman's disease (MCD) [30, 92, 123]. In the present review, the basic data defining HHV8 as a new human tumor virus is presented, and the impact of the virus detection in the diagnosis of HHV8-associated diseases as well as some controversies concerning other diseases possibly associated with HHV8 infection are discussed.

The virus

In contrast to the other human herpes viruses, HHV8 was primarily characterized using molecular biology techniques, i.e., the representational difference analysis [33]. Further analysis and subsequent cloning and sequencing of the complete viral genome revealed that HHV8 belongs to the subfamily of γ -herpes virus, related to Epstein-Barr virus (EBV), and represents the first member of a human γ_2 -herpes virus, genus *Rhadinovirus* [88, 93, 112]. HHV8 is most closely related to herpes virus saimiri, an animal virus causing lymphoproliferative disorders in new-world primates. The genomic structure of HHV8 is shared by all rhadinoviruses and consists of a

G. Cathomas (✉)
Department of Pathology, University of Zürich, Switzerland
e-mail: gieri.cathomas@pty.usz.ch
Tel.: +41-1-2652514, Fax: +41-1-2654416

G. Cathomas
Institute for Clinical Pathology,
Department of Pathology University Hospital,
Schmelzbergstrasse 12, CH-8091 Zürich, Switzerland

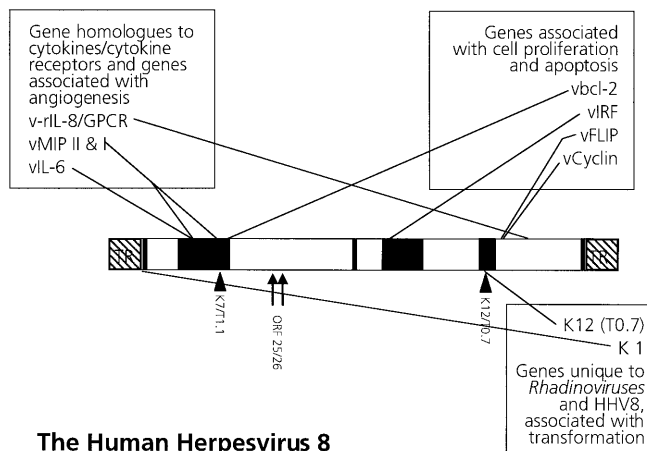


Fig. 1 Schematic representation of the human herpes virus 8 (HHV8) genome showing blocks of coding regions conserved in other herpes viruses (black areas) and regions unique to *Rhadinovirus* or HHV8 (white areas). The position of various genes is indicated as well as the gene position of ORF 25 and 26 used for polymerase chain reaction (PCR) (arrows) and two probes K12/T0.7 and K7/T1.1 suitable for in situ hybridization (arrowheads) [88, 93, 112]. *v* viral; *rIL8/GPCR* interleukin-8 receptor/G-coupled protein receptor; *MIP* macrophage inflammatory protein; *IL-6* interleukin 6; *IRF* interferon regulatory factor; *FLIP* Flice inhibitory protein

central unique gene region flanked by repetitive sequences, containing a high GC DNA content (Fig. 1). The linear viral genome of HHV8 includes the 140.5-kb central coding region and the terminal repeats containing several 801-bp units [93, 112]. In HHV8, two types of genes have been described within the genome: conserved genes similar to other herpes virus and coding for structural and replication-associated proteins, being arranged in blocks (Fig. 1). In the gene regions between these conserved blocks, the viral genome reveals open reading frames (ORFs) unique to rhadinoviruses and HHV8, including a variety of homologues to human genes [93, 112], of which many revealed in vitro functional activity similar to that seen in their natural counterpart. These genes include viral homologues to cytokines and cytokine receptors, such as interleukin 6 (vIL-6) [86, 94], the macrophage inflammatory proteins I and II (vMIP I/II) [19, 86, 94], and the interleukin-8 receptor/G-protein-coupled receptor (vIL-8/GPCR) [7, 9], as well as genes associated with cell proliferation and anti-apoptosis, such as a viral Cyclin D [72], an interferon response factor (vIRF) [55, 86, 140], vbc1-2 [36, 115] and Flice inhibitory protein (vFLIP) [133] (for review see also [117]). Furthermore, HHV8-encoded genes have been shown to induce angiogenesis [5, 9, 19]. Genes unique to HHV8 have been characterized and assigned with the prefix "K" and, using in vitro analysis, at least two of them, K1 and K12 (T0.7/Kaposin), revealed transforming potential in vitro [68, 91]. Transforming activity was further observed in long-term culture of HHV8-infected endothelial cells [49, 90].

Most of the in vitro data have been generated by analyzing permanently HHV8-infected lymphoma cell lines

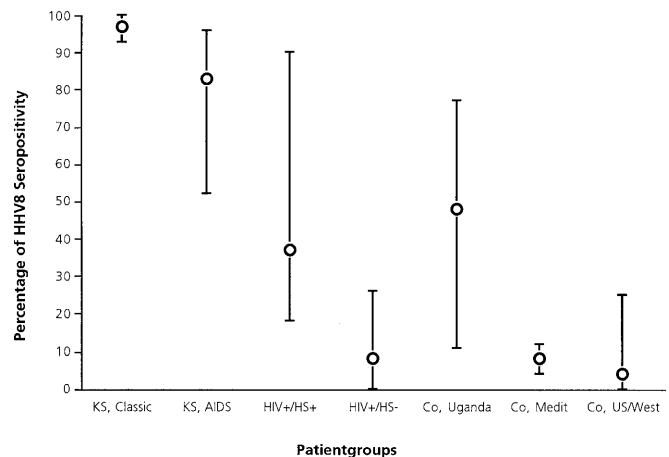


Fig. 2 Human herpes virus 8 (HHV8) seroepidemiology in various patient groups: the circles represent the mean of six studies including different techniques using latent and lytic antigens [34, 57, 66, 70, 106, 119]. The error bars indicate the maximum and minimum values reported by these studies. *KS, classic* classic or endemic Kaposi's sarcoma; *KS, AIDS* Kaposi's sarcoma associated with human immunodeficiency virus (HIV) infection and acquired immunodeficiency syndrome (AIDS); *HIV+/HS+* homosexual patients infected with HIV without Kaposi's sarcoma; *HIV+/HS-* HIV-infected patients without known homosexual or bisexual behavior; *Co, Uganda* control groups originating from Uganda; *Co, Medit* control groups originating from the Mediterranean area; *Co, US/West* control groups originating from the US or Western Europe

[8, 82, 110]. The expression of viral genes in these cell lines can be induced by butyrate or phorbol esters and, based on this response, three classes of HHV8 transcripts have been distinguished [116]. Whereas class-I genes, such as vFLIP or vCyclin D, are constitutively expressed and unaffected by induction, class-III genes, representing predominantly structural viral genes, can be detected only following appropriate stimulation. Class-II genes, finally, as exemplified by K7 (T1.1/nut-1), are constitutively transcribed at low level, but expression increases following induction. In general, class-I genes are basically thought to be associated with latent, class III with lytic infection, whereas class-II genes have been associated with both latent and lytic infection [139]. Although successful primary cultivation of HHV8 from Kaposi's sarcoma tissue has been reported, the use of cell culture systems other than the lymphoma cell lines is very limited so far [51, 109].

Seroepidemiology of HHV8

As for other infectious agents, the detection of antibodies against HHV8 proteins analyzed in various populations provides important data concerning the general epidemiology of the infection as well as important hints to the mode of transmission. In addition, as is the case for other herpes viruses, it is very likely that, following primary infection, HHV8 establishes a latent or persistent infection with the potential to be reactivated under certain

conditions, such as immunosuppression. A number of serosurveys have been performed analyzing various patient groups and cohorts all over the world [34, 66, 70, 106, 119, 120]. To perform the serological assays, basically two sources of antigen have been used: recombinant proteins and HHV8-infected lymphoblastoid cell lines, derived from PEL [102]. With respect to the antigen itself, viral proteins associated with lytic or latent infection have been used, manufactured either as recombinant proteins [119] or derived from uninduced (latent infection) and induced (lytic infection) HHV8-infected lymphoblastoid cell lines [57, 66]. So far, the antibody tests have not been standardized and considerable differences in the seroprevalence of HHV8 within a given population as well as in the interassay correlation have been reported [102]. Nevertheless, most studies gave concordant results, demonstrating that HHV8 is, in contrast to most other herpes viruses, not a ubiquitous human infection, and HHV8 seroprevalence parallels the risk of developing Kaposi's sarcoma (Fig. 2).

Antibodies against HHV8 have been detected in 70–100% of individuals with Kaposi's sarcoma, whereby the detection rate is slightly lower in patients with acquired immunodeficiency syndrome (AIDS)-associated disease than in patients with classic Kaposi's sarcoma [119]. In the general population of the Western World, a range of seroprevalences of 0–20% has been reported [34, 66, 70, 106, 119]. The majority of studies, however, report a seroprevalence of 5–10% in this population and the discrepancies reported may indeed be associated with a lower specificity of some of these tests. Although some studies suggest that assays detecting antibodies against lytic antigen may find more seropositive samples, this could not generally be confirmed [102]. One should keep in mind, however, that as none of the tests detect HHV8 antibodies in all patients with Kaposi's sarcoma, but HHV8 DNA can be detected in all these lesions (see below), the true rate of HHV8 infection in low-risk populations remains to be elucidated. A similar problem can be observed in the typical low-risk population of children in the Western World. Most studies, however, reported the absence or at least a low prevalence of HHV8 antibodies in young children [18, 70, 119].

In high endemic areas, such as Central Africa, a higher seroprevalence in the general population has been reported ranging from 32% to 100% [57, 59, 70, 119, 120]. This is not surprising, as in some areas in Central Africa Kaposi's sarcoma is one of the most common tumors [136]. A higher rate of seroprevalence has further been reported in patients attending clinics for sexually transmitted diseases or in patients with a well-known risk of Kaposi's sarcoma, especially in HIV-positive homosexual men, ranging from 20% to 70% and supporting the concept that HHV8 is a sexually transmitted disease [16, 57, 66, 70, 106, 119]. However, in HIV-infected and uninfected hemophiliacs, the HHV8 seroprevalence does not significantly exceed the prevalence reported for the general population [57, 66, 70, 119].

Generally, seroconversion and seropositivity for HHV8 predicts the risk to develop Kaposi's sarcoma [56, 78, 108, 121]. In a large cohort of 593 men with a seropositivity of 37.6%, the 10-year probability of developing Kaposi's sarcoma was 49.6% [78]. HHV8 can also be transmitted by solid organ and bone-marrow transplantation. Following transplantation, primary infection and reactivation may lead to Kaposi's sarcoma, and these patients have an increased risk of developing the tumor [48, 58, 61, 100, 108]. In a study of renal transplant recipients, within 4 years, Kaposi's sarcoma developed in 2 of 39 HHV8-seropositive patients, all showing seroconversion following transplantation, but in none of the 181 seronegative kidney recipients [108].

Taken together, serological data confirm the strong correlation between Kaposi's sarcoma and HHV8 infection and suggest that the virus is primarily sexually transmitted in countries with low Kaposi's sarcoma prevalence. Other ways of transmission, however, must be present, as suggested by the fact that HHV8 can be detected in young children from endemic areas [3].

HHV8 in Kaposi's sarcoma tissue

Since the original description of Kaposi's sarcoma in 1872, a variety of different clinical forms of this lesion have been described [64]. The classic or endemic form of Kaposi's sarcoma, originally found in older men of Eastern Europe or of Mediterranean origin, usually shows an indolent clinical course. In contrast, the more recently described forms associated with prolonged immunosuppression, as seen in solid organ transplant recipients and especially in patients infected with HIV, show a more aggressive clinical behavior and often disseminate and involve inner organs such as the lung or the gastrointestinal tract. Furthermore, additional variants of Kaposi's sarcoma in Africa have been described. Histologically, all clinical forms of Kaposi's sarcoma show similar features. In the early or patchy stage, jagged and dilated vascular spaces with interstitial inflammatory cells and extravasated red blood cells can be seen. In the more characteristic plaque and finally nodular stage, the tumor is made up of plump spindle cells with irregular slit-like vascular spaces aligned by a recognizable endothelium and filled with erythrocytes [46].

In the original description of the herpes virus-like DNA sequences of HHV8 by Chang and coworkers, a polymerase chain reaction (PCR)-based method, the representational difference analysis, has been used to detect the viral sequences [33]. Although HHV8 can be detected in Kaposi's sarcoma tissue using Southern blots, in the vast majority of subsequent analyses, PCR has been performed to detect fragments of the viral DNA either in fresh tissue samples or formalin-fixed biopsy material [2, 24, 33, 44, 60, 87]. In addition, to increase the sensitivity of the test, a nested PCR, i.e., two consecutive PCR reactions with an inner and outer primer pair, has been used. Although nested PCR can be performed for diagnostic purposes, rigorous precautions and appropri-

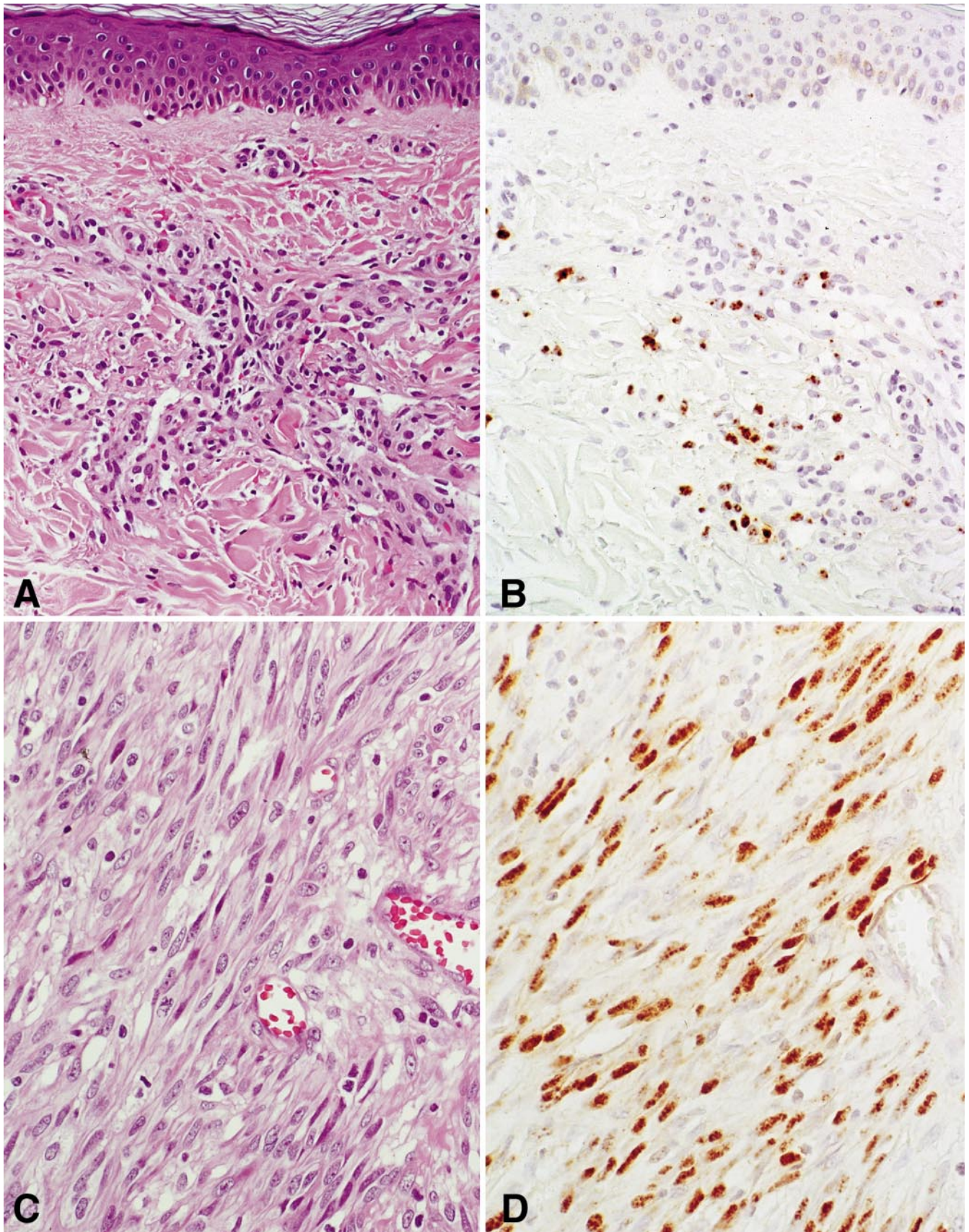


Fig. 3 Human herpes virus 8 (HHV8) and Kaposi's sarcoma: patch or macula stage (A) and nodular stage (C) of Kaposi's sarcoma (hematoxylin and eosin) and in situ hybridization using biotinylated

tyramide signal amplification (B, D). A few positive cells can be seen in the macula stage (B) and a strong staining of most of the spindle cells in the nodular form of Kaposi's sarcoma (D)

ate controls are mandatory to avoid false-positive results. However, so far, no other test achieves equal sensitivity. Using nested PCR, HHV8 DNA can be detected in virtually all Kaposi's sarcoma tissues, including formalin-fixed, paraffin embedded tissue, and in all clinical forms, including the classic, endemic, transplantation-associated and African tumors [2, 22, 23, 24, 33, 44, 60, 63, 87, 95, 127]. Many studies used primer from the minor capsid protein region (ORF26), the originally described region of the HHV8 genome [33]. Primer pairs of other gene regions, especially ORF 25, have been used equally successfully and, although variation within the HHV8 genome has been described, most of these gene regions revealed no major sequence variability and subsequent decrease of the sensitivity of the assay [11, 21, 28]. Most studies were unable to detect HHV8 DNA in mesenchymal and vascular tumors other than Kaposi's sarcoma, including hemangiomas, hemangioendotheliomas, infantile capillary hemangioma and hemangiosarcomas [24, 63, 67, 73, 77, 122], although some controversies exist with respect to hemangiosarcomas [79].

To overcome the problems of false-positive results and to increase the specificity, an in situ hybridization assay can be performed. Using in situ hybridization and PCR in situ hybridization, HHV8 DNA has been shown to be present in the spindle and vascular cells of Kaposi's sarcoma [20, 50, 71]. In addition, using the same technique, HHV8 DNA has been reported to be present in the epidermal cells overlaying Kaposi's sarcoma tissue as well as in pneumocytes of patients with the tumor [50]. Using isotopic in situ hybridization with probes directed against HHV8 RNA, it has been further shown that viral RNA associated with latent infection is expressed in the majority of tumor spindle cells as well as in endothelial cells lining atypical blood vessels [125, 126]. In contrast, only few cells express transcripts associated with lytic infection and at least a subgroup of these cells are of monocytic origin [17, 125]. Nevertheless, for routine use, neither PCR in situ hybridization nor isotopic in situ hybridization are well suited as a diagnostic test. Therefore, non-radioisotopic, colorimetric assays have been applied to detect HHV8 in routinely processed tissue samples [105] (Cathomas et al, unpublished observations). ORF K12 (T0.7/Kaposin) RNA is a suitable target as it is expressed in latently HHV8-infected spindle and endothelial cells of Kaposi's sarcoma. Another target associated with lytic HHV8 infection is ORF K7 (T1.1/nut-1); this transcript is abundantly expressed, albeit in a small number of cells [97, 124, 139] (Cathomas et al, unpublished observations). Using digoxigenin-labeled oligonucleotides, the test revealed a rather low sensitivity, detecting K7 (T1.1/nut-1) RNA in only 63.2% and K12 (T0.7/Kaposin) RNA in 19.2% of Kaposi's sarcoma tissues, and early lesions were rarely positive [75]. To increase the sensitivity, signal amplification using biotinylated thymidine has been successfully applied and, using this more-sensitive technique, latency-associated HHV8 RNAs such as K12 (T0.7/Kaposin) or v-cyclin D can be detected in all

forms and stages of Kaposi's sarcoma samples (Fig. 3) [105] (Cathomas et al, unpublished observations). Using immunohistochemistry, latency-associated HHV8 proteins have also been detected [43, 104], reporting a detection rate of 11 (78.6%) of 14 samples analyzed [43]. Finally, herpes virus particles have been visualized by electron microscopy in Kaposi's sarcoma tissue [97].

In Kaposi's sarcoma tissues, as outlined above, HHV8 can be detected using PCR in 95–100% of cases. It can therefore be concluded that HHV8 DNA is present in all variants of the tumor, and the detection of HHV8 DNA can be used as a diagnostic test for the disease. Failure to detect HHV8 in a given lesion (and a positive internal control to confirm the presence of appropriate DNA) should shed doubts on the primary diagnosis. The detection of HHV8 can further be used as a diagnostic tool in clinical specimens for which the diagnosis of Kaposi's sarcoma is difficult to achieve due to the small size of the biopsy and crash artifacts, as in biopsies of the lung and the gastrointestinal tract (Fig. 4). In addition, the assay can also be applied to fine-needle aspirates [1] and bronchoalveolar lavage fluids (BAL). The detection of HHV8 DNA in BAL of immunocompromised patients has been shown to have a high sensitivity and specificity for the diagnosis of pulmonary Kaposi's sarcoma and the virus may be detected prior to manifest lesions and disappear following successful therapy [12, 25, 128].

Detection of HHV8 in non-tumorous specimens of patients with and without Kaposi's sarcoma

HHV8 DNA can be detected in the blood, especially in the lymphocyte fraction of infected patients and the presence of viral DNA is predictive of a significantly increased risk of developing Kaposi's sarcoma [69, 89, 138]. In non-tumorous tissue of patients with Kaposi's sarcoma elsewhere, HHV8 DNA can be detected by means of PCR in up to 50%; the viral load in these non-tumorous tissues is, however, lower than in tumor tissue and may represent circulating HHV8-infected cells [22, 28, 38, 44]. Nevertheless, the detection of HHV8 DNA in non-tumorous tissue may also lower the specificity of the HHV8 detection by means of PCR as a diagnostic test in patients with Kaposi's sarcoma in another location [28].

Intriguingly, the presence of HHV8 DNA detected using PCR has been reported not only in semen of HIV-infected homosexual men but also in 23–91% of semen and 63% of non-neoplastic prostatic tissue of normal healthy men or patients without evidence of immunosuppression [74, 84]. These findings are important as they would support the concept that HHV8 is transmitted by sexual contact and implicate a widespread infection within the general population. However, subsequent studies were unable to confirm these data in healthy subjects and seroepidemiology makes a widespread infection in healthy, non-homosexual men unlikely [28, 41, 74, 131].

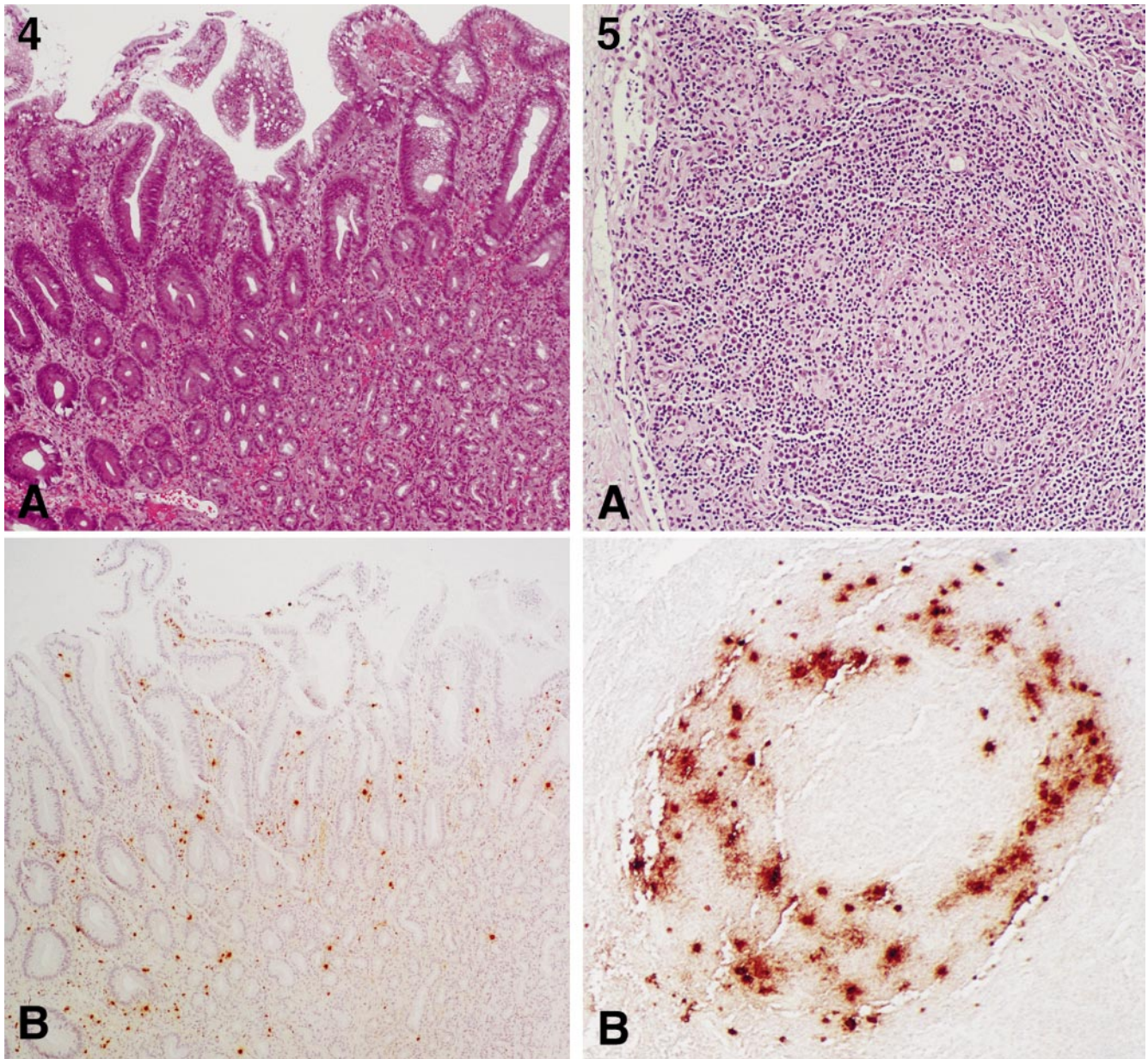


Fig. 4 Gastric involvement of a Kaposi's sarcoma in a patient with acquired immunodeficiency syndrome (AIDS): hematoxylin and eosin and in situ hybridization to detect latency-associated human herpes virus 8 (HHV8) RNA

Fig. 5 Acquired immunodeficiency syndrome (AIDS)-associated multicentric Castleman's disease (**A**, hematoxylin and eosin, frozen section) and in situ hybridization using a probe directed against a RNA transcript associated with lytic infection (**B**). The probe reveals a large number of positive cells in the mantle zone of a lymphoid follicle

PEL and MCD

Two additional diseases have been associated with HHV8, the body-cavity-based-lymphoma (BCBL), later referred to as PEL and the MCD. PEL is a rare malignant non-Hodgkin's lymphoma, emerging as serous pleural and pericardial effusion or ascites, usually without a de-

tectable mass or lymph-node involvement [4, 30, 65, 92]. However, solid tumor masses of PEL have been described in lymph nodes, lung and the gastrointestinal tract [39, 65, 92]. Meta- or synchronic Kaposi's sarcoma is common [4, 30, 65]. The tumor is associated with HIV-infection but PEL in HIV-negative patients has been described [32, 92]. PEL often shows co-infection with EBV, but EBV-negative forms also exist, especially in HIV-negative patients [8]. Morphologically, the PEL bridges large-cell immunoblastic lymphoma and anaplastic large-cell lymphoma [4, 30, 65, 92]. The tumor cells are polymorphous, with abundant cytoplasm often with a clear perinuclear Golgi zone. Most of the nuclei are round to oval with prominent nucleoli, a subset of cells show highly irregular, polylobular or multiple nuclei. The tumor cells express CD45, but there is frequently an absence of other B-cell-associated antigens. As the ma-

jority of tumors are also positive for CD30, CD38 and epithelial membrane antigen (EMA), it was suggested to put PEL in the group of mature plasma cell neoplasms [62]. Clonal immunoglobulin gene rearrangement is present, but a c-myc gene rearrangement is missing [4, 30, 65, 92]. In addition, a PEL of the T-cell phenotype has been reported [114]. HHV8 is thought to be invariably associated with this lymphoma, and the detection of HHV8 can therefore be used for the diagnosis of this non-Hodgkin's lymphoma. The presence of HHV8 may further be helpful to distinguish PEL from pyothorax-associated lymphoma (PAL), another malignant non-NHL associated with malignant effusions [6]. A number of cell lines deriving from PEL have been established, which can maintain the virus in vitro [8, 31, 110]. These cell lines have been important in the study of viral replication and as a base for serological assays (see above). In contrast, HHV8 DNA has rarely been detected in other forms of malignant non-Hodgkin's lymphoma in patients with or without immunosuppression [26, 30, 52].

HHV8 DNA has been further detected in most patients with MCD associated with HIV infection [123]. In HIV-negative patients, HHV8 was detected in about 40% of the multicentric variant of this disease, but in the localized form of Castleman's disease, HHV8 can only rarely be detected [10, 123]. MCD, a non-neoplastic angiofollicular lymphoid hyperplasia, usually of the plasma cell or mixed plasma cell/hyaline vascular type [96, 123], affects multiple lymphoid organs and may be associated with a number of diseases showing immunosuppression or immuno-dysregulation (reviewed in [101]). Recently, the presence of HHV8 has further been reported in 6 of 7 patients with MCD in POEMS' syndrome [11]. Although the precise pathogenesis of the disease remains to be elucidated, extensive production of cytokines has been reported in MCD, especially of IL-6, and HHV8-derived vIL-6 was detected in the lymph node of HHV8 by means of immunohistochemistry [98] and PCR [132]. In contrast to Kaposi's sarcoma, lymph nodes of HHV8-associated MCD reveal in the mantle zone of lymphoid follicles a significant expression of HHV8 RNA associated with lytic infection, and the pattern of expression is characteristic of HHV8-associated MCD (Fig. 5) [124] (Cathomas et al, unpublished observations).

HHV 8 in other diseases

There are a number of data reporting the presence of HHV8 DNA in various other diseases and lesions. The most intriguing is the presence of HHV8 in cultured bone-marrow stromal dendritic cells [111] and bone-marrow biopsies [113] of patients with multiple myeloma and in a proportion of patients with monoclonal gammopathy of unknown significance (MGUS) [111]. These data, have been confirmed by some groups [35, 54], whereas others have been unable to detect evidence of HHV8 infection in these patients, either using PCR or serological tests [27, 99, 130, 134], and a fierce contro-

versy has emerged concerning the role of HHV8 in multiple myeloma [15, 129]. To explain these conflicting results, differences in the techniques applied by the various groups or other so-far unknown viruses have been incriminating, but further data are urgently needed to define the role of HHV8 in this disease.

Additional reports describe the detection of HHV8 DNA in epithelial skin tumors following solid organ transplantation [103], pemphigus vulgaris/foliaceus [80], sarcoidosis [40] and angiolymphoid hyperplasia [76]. Most of these findings have, however, not been confirmed by other groups [21, 26, 29, 37, 85, 107]. It remains to be seen whether these controversial reports, often based on the detection of HHV8 DNA by means of PCR, originate in false-positive results generated by nested PCR or are due to marked regional differences in the prevalence of HHV8 [85]. Nevertheless, based on the discrepancies reported and the fact that, in contrast to Kaposi's sarcoma, many groups failed to regularly detect HHV8 in these lesions, it is unlikely that HHV8 is involved in the basic pathogenesis of these diseases.

HHV8, a human tumor virus?

Due to the long incubation period and the fact that only a subgroup of infected patients finally develop a tumor, it is difficult to prove the link between a given virus and an associated neoplasm. Based on the famous postulate of Robert Koch, Evans and Müller proposed a number of criteria to prove the causal relationship of virus and tumor [47]: the geographic distribution of the infection should cover similar areas as the tumor; markers of viral infection should precede the development of the tumor; and the rate of infection should be higher in patients with than without the tumor [47]. In addition, the quantity of viral markers indicated by antibody titers or viremia should be increased in the tumor population relative to the matched controls, and prevention of the infection, such as by vaccination, should decrease the tumor incidence. Besides these epidemiological points, virological aspects should also be fulfilled, including the presence of viral nucleic acids in most tumor tissue samples (but not in normal cells) as well as experimental evidence, such as the transformation capacity of the virus (or viral genes) and the possibility of experimental induction of tumors in a susceptible animal system [47].

As outlined above, for HHV8, a number of these criteria have been already fulfilled. The seroepidemiology parallels the risk of Kaposi's sarcoma in terms of geographical distribution as well as within different patient groups with a well-known risk of developing the tumor. In addition, it has been shown that the HHV8 antibody as well as the detection of HHV8 DNA by means of PCR precedes the development of Kaposi's sarcoma, and patients with HHV8 infection have a significantly increased risk of developing the tumor, as has been shown in HIV-infected patients and in transplant recipients [78, 108]. HHV8 DNA can be detected in all tumor tissue,

Table 1 Viruses associated with human tumors. *HPV* human papillomavirus; *HBV* hepatitis B virus; *HCV* hepatitis C virus; *HTLV I* human T-cell leukemia virus I; *EBV*, *HHV5* Epstein-Barr-virus; *PTLD* post-transplantation lymphoproliferative disease;

Virus	Family	Non-malignant diseases	Associated malignancies	Co-factors
HPV	Papovaviridae	Warts, laryngeal papillomatosis	Epidermoid cancer of cervix, anus, vulva and penis	
HBV	Hepadnavirus	Chronic hepatitis Cirrhosis	Hepatocellular carcinoma	Aflatoxin, Alcoholism Co-infection with HCV
HCV	Flaviviridae	Chronic hepatitis Cirrhosis	Hepatocellular carcinoma	Alcoholism Co-infection with HBV
HTLV I	C-Retrovirus	Tropical spastic paresis	Adult T-cell leukemia	
EBV, HHV5	γ -Herpes virus	Infectious mononucleosis Oral hairy leukoplakia	Burkitt's lymphoma (endemic form) PTLD X-linked lymphoproliferative disease Nasopharyngeal carcinoma Hodgkin's disease AIDS-associated CNS-lymphoma Leiomyosarcoma in children with AIDS	Malaria Immunosuppression Gene defects
Human herpes virus 8 (HHV8) Kaposi's sarcoma-associated herpes virus (KSHV)	γ_2 -Herpes virus	Multicentric Castleman's disease	Kaposi's sarcoma Primary effusion lymphoma	Immunosuppression

and there is at least some evidence that HHV8 has a transforming capacity in vitro [49, 68, 91].

Kaposi's sarcoma itself, however, is a rather peculiar lesion and even the question whether Kaposi's sarcoma is really a neoplastic or basically a reactive proliferation remains a controversial issue [53]. Several studies have shown high levels of cytokines and chemokines within Kaposi's sarcoma lesions and especially the dependence on these factors to maintain cell proliferation (reviewed in [45]). It is therefore very likely that, as for other tumors, cofactors are an important prerequisite for the development of the lesion, of which immunosuppression is the most obvious. A possible explanation for the difference between HHV8 infection and the traditional viral transforming pathway of other tumor viruses is the recent finding that inflammatory cytokines found in Kaposi's sarcoma lesions reactivate latent HHV8 infection [83]. It has therefore been proposed that latently infected cells exposed to sites of inflammation with an increased cytokine environment leads to the reactivation of HHV8 and subsequent expression of potential pathogenic genes as vIL6. This lytic infection subsequently re-infects other cells, maintaining, especially in the context of immunosuppression and immuno-dysregulation, a cycle of lytic and latent infection, sustaining the proliferative stage of Kaposi's sarcoma [81].

Much less is known about the pathogenesis of PEL, a rare disease. However, the fact that cell lines of this type of lymphoma maintain replicative virus also in the EBV-negative forms makes it likely that this tumor is also basically caused by HHV8. Taken together, the data available today points in the direction that HHV8 is indeed the cause of Kaposi's sarcoma and PEL, and can be seen as a new virus associated with human tumors (Table 1).

In conclusion, the most recently detected human herpes virus, HHV8, is closely linked to all forms of Kaposi's sarcoma. The total of epidemiological evidence and the molecular and cellular biology data strongly suggest that HHV8 is a new human oncogenic virus directly involved in the pathogenesis of Kaposi's sarcoma. This close correlation makes the detection of HHV8 a useful diagnostic marker, especially using in situ hybridization and eventually immunohistochemistry. In addition, there is strong evidence that HHV8 is the cause of a rare malignant non-Hodgkin's lymphoma, PEL, and subgroup of MCDs. Again, the detection of the virus in this lesion is a helpful tool in the diagnosis of these diseases. A number of questions, however, remain to be answered, especially relating to the precise epidemiology, the mode of transmission in the general population, and the cofactors leading to the development of HHV8-associated diseases in persons infected with the virus. In addition, the role of HHV8 in other diseases, especially in the multiple myeloma, has to be clarified. Finally, the better understanding of the pathogenesis of HHV8 infection will ultimately lead to more specific therapeutic approaches and, hopefully, to a vaccine. In any case, the detection of HHV8 has opened a new exciting field in viral oncogenesis.

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