Human Parainfluenza 2 & 4: clinical and genetic epidemiology in the UK, 2013-2017, reveals distinct disease features and co-circulating genomic subtypes

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Abstract

Background Human Parainfluenza viruses (HPIV) comprise of four members of the genetically distinct genera of Respirovirus (HPIV1&3) and Orthorubulavirus (HPIV2&4), causing significant upper and lower respiratory tract infections worldwide, particularly in children. However, despite frequent molecular diagnosis, they are frequently considered collectively or with HPIV4 overlooked entirely. We therefore investigated clinical and viral epidemiological distinctions of the relatively less prevalent Orthorubulaviruses HPIV2&4 at a regional UK hospital across four autumn/winter epidemic seasons. Methods A retrospective audit of clinical features of all HPIV2 or HPIV4 RT-PCR-positive patients, diagnosed between 1st September 2013 and 12th April 2017 was undertaken, alongside sequencing of viral genome fragments in a representative subset of samples. Results Infection was observed across all age groups, but predominantly in children under nine and adults over 40, with almost twice as many HPIV4 as HPIV2 cases. Fever, abnormal haematology, elevated C-reactive protein and hospital admission were more frequently seen in HPIV2 than HPIV4 infection. Each of the four seasonal peaks of either HPIV2, HPIV4 or both, closely matched that of RSV, occurring in November and December and preceding that of Influenza A. A subset of viruses were partially sequenced, indicating co-circulation of multiple subtypes of both HPIV2&4, but with little variation between each epidemic season or from limited global reference sequences. Conclusions Despite being closest known genetic relatives, our data indicates a potential difference in associated disease between HPIV2 and HPIV4, with more hospitalisation seen in HPIV2 mono-infected individuals, but a greater overall number of HPIV4 cases.

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