Improvement and application of nested-PCR technique using consensus-degenerate primers to detect human herpes virus in plasma samples from hematopoietic stem cell transplantation (HSCT) patients

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Human herpes viruses (HHVs) are an important cause of infections in transplantation and immunocompromised patients in general. This group of virus consists in three subfamilies: α-herpesvirinae, β–herpesvirinae and γ–herpesvirinae which include the eight human herpes virus species. Currently, the diagnosis of infectious diseases have been a considerable advance after molecular techniques implantation, especially the polymerase chain reaction (PCR), once it presents high sensitivity and specificity to detect low quantities of nucleic acids. The use of consensus-degenerate primers in PCR has been used as an efficient alternative for the detection and identification of Herpes viridae family members in clinical samples. The aim of this study was to improve the nested-PCR (N-PCR) technique using consensus-degenerate primers to detect human herpes virus sub-families. Forty plasma-DNA samples from HSCT patients were analyzed using N-PCR technique with degenerate primers in both reactions. These primers were designed from highly conserved amino acid sequences of herpesviral DNA polymerase gene. The results show that 8/40 (20%) were positive to α-herpesvirinae and/or γ–herpesvirinae; 19/40 (47.5%) were positive to β–herpesvirinae and 5/40 (12.5%) presented coinfection with the three subfamilies. The development and improvement of N-PCR using consensus-degenerate primers have been fundamentally important in helping the clinical diagnosis, therapy, classification and epidemiological studies of viruses and to discover new herpesvirus species.

Biography
Talita Cristina Dellariva completed her degree in Biological Sciences from State University of Campinas (UNICAMP) in 2013. She has been working on her Master’s degree in Clinical Medicine in the Faculty of Medical Sciences, State University of Campinas, São Paulo, Brazil.

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