Abstract

In patients after allogeneic haematopoietic stem cell transplantation (HSCT) is a human cytomegalovirus (CMV) one of the most important viral pathogens. Its detailed characteristic could provide information about the impact of each CMV genotype on overall survival of the patient, and some serious complications, such as graft versus host disease (GvHD).

This thesis deals with retrospective genetic analysis of samples from 1877 patients transplanted at the Clinic of Pediatric Hematology and Oncology, University Hospital Motol and the Institute of Hematology and Blood Transfusion since 2002. DNA from biological samples (especially whole blood) was isolated kit Qiagen DNA Blood Mini or Qiagen DNA Mini and samples were prospectively detected presence of CMV DNA. Samples were subsequently stored at -20 °C. Genotyping was performed using real-time PCR technologies to the genes of 2 structural proteins glycoprotein B, glycoprotein H and using sequence specific primers and probes.

In 1343 samples (71.6%) from 390 patients there was only one strain of CMV; in 256 (13.6%) samples from 113 patients have detected mixed infection caused by two or more strains of CMV. The most common genotype demonstrated in "single" infection was in pediatric and adult patients gB1/gH2 detected in 118 (28.4%) patients. Most frequently detected combination of genotypes in mixed infections, the combination gB1/gH1,2 detected in 24 (15.8%) patients.

Keywords
human cytomegalovirus, herpesvirus, genotype, haematopoietic stem cell transplantation, allogeneic