Detection of Human Herpesvirus 6 by Molecular Methods in Specimens from Patients Diagnosed with Meningitis

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Introduction. Virus infection is one of the causes of central nervous system (CNS) diseases. Human herpesvirus 6 (HHV-6) may infect the CNS during primary infection, and the following reactivation from a latent state may cause the disease of CNS. Especially in immunosuppressed patients the infection can take a life-threatening course, and, therefore, early diagnosis of herpesvirus-associated neurological diseases should have high priority.

Aim. The aim of this study is to detect the presence of HHV-6 infection in patients with clinically diagnosed meningitis.

Material and Methods. Whole blood and cerebrospinal fluid (CSF) DNA samples from 18 patients (13 female and 5 male; mean age – 55 years) with clinically diagnosed meningitis and whole blood from 109 practically healthy blood donors (43 female and 66 male; mean age – 31 years) were studied for the presence and type of HHV-6, viral load and mRNA expression using nPCR, real-time PCR and RT-PCR, respectively.

Results. HHV-6 genome sequence was detected in 9/18 (50.0%) whole blood DNA samples from patients and 10/109 (9.1%) practically healthy blood donors. In whole blood DNA samples from patients with meningitis both HHV-6 types were detected: 5/9 - HHV-6B and 4/9 - HHV-6A. High HHV-6 load was detected in 1/9 patient and in 1/10 control group individual (1170.2 copies/1x106 cells and 7677.00 copies/1x106 cells, respectively). In 3/9 patients the average viral load was 338.16 copies/1x106 cells (from 234.25 to 537.34 copies/106 cells). In 5/9 patients and 8/10 donors viral load did not exceed 10 copies/1x106 cells. mRNA expression was detected in 6 out of 9 (66.6%) patients: in one patient HHV-6 early (U41), and immediate early (U89/U90) gene expression was found but in 5 patients only immediate early gene expression. HHV-6 mRNA expression was not detected in any of donor samples. HHV-6 was not detected in any of CSF DNA samples.

Conclusion. HHV-6 genomic sequence was demonstrated significantly more often in DNA of patients with clinically diagnosed meningitis in comparison to practically healthy blood donors (p = 0.0001). Due to the high detection rate of HHV-6 infection its potential pathogenic role in the development of meningitis could not be excluded.

