Detection of Epstein–Barr Virus DNA in respiratory specimens from patients with chronic obstructive pulmonary disease by quantitative PCR


Purpose: Data from a previous study suggested a possible association between active EBV infection and Chronic Obstructive Pulmonary Disease (COPD). A cross-sectional study to investigate this observation was undertaken.

Methods: Patients with early clinical symptoms of COPD and controls (‘healthy smokers’ with normal spirometry) were recruited. Combined nasal/oropharyngeal swabs and induced sputums were obtained from each subject. Total nucleic acids were extracted from these specimens, and a TaqMan qPCR assay was used to detect and quantify EBV DNA. Specimen extracts were also tested for the presence of 8 human herpes viruses (HSV-1, HSV-2, VZV, CMV, EBV, HHV-6A, HHV-6B, HHV-7) using the Mobidiag® Prove-it’ tube array platform.

Results: EBV DNA was detected significantly more often amongst the COPD group (23/45 swabs and 33/43 sputums) than the control group (13/45 swabs and 20/42 sputums). P = 0.052 and 0.007 for swabs and sputums respectively (Fisher’s Exact). EBV copy numbers varied widely (over a 4-log range for swabs and a 5-log range for sputums) and there was no significant difference in geometric mean copy number between the study groups. Data from the Prove-it’ tube array platform will also be presented.

Conclusion: Active EBV infection was more common in the disease group than the control group, although there was no association with virus copy number.

Influenza A viruses host ultrastructural nuclear modifications: specific patterns between avian and human strains?

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Purpose: During the 1970s, electron microscopy investigations revealed that human influenza induced drastic modifications of the architecture and the molecular composition of the host cell nucleus and cytoplasm during infection (reviewed in Josset et al., 2008). Many other viruses induce such important remodeling in order to lead optimal infectious cycle (Hiscox et al., 2007). Our purpose was to characterize and compare the host ultrastructural modifications induced by human and avian influenza A viruses in order to correlate these phenotypes with their virulence and host adaptability.

Methods: We infected human pulmonary epithelial AS49 cell line and Chick Embryo Fibroblast primary cells (CEF) with human (A/NewCaledonia/20/99 H1N1 and A/Moscow/10/99 H3N2) and avian (A/Finch/England/2051/94 H5N2, A/Turkey/582/2006 H5N1 and A/chicken/Belgium/2003 H7N7) viruses. Electron microscopy investigations focused on nuclear and nucleolar ultrastructural modifications were performed on Epon sections of glutaraldehyde fixed cells.

Results: Both avian and human influenza viruses specifically alter the nucleus and particularly the nucleolus of infected cells. The regular functional sub-domains of nucleolus become progressively undetectable during the infection. Moreover, several types of viral induced structures with specific morphology can be observed. Altogether, our observations show two seemingly emerging patterns of remodelled nucleus, depending on the human or the avian virus origin.

Conclusions: These specific ultrastructural modifications could probably result from differential hijacking of the host nuclear machinery by influenza viruses. The molecular composition of viral induced structures need to be characterized in order to determine their functional significance in regard to the virulence and the host adaptability of influenza strains.