Epidemiology of two human protoparvoviruses, bufavirus and tusavirus Abstract

Two human parvoviruses were recently discovered by metagenomics in Africa, bufavirus (BuV) in 2012 and tusavirus (TuV) in 2014. These viruses have been studied exclusively by PCR in stool and detected only in patients with diarrhoea, although at low prevalence. Three genotypes of BuV have been identified. We detected, by in-house EIA, BuV1-3 IgG antibodies in 7/228 children (3.1%) and 10/180 adults (5.6%), whereas TuV IgG was found in one child (0.4%). All children and 91% of the adults were Finnish, yet interestingly 3/6 adults of Indian origin were BuV-IgG positive. By competition EIA, no cross-reactivity between the BuVs was detected, indicating that the BuV genotypes represent distinct serotypes. Furthermore, we analysed by BuV qPCR stool and nasal swab samples from 955 children with gastroenteritis, respiratory illness, or both, and found BuV DNA in three stools (0.3%) and for the first time in a nasal swab (0.1%). This is the first study documenting the presence of BuV and TuV antibodies in humans. Although the seroprevalences of both viruses were low in Finland, our results indicate that BuV infections might be widespread in Asia. The BuVspecific humoral immune responses appeared to be strong and long-lasting, pointing to systemic infection in humans.