GENOMIC DIVERSITY OF EPSTEIN-BARR VIRUS HARBORED IN PBMC, PLASMA AND SALIVA OF CHILDREN WITH EBV-ASSOCIATED LYMPHOPROLIFERATIVE DISEASES

Ka Wo Wong[1], Janice KP Lam[1], Kwok Hung Chan[2], Wanling Yang[1], Alan KS Chiang[1]

Department of Paediatrics and Adolescent Medicine1, Department of Microbiology2, Li Ka Shing Faculty of Medicine, The University of Hong Kong, Hong Kong, China

E-mail of presenting author: cyruswkw@hku.hk

Epstein-Barr virus (EBV) is a double-stranded gamma-herpesvirus with a 172 kb genome that persists in more than 90% of the world's population. Primary EBV infection may give rise to several lymphoproliferative diseases (LPDs) including infectious mononucleosis (IM), haemophagocytic lymphohistiocytosis (HLH) and post-transplant lymphoproliferative disease (PTLD). EBV primarily infects human B cells in submucosal secondary lymphoid tissues such as the tonsils. EBV can be detected in whole blood, plasma and saliva. In this study, we aim to assess the genomic diversity of EBV harbored in peripheral blood mononuclear cells (PBMC) and other biological compartments such as plasma and saliva. The EBV genomes harbored in PBMC, plasma and saliva in 67 IM, 29 HLH and 29 PTLD patients are sequenced. Among these patients, 38 IM, 10 HLH and 17 PTLD have at least two biological compartments with genomic sequencing depth of more than 20 fold for comparison (PBMC: range of sequencing depth, 20.2 – 2,587 fold; median, 371 fold; plasma: range of sequencing depth, 22 – 6,602 fold; median, 245 fold; saliva: range of sequencing depth, 22 – 20,665 fold; median, 2,666 fold). The median of pairwise variant similarity of EBV genomes in 182 healthy adult donors of the Hong Kong population, which represents inter-individual genomic variation, is 46% as compared to 98% variant similarity of EBV in the PBMC, plasma and saliva of individual IM, HLH and PTLD patients, indicating that the EBV genomes harbored in the three biological compartments within the same individuals are highly similar. The pattern of unique variants in each biological compartment is further assessed by pairwise intra-host sample comparison. No variant is found to be compartment-specific.