HHV-6 DNA level in CSF due to primary infection differs from that in chromosomal viral integration and has implications for the diagnosis of encephalitis

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ABSTRACT

The prevalence and concentration of human herpesvirus 6 (HHV-6) DNA in the cerebrospinal fluid (CSF) of the immunocompetent in primary infection was compared with that in viral chromosomal integration. Samples from 510 individuals with suspected encephalitis – 200 young children and 310 older children/adults – and 12 other patients were tested. HHV-6 DNA concentration (log_{10} copies/ml) was measured in CSF, serum and whole blood using PCR. Serum HHV-6 IgG antibody was measured by indirect immunofluorescence. Primary infection was defined by antibody seroconversion and/or low concentration HHV-6 DNA (<3.0 log_{10} copies/ml) in a seronegative serum. Chromosomal integration was defined by high concentration viral DNA in serum (≥3.5 log_{10} copies/ml) or whole blood (≥6.0 log_{10} copies/ml).

The prevalences of CSF HHV-6 DNA in primary infection and chromosomal integration were 2.5% and 2.0% respectively in the young children (<2 years) and 0% and 1.3% respectively in the older children/adults. The mean concentration of CSF HHV-6 DNA in 9 children with primary infection was significantly lower (2.4 log_{10} copies/ml) compared to that (4.0 log_{10} copies/ml) of 21 patients with viral chromosomal integration. Only HHV-6B DNA was found in primary infection whereas in viral integration 4 patients had HHV-6A and 17 HHV-6B.

Apart from primary infection, chromosomal integration is the most likely cause of HHV-6 DNA in the CSF of the immunocompetent. Our results show that any
diagnosis of HHV-6 encephalitis or other type of active central nervous system infection should not be made without first excluding chromosomal HHV-6 integration by measuring DNA load in CSF, serum and/or whole blood.
INTRODUCTION

Not long after its discovery in 1986 (32), human herpesvirus 6 (HHV-6) was associated with neurological disease when primary infection was described in a liver transplant patient with grand mal fits (44). At that time primary infection, although usually silent, was known sometimes to cause exanthem subitum (50). However, in the next decade there were further reports of primary infection and neurological disease, especially in young immunocompetent children with fever and seizures (19,23,35,43). Additionally, occasional cases of encephalitis were diagnosed in young children with primary infection [for review see (51)]. Most recently, primary HHV-6 infection has been shown to be an important cause of the neurological emergency of status epilepticus with fever in children up to 2 years old (41).

Primary HHV-6 infection almost invariably occurs in the first 2 years of life (19,45,52) but rare cases of encephalitis, presumed due to HHV-6 reactivation, have been reported in immunocompetent older children and adults (28). In the absence of primary infection, the key finding linking HHV-6 to these cases was the detection of viral DNA in cerebrospinal fluid (CSF) by polymerase chain reaction (PCR) leading to the assumption that HHV-6 was replicating in the central nervous system (CNS). However, this interpretation has been questioned in view of the phenomenon of HHV-6 chromosomal integration (8,46).
HHV-6 is the only human herpesvirus found integrated into host chromosomes (10,37,38). The occasional individual with such integration is easily identifiable since every leucocyte inevitably contains viral sequences and there are thus characteristically persistent high levels of HHV-6 DNA in both serum and whole blood (8,46). Since normal CSF, i.e. in the absence of inflammation, contains a few leucocytes it is only to be expected that, in cases of HHV-6 integration, viral DNA will be present in CSF even though there is no viral replication. This is in sharp contrast to the usual scenario in immunocompetent persons in whom after primary infection HHV-6 virus persists throughout life and is only found in the infrequent leucocyte (7) and hence viral DNA is not normally found in CSF.

Thus, when assessing the significance of viral DNA in CSF and its relationship to neuropathogenesis, chromosomal HHV-6 integration must be distinguished from primary infection in young children, and from putative virus reactivation in older individuals. In this context it is also important to differentiate HHV-6 variant A (HHV-6A) from B (HHV-6B) as either virus may be chromosomally integrated (8,46) whereas only HHV-6B is found in primary infection in young children (14). We now report on the prevalence and concentration of HHV-6A and B DNA in the CSF of immunocompetent patients with suspected encephalitis and compare the findings in primary infection with those in viral chromosomal integration. The implications for diagnosis of HHV-6 encephalitis are discussed.
MATERIALS & METHODS

Patients

Group 1 – Routine Diagnosis Patients. These were 510 immunocompetent patients of all ages with neurological illness whose serum and CSF samples had been referred between October 1998 and September 2003 for routine diagnosis of HHV-6 infection. This group includes children aged 2 months to 3 years reported to a British Isles-wide Survey between October 1998 and September 2001 because of suspected encephalitis (41).

Group 2 – Referred HHV-6 Patients. These were 12 immunocompetent patients found to have viral DNA in their CSF with presumed HHV-6 encephalitis. Samples of whole blood and/or serum, and CSF from these patients had been sent to us for further investigation between October 1998 and September 2005.

The samples from both groups of patients had originated from all over the British Isles and informed consent was obtained in the usual way by the referring clinician in accordance with good clinical practice.

Semi-quantitative PCR for HHV-6.

Nucleic acid [both RNA and DNA] was extracted from serum or CSF using the QIAmp RNA Mini Kit [Qiagen Ltd, Crawley, UK] and the extract tested for HHV-6 DNA using a nested PCR (22). As previously described (47), the amount of viral DNA in positive specimens was estimated semi-quantitatively by PCR using serial
10-fold dilutions. The result was expressed as log_{10} copies/ml. This method was used on samples up to 2003 after which it was superseded by the quantitative PCR described below.

Quantitative PCR for HHV-6

DNA was extracted from whole blood, serum, or CSF using the QIAamp DNA Mini Kit [Qiagen Ltd, Crawley, UK]. Five µl of nucleic acid extract was tested for HHV-6 DNA. A TaqMan PCR was performed using an ABI 7700 Sequence Detector [Applied Biosystems]; amplification primers were U67F, 5’-GGCTAGAACGTATTTGCTGCAGA-3’ and U67R, 5’-AATGTACGTCCCCGAAATGG-3’ and the TaqMan probe was U67P, 5’-(FAM)CGTTTCGCGGACTCAAGATCAACAAGTT(TAMRA)-3’. A 73 base pair sequence of the U67 open reading frame was amplified (8). The lower limit of detection was 5 copies/reaction. Control standards were known copy numbers of plasmid cloned amplicon. All samples were tested in duplicate and the mean used to calculate the HHV-6 DNA concentration which was expressed as log_{10} copies/ml of original sample.; the mean difference between replicates was 8%.

Determination of HHV-6 DNA copies/cell

Five µl of DNA extract from whole blood, serum or CSF were subjected to quantitative HHV-6 PCR and the result compared with the result of quantitative PCR for human β-globin (25). The HHV-6 PCR (8) amplifies DNA from part of the HHV-6 U67 gene, of which there is only one copy per virus genome (16). Since
there are 2 copies of β-globin/cell, the number of viral DNA copies/cell is 2 x HHV-6 DNA copies/β-globin DNA copies (46).

**Variant typing of HHV-6**

Restriction enzyme analysis of PCR products was used to distinguish HHV-6A from B as previously described (22).

**Definitions**

*Primary HHV-6 infection.* Validated tests for HHV-6 antibody avidity (42,45,48) and DNA (47) were used. As described elsewhere (41,47), the diagnosis of primary HHV-6 infection was based on seroconversion to HHV-6 IgG between acute and convalescent sera and/or PCR to detect low level HHV-6 DNA i.e. concentration <3.0 log<sub>10</sub> copies/ml in an acute seronegative serum.

*High level serum HHV-6 DNA.* A serum HHV-6 DNA concentration of >3.5 log<sub>10</sub> copies/ml was defined as high based on the 95% confidence limits for the mean level found in individuals with persistent high levels HHV-6 DNA (24,46,47).

*High level whole blood HHV-6 DNA.* An HHV-6 DNA concentration of >6.0 log<sub>10</sub> copies/ml in whole blood was defined as high (8,46)

*HHV-6 chromosomal integration.* In this situation there is ≥ 1 copy of HHV-6 DNA/leucocyte and consequently a high viral DNA concentration in whole blood. Similarly in serum there is ≥1 copy of HHV-6 DNA/lysed leucocyte and the level
of HHV-6 DNA is high although about 50-fold lower than that of whole blood. These high levels define viral chromosomal integration and are not seen in other circumstances. (46).

Statistics
The exact confidence limits for proportions were calculated using the method of Armitage & Berry (3). The t distribution was used to calculate the 95% confidence limits for a sample mean. The significance of the difference between two sample means was estimated using the paired t test and the Mann Whitney two sample rank sum test.
RESULTS

HHV-6 DNA in the CSF and Serum of Immunocompetent Children with Primary Infection

Table 1 shows the results of testing CSF and acute phase serum from the 9 patients in Group 1 (Routine Diagnosis Patients – P1-9) with primary infection (see Definitions, Methods). All were young children <2 years old and all presentations were similar involving fever and convulsions sometimes accompanied by rash.

**HHV-6 DNA in CSF.** Five of the 9 children (56%) had HHV-6 DNA detected in the CSF. In the 4 cases where there was sufficient CSF for further tests the mean concentration was 2.4 log\(_{10}\) copies/ml (95% confidence limits 1.0-3.7) and the variant was B. The cell count was known for all but one of the CSFs tested (median <1 x 10\(^3\) leucocytes/ml; range <1-2).

**HHV-6 DNA in serum.** Seven of the 9 children had low level HHV-6 DNA, i.e. <3.0 log\(_{10}\) copies/ml, detected in the acute phase serum; in each case this was variant B. Viral DNA was not detected in any convalescent serum.

**HHV-6 DNA in the CSF, serum and whole blood of immunocompetent children and adults with viral chromosomal integration.**

Table 2 shows the results of testing for viral DNA in CSF, whole blood and serum from 21 children and adults with high level HHV-6 DNA in serum and/or whole...
blood, i.e. viral chromosomal integration (see Definitions, Methods); these comprised 9 patients found to have such high level viral DNA in Group 1 (Routine Diagnosis Patients - HL8-11, HL14, HL16-18 & HL 20) and all of the 12 Referred HHV-6 Patients in Group 2 (HL1-7, HL12, HL13, HL15, HL19 & HL21). In all, 4 of these 21 patients had HHV-6A and 17 HHV-6B. The patients' neurological illnesses were diverse ranging from fever and convulsions to suspected encephalitis (confirmed in 2 patients as herpes simplex encephalitis).

**HHV-6 DNA in CSF.** HHV-6 DNA was detected in 20 of the 21 patients' CSF (24/26 CSF samples; Table 2). Of the 26 CSF samples tested, the leucocyte count was known for 17 (median 5 x 10^3 leucocytes/ml; range <1-65). There were four samples with a cell count of <1 x 10^3/ml and these included the 2 samples in which HHV-6 DNA was not found; in patient HL20, who had herpes simplex encephalitis, HHV-6 DNA was not detected in the first CSF which contained <1 x 10^3 leucocytes/ml but was found in the later CSF with many more leucocytes namely, 50 x 10^3 leucocytes/ml. In patients HL6, HL9 and HL15, samples had been taken long after the onset of illness, i.e. between 107 and 371 days later, yet all contained HHV-6 DNA.

In 16 samples there was sufficient CSF to quantify the HHV-6 DNA and the mean concentration was 4.0 log_{10} copies/ml (95% confidence limits 3.5-4.5); this is the equivalent of an average of at least one copy/CSF leucocyte and at least a log higher than the mean HHV-6 DNA CSF concentration in primary infection.
(P=0.008, paired t test; P=0.02, Mann Whitney two sample rank sum test). In 2
cases there was sufficient material to carry out a β-globin PCR and hence
estimate the HHV-6 DNA copies/CSF leucocyte for each individual sample; in
both cases this was ≥1.

**HHV-6 DNA in serum and/or whole blood.** All 21 patients had high level HHV-6
DNA in every sample tested. For 12 of these, persistent high level HHV-6 DNA
was demonstrated since more than one sample was available (Table 2); in the
case of HL19 high level persistence was documented in serum for over 4 years.

**Prevalence of HHV-6 DNA in the CSF of Immunocompetent Patients with
Neurological Illness**

Table 3 shows the results for the 510 patients in Group 1 (Routine Diagnosis
Patients); these comprised 200 children <2 years old and 310 older
children/adults. Of the young children whose CSF contained HHV-6 DNA, 5 (P3,
P5, P6, P8, P9 - Table 1) had primary HHV-6 infection and 4 (HL8-10 & HL14 –
Table 2) had high level serum HHV-6 DNA and thus viral chromosomal
integration (see Definitions, Methods). Of the older children/adults whose CSF
contained HHV-6 DNA, there were no cases of primary infection but 4 (HL16-18
& HL20 – Table 2) had high level serum HHV-6 DNA, i.e. viral chromosomal
integration. The prevalence of HHV-6 DNA in CSF associated with HHV-6
chromosomal integration was 2.0% (95% confidence limits 0.6-5.0) in the young
children and 1.3% (95% confidence limits 0.4-3.3) in the older children/adults; the

overall prevalence for all ages was 1.6% (95% confidence limits 0.7-3.1).
DISCUSSION

In this study of HHV-6 DNA in CSF, we compare the results in primary infection with those in viral chromosomal integration. Primary infection, always with HHV-6B, occurs early in life in almost all persons and may sometimes be accompanied by symptoms, i.e. fever and convulsions with or without a rash. In contrast, no disease has yet been causally linked to HHV-6A nor has the time of first infection with this variant ever been identified. In primary infection with variant B, viral DNA appears transiently in serum at a low level followed by antibody seroconversion (41,47). Thereafter HHV-6 becomes latent, virus is not detected in serum and viral DNA is present at the low level of around 1 copy per 10^4 - 10^5 leucocytes (7) but not in other cell types such as hair follicles (46).

On the other hand, in HHV-6 chromosomal integration, both peripheral blood leucocytes and hair follicle cells have a high viral load (37) and, as we have recently shown, this results from ≥ 1 copy of HHV-6 DNA in each of these cell types (46) suggesting that every cell in the body contains virus. In fact it seems that cases of chromosomal HHV-6 integration are usually inherited in the germ line and passed from parent to child (10,37). Other notable features of viral chromosomal integration are the presence not only of variant B but sometimes variant A instead (8,11,37,46) and persistent high level HHV-6 DNA in whole blood and serum (46) which in the latter case is at least 100-fold higher than that observed briefly in primary infection (47).
Thus, 21 subjects with HHV-6 chromosomal integration were identified in this study because of high viral DNA load in whole blood and/or serum (Table 2). Indeed, for 12 of the patients persistence of this high level HHV-6 DNA was also documented. In 4 patients chromosomal integration was confirmed by fluorescent in situ hybridisation on chromosome preparations and ≥1 copy of HHV-6 DNA/cell or lysed cell in hair follicles and whole blood/serum, respectively (8). A fifth patient had ≥1 copy of viral DNA/cell or lysed cell in whole blood and serum but hair follicles and chromosome preparations were not tested. Moreover another 2 patients must have inherited viral integration from their mothers since these also had high level serum HHV-6 DNA.

Turning now to our findings on CSF in primary infection, HHV-6 DNA was only detected in about half (56%) of CSF samples, and at a low mean concentration of 2.4 log_{10} copies/ml. This presumably reflects the concurrent and similarly brief low level HHV-6 DNA in serum or plasma seen in the first few days of primary infection (6,36,47). Indeed it has been previously reported that HHV-6 DNA appears transiently in CSF at this time (35).

Notably, almost all of the CSFs (92%) from the 21 patients with viral chromosomal integration contained HHV-6 DNA and, unlike primary infection, where more than one CSF was available for testing HHV-6 DNA was shown to persist in every case even up to a year after the original onset of illness. The mean CSF viral DNA concentration for all samples was 4.0 log_{10} copies/ml and
more than 10-fold higher than that in primary infection. On the basis of the median CSF cell count it could be calculated that, as expected for viral integration, there was on average at least one HHV-6 copy/CSF leucocyte and this was also confirmed for 2 individual samples by comparing HHV-6 and human β-globin concentrations. HHV-6 DNA could even be detected in normal CSF with no evidence of inflammation, i.e. the CSF cell count was ≤5 \times 10^3/ml. However, when the cell count was at its lowest, i.e. <1 \times 10^3 cells/ml, only half of the samples tested contained detectable HHV-6 DNA presumably because our test was at the limit of sensitivity.

HHV-6 DNA in CSF is usually taken to indicate active infection but in chromosomal viral integration there is no evidence to date of virus replication \((27,38)\). Thus, many of our patients with integrated virus were initially given a misdiagnosis of HHV-6 encephalitis because of viral DNA in CSF, although they had disparate symptoms, final diagnoses and outcomes including 2 confirmed cases of herpes simplex encephalitis one of whom died (Table 2). It is also worth noting that ganciclovir therapy with its frequent adverse effects was initiated unnecessarily in one case because of such a misdiagnosis (case report submitted elsewhere).

Similar confusion has probably arisen in the literature. Several cases from a large study of patients of all ages with focal encephalitis were attributed to HHV-6 because viral DNA was detected in CSF (28) but in the absence of quantitative
measurement of HHV-6 DNA, it is difficult to differentiate primary infection from viral integration and the role of the virus is unclear. Turning to older individuals in whom primary infection is extremely unlikely, there are a handful of case reports describing in all 11 immunocompetent adults and one teenager. All had clinically defined encephalitis and HHV-6 DNA in their CSF (4,5,13,21,26,29,30,33,39) and in each case the diagnosis was given as HHV-6 encephalitis but viral integration had not been considered. Viral DNA load in CSF was measured in 7 patients; low level HHV-6 DNA was found in 2 of these but in both primary infection was excluded (29,30) suggesting viral reactivation. The remaining 5 had high viral DNA levels (≥ 4.0 log_{10} copies/ml) (5,21) which, although not noted in the reports, is equivalent to at least one viral copy/CSF leucocyte strongly suggesting chromosomal HHV-6 integration. Moreover, in one of these 5 patients HHV-6 DNA persisted in CSF for at least 55 days despite therapy with ganciclovir, and was also in serum at high level – in this case ≥ 5.0 log_{10} copies/ml (5). Thus, unrecognised chromosomal viral integration may often account for HHV-6 DNA in CSF.

Additional support for the idea that chromosomal HHV-6 integration commonly results in viral DNA in CSF in immunocompetent individuals comes from instances in which the HHV-6 variant was typed. There are a remarkable number of cases of encephalitis in immunocompetent adults attributed to variant A, 6 in all (4,13,26,29,30,39), as opposed to one attributed to variant B (5,28). As previously discussed HHV-6B, not HHV-6A, is responsible for primary infection in
childhood whereas either variant A or B can be integrated into human chromosomes. These findings are once again confirmed in the present paper where only HHV-6B was detected in the CSF in primary infection whereas variant A was found in the CSF of some of our patients with evidence of integrated virus and variant B in others. It may therefore be concluded that when HHV-6A rather than B DNA is detected in CSF this most likely indicates viral integration. Such integration may well account for the mistaken idea (18) that since HHV-6A tends to persist in CSF it is more neurotropic than variant B.

Regarding the 1.6% prevalence of HHV-6 DNA in the CSF due to chromosomal integration in our immunocompetent patients, there was no appreciable difference between young children < 2 years old and older children/adults, i.e. 2.0 and 1.3% respectively, findings suggesting that viral integration is always acquired very early in life and consistent with vertical transmission i.e. inheritance. As expected for a common cause of neurological disease in young children (41), primary infection was also responsible for viral DNA in the CSF of this age group. In contrast, viral chromosomal integration was the main cause of HHV-6 DNA in the CSF of older children and adults who were past the age for primary infection.

Of the prior surveys of the prevalence of HHV-6 DNA in the CSF of predominantly immunocompetent populations, all, as in our case, were based on samples referred for diagnosis of suspected viral CNS infection. The results
were variously 0.05% (1/2161) (31), 0.3% (1/320) (15), 1.2% (9/753), (12), 1.5% (6/407) (34) and 2.8% (3/106) (20). All but one of these surveys included at least some young children but without analysis for differences due to age. However, two further studies did analyse their results in this way. In one case (2) a prevalence of 2.0 % (3/148) was found in children <2 years but all 3 subjects were less than 2 months old suggesting acquisition at birth i.e. chromosomally inherited HHV-6. Isaacson et al. (21), divided their results into those for young children ≤3 years old (0%; 0/98) and older children and adults (0.4%; 4/902) thus excluding HHV-6 DNA in CSF due to primary infection in the latter group. In summary, although not considered as a possibility by the authors, the prevalences in all the above studies are of the same order as that attributed by us to HHV-6 chromosomal integration suggesting that in most of these instances HHV-6 DNA in CSF resulted from this phenomenon.

Although neither our survey of HHV-6 DNA in CSF nor those discussed above included normal controls, the prevalence in such controls due to viral integration should be between 0.7% (95% 0.2-2.1) and 1.5% (95% confidence limits 0.7-2.8) as judged by our two separate reports of high level serum or plasma HHV-6 DNA, i.e. presumed chromosomal integration, in control populations (24,47). Further support for these estimates comes from the reported prevalences of between 0.9-1.6% for congenital HHV-6 infection (1,9,17), i.e. presumed chromosomal integration. All these frequencies are remarkably similar to the finding in CSF of 1.6% (95% confidence limits 0.7-3.1) in our samples from
immunocompetent patients of all ages with various neurological symptoms. Davies et al. (12) attempted to solve the problem of controls in their study of suspected CNS infections by using clinical and laboratory criteria to define a group of patients unlikely to have CNS viral infection, and found a prevalence of 0.3% (95% confidence limits 0.01-2.8) for HHV-6 DNA in CSF, a finding no different from ours. The only other information comes from controls without CNS disease (40) in whom one individual out of 107 (95% confidence limits 0.02-5.1) had HHV-6 DNA persisting in two CSF samples collected 4 months apart presumably because of viral chromosomal integration. From the limited evidence available the prevalence of HHV-6 DNA in the CSF due to viral chromosomal integration in those with suspected viral CNS infection is the same as that in controls suggesting that such integration does not predispose to neurological disease.

It may be concluded therefore that where HHV-6 DNA is detected in the CSF of immunocompetent patients it is commonly due to chromosomal viral integration resulting in a mistaken association with encephalitis. This is especially so for older children and adults in whom primary infection, the other common cause of HHV-6 DNA in CSF, is exceptionally rare. A recent editorial commentary (49) asked ‘Human herpesvirus 6 infection of the central nervous system: is it just a case of mistaken association?’ The present findings go a long way towards answering this question; our results show that any diagnosis of HHV-6 encephalitis should not be made without first excluding chromosomal HHV-6 integration by
measuring DNA load in CSF, serum and/or whole blood. Further support for such integration would be provided by the detection of HHV-6 DNA in hair follicle cells.
ACKNOWLEDGEMENTS

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Reference List


TABLE 1. Frequency of HHV-6 DNA in the CSF of Immunocompetent Children with Primary Infection.

<table>
<thead>
<tr>
<th>Patient no./sex</th>
<th>Age at onset of illness</th>
<th>Acute phase serum HHV-6 DNA/variant</th>
<th>Days after onset of illness sample taken</th>
<th>CSF HHV-6 DNA/variant/ log_{10} HHV-6 DNA copies/ml</th>
<th>Clinical details</th>
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<tbody>
<tr>
<td>P1/F^{b}</td>
<td>4 months</td>
<td>+/B</td>
<td>0</td>
<td>-</td>
<td>Fever, rash, ?encephalitis/ meningitis</td>
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<tr>
<td>P2/M^{b,d}</td>
<td>9 months</td>
<td>+/B</td>
<td>0</td>
<td>-</td>
<td>Fever, convulsions</td>
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<tr>
<td>P3/F^{d}</td>
<td>10 months</td>
<td>-</td>
<td>1</td>
<td>+/B/1.6</td>
<td>Fever, convulsions</td>
</tr>
<tr>
<td>P4/F^{d}</td>
<td>11 months</td>
<td>+/B</td>
<td>0</td>
<td>-</td>
<td>Fever, rash, convulsions</td>
</tr>
<tr>
<td>P5/M^{b,d}</td>
<td>11 months</td>
<td>+/B</td>
<td>3</td>
<td>-</td>
<td>Fever, rash, convulsions</td>
</tr>
<tr>
<td>P6/M^{b,d}</td>
<td>1 year</td>
<td>+/B</td>
<td>1</td>
<td>+/B/2.6</td>
<td>Fever, convulsions</td>
</tr>
<tr>
<td>P7/F^{b,d}</td>
<td>1 year 3 months</td>
<td>-</td>
<td>1</td>
<td>+/nt/nt</td>
<td>Fever, rash, convulsions</td>
</tr>
<tr>
<td>P8/M^{d}</td>
<td>1 year 8 months</td>
<td>+/B</td>
<td>1</td>
<td>+/B/1.6</td>
<td>Fever, encephalopathy</td>
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</table>

^{a} Further details for patients have been reported elsewhere (41,47).

^{b} Primary infection defined by low concentration HHV-6 DNA, i.e. <3.0 log_{10} HHV-6 DNA copies/ml in an acute seronegative serum.

^{c} Day of onset of illness unknown so day of first sample defined as 0.

^{d} Primary infection defined by seroconversion to HHV-6 IgG between acute and convalescent sera.

nt = not tested
TABLE 2. Frequency of HHV-6 DNA in the CSF of Immunocompetent Patients with High Level Viral DNA in Serum and/or Whole Blood.

<table>
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<tr>
<th>Patient no./sex</th>
<th>Age at onset of illness</th>
<th>High level a) HHV-6 DNA</th>
<th>Clinical Details</th>
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<td>3/186 5</td>
</tr>
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<td>+/B +/B/B nt/3/186 5</td>
<td>+/nt/4.1</td>
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<td>+/nt/4.6</td>
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<td>HL6/F</td>
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</tr>
<tr>
<td>HL11/M</td>
<td>1 year 1 month</td>
<td>+/B nt</td>
<td>1/0 2</td>
</tr>
<tr>
<td>HL12/ NK</td>
<td>1 year 1 month</td>
<td>+/B nt</td>
<td>1/0 0</td>
</tr>
<tr>
<td>HL13/F</td>
<td>1 year 3 months</td>
<td>+/B nt</td>
<td>1/0 0</td>
</tr>
<tr>
<td>HL14/M</td>
<td>1 year 11 months</td>
<td>+/B nt</td>
<td>10/452 1</td>
</tr>
<tr>
<td>HL15/F</td>
<td>2 years 9 months</td>
<td>+/A nt</td>
<td>3/9 180</td>
</tr>
<tr>
<td>HL16/M</td>
<td>4 years</td>
<td>+/B nt</td>
<td>2/15 0</td>
</tr>
<tr>
<td>HL17/M</td>
<td>4 years</td>
<td>+/B nt</td>
<td>1/0 0</td>
</tr>
<tr>
<td>HL18/F</td>
<td>12 years</td>
<td>+/A nt</td>
<td>5/553 0</td>
</tr>
<tr>
<td>HL19/M</td>
<td>23 years</td>
<td>+/B +/B/nt 6/1701 6 25</td>
<td>+/nt/3.6</td>
</tr>
<tr>
<td>HL20/F</td>
<td>52 years</td>
<td>+/B nt</td>
<td>1/0 0</td>
</tr>
<tr>
<td>HL21/F</td>
<td>58 years</td>
<td>+/B +/B/nt 2/3 1</td>
<td>+/B/5.5</td>
</tr>
</tbody>
</table>

nt = not tested  a) >3.5 log_{10} copies/ml in serum; >6.0 log_{10} copies/ml in whole blood b) High level in every sample tested; c) See (47) for more detail; d) Mother has high level serum HHV-6 DNA; e) HHV-6 chromosomal integration identified by fluorescent in situ hybridization & ≥1 HHV-6 DNA copy/hair follicle cell (46); f) ≥1 HHV-6 DNA copy/cell or lysed cell (46); g) Detected in lymphoblastoid cell line derived from this patient’s blood; h) Onset date unknown so day of first sample defined as 0.
TABLE 3. Prevalence of HHV-6 DNA in the CSF of Immunocompetent Patients.

<table>
<thead>
<tr>
<th>No. patients tested</th>
<th>Age (years)</th>
<th>No. patients with HHV-6 DNA in CSF (prevalence(^a))</th>
<th>No. patients with HHV-6 DNA in CSF &amp; HHV-6 primary infection (prevalence(^a))</th>
<th>No. patients with HHV-6 DNA in CSF &amp; high level serum HHV-6 DNA(^b) (prevalence(^a))</th>
<th>No. patients with HHV-6 DNA in CSF &amp; indeterminate status (prevalence(^a))</th>
</tr>
</thead>
<tbody>
<tr>
<td>200</td>
<td>&lt;2(^c)</td>
<td>14 (7.0%)</td>
<td>5 (2.5%)</td>
<td>4 (2.0%)</td>
<td>5(^d) (2.5%)</td>
</tr>
<tr>
<td>310</td>
<td>≥2(^e)</td>
<td>6 (1.9%)</td>
<td>0 (0%)</td>
<td>4 (1.3%)</td>
<td>2(^f) (0.6%)</td>
</tr>
</tbody>
</table>

\(^a\) No. with HHV-6 DNA/No. tested

\(^b\) >3.5 log\(_{10}\) HHV-6 DNA copies/ml

\(^c\) Median age 0.9 years (range 0-1.9)

\(^d\) 2 cases serum not available; 1 case high level serum HHV-6 DNA excluded; 1 case primary infection excluded; 1 case high level serum HHV-6 DNA excluded & primary infection excluded.

\(^e\) Median 37 years (range 2-88)

\(^f\) 1 case serum not available; 1 case high level serum HHV-6 DNA excluded & primary infection excluded by antibody tests.