

Abstract

Human Herpes Virus 6 (HHV-6) consists of two closely related DNA viruses: HHV-6A and HHV-6B. The primoinfection proceeds at an early childhood usually as sixth exanthem disease or without any clinical symptoms. Both HHV-6 viruses are able to integrate to human genome using recombinant mechanisms which is unique compared to other human herpesviruses. The aim of the thesis is to study Ci-HHV-6 in a group of patients with malign disease and in the healthy population. We analysed 812 patients with malign disease and 420 healthy subjects from general population. The Ci-HHV-6 was assessed by real-time PCR, the specific localization of Ci-HHV-6 was determined using fluorescent *in situ* hybridization (FISH). Using comparative study, we did not identify significant difference between frequency of Ci-HHV-6 in patients with malign disease (1.11%) and healthy subjects (0.95%) (P-value 0.8). Consequently, we proved the heritability of Ci-HHV-6 in affected families. We determined the localization of Ci-HHV-6 to telomeric regions of chromosomes 2 and 18. We studied the production of viral proteins in the subjects with Ci-HHV-6. In this work, we conducted the first epidemiological study of Ci-HHV-6 in the Czech Republic. We also introduced novel methods which contribute to better characterization of this phenomenon.