

Clinical Impact and Epidemiology of Emerging Human Parvoviruses

Maria Söderlund-Venermo

Department of Virology, University of Helsinki, Finland

Modern sequencing methods have revealed an expanding range of novel human parvoviruses. In 2005, parvovirus 4 (PARV4) of *Tetraparvovirus* genus was discovered in blood, and human bocavirus 1 (HBoV1) of *Bocaparvovirus* genus, in pediatric respiratory samples. PARV4 is, in the western world, mainly detected in injecting drug users and hemophiliacs, but has not been associated with any specific symptoms, whereas HBoV1 causes mild to life-threatening respiratory tract infections in children. Three more bocaviruses (HBoV2–4) were discovered in stool, without clear clinical associations. Bufavirus (BuV), discovered in 2012, was the first human parvovirus in the *Protoparvovirus* genus followed by two other novel viruses, tusavirus (TuV) in 2014 and cutavirus (CuV) in 2016. These three protoparvoviruses were all originally discovered in feces of diarrheic children, and BuV has been associated with gastrointestinal symptoms. CuV, however, was observed also in 4 out of 15 cutaneous T-cell lymphoma (CTCL) skin lesions and in one melanoma. To study the epidemiology and disease associations of CuV, BuV and TuV, we analyzed serum samples by IgG EIAs and searched by multiplex qPCR for viral DNA in stools of children with and without gastroenteritis or respiratory tract infection and in skin biopsies of CTCL patients, immunosuppressed organ-transplant recipients, and immunocompetent healthy adults. CuV DNA positivity clearly associated with CTCL, whereas all skin samples were negative for BuV and TuV DNA. We further studied BuV-, TuV- and CuV-IgG seroprevalences in various human populations on four continents, and found a striking geographic difference in BuV IgG prevalence, varying from 2% in Northern Europe to 85% in the Middle East. Conversely, CuV IgG showed evenly low prevalences in all countries studied and TuV IgG was entirely absent. These results provide new insights on the global distribution and endemic areas of human protoparvoviruses.