Kaposi’s sarcoma associated herpes virus (KSHV/HHV 8): epidemiology, molecular biology and tissue distribution

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Introduction

Although first described in 1872, Kaposi’s sarcoma remains a neoplasm of uncertain histogenesis.1 The lesion is considered by some experts to be a vascular neoplasm and by others, a reactive vasoproliferative condition. Currently, the debate still rages over the precise cell of origin of Kaposi’s sarcoma—that is, whether it is of lymphatic or true endothelial cell origin.

Clinically, Kaposi’s sarcoma is often multifocal and the spindle cells of these individual lesions have been shown to be clonal in origin.2 It is also known that Kaposi’s sarcoma lesions can regress spontaneously, especially when immunosupressive treatment is discontinued, thereby suggesting that the growth of Kaposi’s sarcoma is controlled by host factors. In addition, at least one group has observed regression of Kaposi’s sarcoma lesions when patients are treated with the anti-herpes viral drug Foscarnet.3 The role of cytokines has also been explored, as has the contribution of the HIV Tat protein which may act in a synergistic manner (see later). Epidemiological evidence suggests an infectious aetiology for Kaposi’s sarcoma, which is supported by the clustering of the disease in well-defined populations (men with AIDS and homosexual men) and its relation to immunosuppression.4 Many agents have been investigated as possible aetiological factors, including human papilloma virus, cytomegalovirus and Epstein-Barr virus (EBV), but no convincing association has ever been established.

Kaposi’s sarcoma associated herpes virus (KSHV)/human herpes virus type 8 (HHV8)

In 1994, Chang et al5 documented the presence of a previously undescribed virus in Kaposi’s sarcoma tissue samples (fig 1). This Kaposi’s sarcoma associated herpes virus (HHV8) was discovered using representation difference analysis which permits the discrimination of DNA sequences which are present in tumour tissue from ones that are absent in normal DNA from the same patient. The newly described virus shows similarity to two other gamma herpes viruses—herpes virus saimiri (HVS) and EBV.6

Viral genetic analysis demonstrates that the agent is a gamma II herpes virus (genus Rhadinovirus) and is the first member of this genus known to infect humans (fig 2). HHV8 has been partially sequenced recently and many regions show sequence homology at the DNA level to both EBV and HVS.

Tissue distribution of HHV8

Using PCR, HHV8 is found in more than 90% of HIV associated Kaposi’s sarcoma lesions as well as in classic Kaposi’s sarcoma, and endemic and post-transplant associated Kaposi’s sarcoma.7-12 HHV8 has also been described in two AIDS related lymphoproliferative disorders: body cavity based lymphomas (BCBL or primary effusion lymphomas) and multicentric Castleman’s disease (MCD) which itself is related to the development of Kaposi’s sarcoma.13-14

BCBLs are a unique group of non-Hodgkin’s lymphomas, largely confined to HIV

Figure 1 (A) HHV8 amplicons in Kaposi’s sarcoma (KS) identified by PCR ISH, showing positive signals in KS spindle cells (arrow). (B) HHV8 identified by non-isotopic in situ hybridisation (NISH) in the BCP-1 cell line derived from a BCBL showing two discrete intranuclear signals (arrows). (C) HHV8 amplicons identified in a BCBL derived cell line showing the characteristic herpes-like viral particles.
lesions, including squamous carcinomas, other groups, including our own, have disputed this.21,22

**HHV8 in Kaposi’s sarcoma**

In Kaposi’s sarcoma lesions, HHV8 infects spindle and endothelial cells, as demonstrated by PCR in situ hybridisation (PCR-ISH), and the majority of these cells seem to be latently infected.23–24 Viral DNA is generally absent from non-Kaposi’s sarcoma tumours and other tissue specimens from individuals lacking Kaposi’s sarcoma risk factors. However, viral DNA can be found in circulating B cells in approximately 50% of AIDS patients with and 7% of AIDS patients without Kaposi’s sarcoma.25 In 1984, Walter et al demonstrated herpes-type virus particles in a Kaposi’s sarcoma tumour specimen by electron microscopy, but were unaware of the importance of their finding.26

**Cell culture and HHV8**

Initially, investigators were unable to detect HHV8 sequences in cell lines derived from Kaposi’s sarcoma samples, which cast doubt on the significance of HHV8 in its pathogenesis. Nikoloff et al have now successfully established tumour cell lines from Kaposi’s sarcoma lesions, in which HHV8 can be isolated and propagated under certain defined conditions.27 This is an important development as the ability to grow HHV8 permits experimentation to determine whether HHV8 is directly capable of causing Kaposi’s sarcoma, or whether the presence of other co-factors, such as HIV, cytokines or some undefined cellular factor, is required. In addition, the propagation of HHV8 in vitro is an extremely important step in providing necessary viral antigens for use in immunoassays (see later).

In 1996, Renne et al demonstrated HHV8 virion production by activated BCBL cells (BCBL-I) stimulated by phorbol esters.28 They were also able to visualise HHV8 virions in cell lysates from such lymphomatous cells. However, as early as 1972 these virions may have been visualised by Giraldo et al.29

**Serology and seroepidemiology of HHV8**

Recently, Kedes et al30 and Gao et al31 provided the first evidence of direct seroprevalence of HHV8 and its distribution in Kaposi’s sarcoma risk groups. Kedes et al, using an immunofluorescence assay which detects antibodies directed against latency associated nuclear antigens (LANA) in B cells latently infected with HHV8, examined serum samples of 913 patients from different Kaposi’s sarcoma risk population cohorts. Their results showed that HHV8 is not a ubiquitous infection in the general population, which contrasts clearly with the known properties of other herpes viruses (such as EBV) in that they infect a relatively large proportion and remain in a latent state throughout the life of the host.

HHV8 seropositivity is high in AIDS patients with Kaposi’s sarcoma and in HIV positive homosexual men without Kaposi’s sarcoma.32 However, HHV8 seroprevalence in

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**Figure 2** Phylogenetic tree of HHV8 based on comparison of amino acid sequences of the major capsid protein of HHV8 (adapted from Moore et al).
Table 1: Summary of seroepidemiology of HHV8

<table>
<thead>
<tr>
<th>Reference</th>
<th>Cell lines</th>
<th>Array</th>
<th>Kaposi’s sarcoma subtypes (% positive HHV8)</th>
<th>Controls (% positive HHV8)</th>
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<tbody>
<tr>
<td>Moore et al</td>
<td>HBL-6 (adsorbed serum)</td>
<td>IFA</td>
<td>Higher in AIDS related KS (14) versus controls (16)</td>
<td>STD-HIV negative (8%)</td>
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<td></td>
<td>BCBL-1 cells</td>
<td>LANA</td>
<td>57/45 AIDS related KS (82%)</td>
<td>HIV positive blood donors (30%)</td>
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<td></td>
<td>BCP-1 cells</td>
<td>LNA</td>
<td>AIDS related KS (US) 88%</td>
<td>HIV positive haemophiliacs (3%)</td>
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<td>AIDS related KS (Italy) 71%</td>
<td>HIV negative haemophiliacs (US) 0%</td>
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<td>AIDS related KS (Uganda) 78%</td>
<td>Blood donors (US) 0%</td>
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<td>HIV negative KS (Italy) 100%</td>
<td>Blood donors (Italy) 4%</td>
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<td>HIV negative KS (Uganda) 100%</td>
<td>HIV positive homosexual (18%)</td>
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<td>HIV positive haemophilic (0%)</td>
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<td>Blood donors (0%)</td>
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<td>high EBV titres (0%)</td>
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<td>7/54 (15%) HIV positive</td>
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<td>Miller et al</td>
<td>BC-1 cells; n-bunrayte inducible antigen (p40)</td>
<td>IFA</td>
<td>32/48 AIDS related KS (67%)</td>
<td>HIV positive homosexual (90%)</td>
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<td></td>
<td>BCP-1 cells</td>
<td>lytic and latent antigens</td>
<td>American (96%)</td>
<td>HIV positiveive IVDU (23%)</td>
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<td>African (100%)</td>
<td>children (US) (4%)</td>
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<td></td>
<td></td>
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<td>(lytic antibodies)</td>
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<td>Ivory Coast (100%)</td>
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<td>HIV positive homosexual (33%)</td>
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<td>HIV positive STD (8.43%)</td>
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<td>HIV negative Ugandan (35.3%)</td>
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<td>US blood donors (5%)</td>
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<td>UK donors (1.6%)</td>
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HIV negative patients with syphilis and in women without sexual exposure (bisexual partners) is low. HIV negative blood donors also have low seroprevalence rates, as do HIV infected haemophiliacs and transfusion recipients (2–4%).

Gao et al investigated the seroprevalence of HHV8 in North American, Italian and Ugandan populations, again using indirect immunofluorescence antibody assays. They were based on the EBV negative, HHV8 infected BCBL cell line, BCP I. The authors detected HHV8 antibodies in approximately 90% of patients with AIDS associated Kaposi’s sarcoma and in 30% of AIDS patients without Kaposi’s sarcoma, which concurred with the study of Kedes et al. Their findings in the Italian cohort were similar. Interestingly, they found high seroprevalence rates (51%) in patients without Kaposi’s sarcoma in Uganda, which is not surprising in the view of the fact that endemic Kaposi’s sarcoma is extremely prevalent in Ugandan locales. In the higher, the higher than expected seroprevalence of HHV8 found in the Italian cohort parallels the incidence of classic Kaposi’s sarcoma in these regions.

The presence of such specific antibody responses does denote past exposure to HHV8 and may indicate ongoing latent infection. Importantly, Gao et al demonstrated that seroconversion occurred during the adult life of the patients examined. From this seroepidemiological data, it is reasonable to conclude that the distribution of HHV8 does conform epidemiologically to that of a sexually transmissible agent and seems to link itself intimately with the risk of developing Kaposi’s sarcoma. This is supported by the documentation of HHV8 seroconversion in a cohort of HIV positive homosexual men prior to the development of overt Kaposi’s sarcoma (table 1).

Molecular biology of HHV8
To establish causation, it is important to demonstrate the presence of HHV8 in patients before they develop Kaposi’s sarcoma. This has been demonstrated clearly by the seroprevalence data. However, the presence of HHV8 seropositivity and the presence of HHV8 in Kaposi’s sarcoma lesions does not establish a direct role for the virus in the pathogenesis of Kaposi’s sarcoma.

Zhong et al have examined the pattern of HHV8 gene expression in Kaposi’s sarcoma and found it to be highly restricted. These authors characterised two small transcripts that represent the bulk of the virus specific RNA, transcribed from over 120 kilobases of the HHV8 genome in infected cells. One of the isolated transcripts is predicted to encode a small membrane protein, whereas the other is an unusual polyadenylated RNA that accumulates in the nucleus in high copy numbers. The pattern of viral gene expression suggests that most infected cells in Kaposi’s sarcoma are latently infected and that lytic viral replication is likely to be restricted to a much smaller subpopulation of cells.

Clearly, many factors are involved in the pathogenesis of Kaposi’s sarcoma. It is known that several cytokines acting in an autocrine/paracrine manner play a direct role in the pathogenesis of Kaposi’s sarcoma. Cultured Kaposi’s sarcoma cells secrete and require certain cytokines, including basic fibroblast growth factor (bFGF), interleukin 6 (IL6) and platelet derived growth factor (PDGF). In addition, mRNA from IL6 and PDGFβ receptor, PDGFPα, and PDGFβ are expressed in high quantities in Kaposi’s sarcoma lesions in vivo. It is also interesting that Ensoli et al have demonstrated that HIV contributes to the intitial proliferation of endothelial cells. They have also shown that the Tat protein of HIV I can...
Kaposi's sarcoma associated herpes virus

Figure 3  Possible role of HHV8 in Kaposi's sarcoma, BCBL, and Castleman's disease. CD40, cyclin D1, bcl-2, and bcl-2 are up-regulated in Kaposi's sarcoma, suggesting possible interaction with HHV8. The v-cyclin gene (ORF 72 of HHV8) may act as a cell growth factor/oncogene.

Co-operate with bFGF to induce the formation of Kaposi's sarcoma-like lesions in nude mice, and that the protein directly increases the proliferation of endothelial cells in Kaposi's sarcoma cell lines. However, it is clear from epidemiological data that HIV infection is not an absolute requirement as HIV-negative patients commonly develop Kaposi's sarcoma.

Other factors involved in the development of Kaposi's sarcoma

For the development of angioproliferative lesions such as Kaposi's sarcoma, cytokines, extracellular matrix molecules and integrins are required. Integrins are known to modulate angiogenesis by directly influencing apoptosis. This is an extremely complex process involving proteins that prolong cell survival (bcl-2 and bcl-x) as well as proteins that promote apoptosis (bcl-x and bax). In Kaposi's sarcoma, it is known that bcl-x is present in endothelial and spindle cells and its expression can be directly influenced by certain cytokines. Bcl-2 is detected in Kaposi's sarcoma lesions, but at lower levels than bcl-x (fig 3).

Increased expression of CD40, a member of the tumour necrosis factor receptor/nerve growth receptor family, in Kaposi's sarcoma tumour cells and in vessels adjacent to Kaposi's sarcoma lesions has been described. CD40 is a signalling molecule which is involved in the inhibition of apoptosis, the induction of cell surface antigen expression and B-cell proliferation, adhesion and differentiation. In B cells, CD40 expression can induce the production of cell survival products such as bcl-x. The important question is what precisely causes increased CD40 expression in Kaposi's sarcoma. Is it caused by cytokines such as γ interferon or β interferon or does HHV8 directly increase expression?

Indeed, it is known that EBV-LMP-1 can result in increased expression of CD40. Is it possible that HHV8 acts in an analogous manner? In addition, other EBV gene products, including LMP-1, which induces bcl-2 expression in B cells, and bhrf-1, which can function as an anti-apoptotic protein, are known to protect virally infected cells from apoptosis.

What is the role of HHV8 in the development of Kaposi's sarcoma?

What is the role of HHV8 in the pathogenesis of Kaposi's sarcoma or BCBL or MCD? There are four possible modes of action.

1. HHV8 may not be oncogenic, but may infect specific B cells that proliferate and respond to developing malignancy, be this Kaposi's sarcoma or BCBL. If this is true, then HHV8 should be detected in serological tests, as demonstrated by Kedes et al and Gao et al. However, its apparent restriction to patients with Kaposi's sarcoma, BCBL and MCD, and absence in other tumour groups tends to contradict this hypothesis.

2. HHV8 infected B cells may have an indirect role in certain defined malignancies, such as Kaposi's sarcoma and BCBL, by enhancing the initial transforming event. A similar promoting role for EBV in some lymphomas (many of which contain EBV) has been suggested, but this effect would seem to be rather specific and tumour restrictive.

3. HHV8 infected B cells may produce cytokines initially causing proliferation of resting endothelial cells, which then promotes transformation/differentiation into the spindle cell phenotype classically seen in Kaposi's sarcoma. Such cytokine production may also be involved in the pathogenesis of BCBL and MCD.

4. HHV8 is involved directly in the proliferation of endothelial cells with activation of endothelial cells and differentiation to spindle cell morphology, and thereby to the formation of Kaposi's sarcoma. This may be mediated by specific cytokines and proteins involved in apoptosis and anti-apoptosis and/or specific gene products involved in cell division. Alternatively, HHV8 may interact with an undefined cellular factor. Sequence analysis of HHV8 has identified several viral genes which are homologous to genes encoding cell cycles and some G protein coupled receptors. Interestingly, HHV8 shares a v-cyclin gene with HVS, which seems to code for a cyclin similar to cyclin D1. IL6 coding regions have also been identified. These and other as yet undefined sequences may provide HHV8 with direct oncogenic ability.

In conclusion, we believe that there is increasing evidence to suggest that HHV8 may be the transmissible infectious agent for Kaposi's sarcoma and, by acting in synergy with other cytokines or by the expression of viral genes or cellular sequences, is intimately involved in the pathobiology of Kaposi's sarcoma.

Kaposi's sarcoma associated herpes virus