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Partial sequencing of the VP2 capsid gene for direct enterovirus genotyping in clinical specimens

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Abstract

Typing of human enterovirus (EV) remains a major goal for diagnostic and epidemiological purposes. Whereas sequencing of the VP1 coding region is the reference standard for EV typing, a method relying on sequencing of the VP2 coding region has been proposed as an alternative; however, this has been validated only on cell culture supernatants. To avoid the selection of cultivable strains and to quicken the identification step, a new semi-nested PCR method targeting the VP2 region was developed by use of the CODEHOP strategy. After validation of the method on reference and clinical strains, a total of 352 clinical specimens found to be positive for EV RNA (138 with the GeneXpert EV kit and 214 with the Enterovirus R-gene kit) during a 3-year period (2010–2012) were analysed prospectively for VP2 genotyping. Overall, 204 (58%) specimens were typeable. A higher proportion of throat swab/stool specimens than of cerebrospinal fluid (CSF) specimens was found to be typeable (94 of 142 (66.2%) vs. 83 of 169 (49.1%), respectively, p <0.01 by the chi-square test). Moreover, the median C_t value obtained was lower for typeable specimens than for untypeable specimens (32.20 vs. 33.01, p <0.05, and 25.96 vs. 31.74, p <0.001, for the GeneXpert and R-gene tests, respectively, by the Mann–Whitney–Wilcoxon test). These results suggest that, in cases of EV meningitis, a peripheral specimen (i.e. throat swab or stool) that is susceptible to exhibiting a higher viral load should be used in preference to CSF for identifying the causative EV genotype by use of the VP2 typing method without cell culture isolation.

Monitoring progress toward measles elimination by genetic diversity analysis of measles viruses in China 2009–2010

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With the achievement of high coverage for routine immunization and supplementary immunization activities (SIAs), measles incidence in mainland China reached its lowest level in 2010. The proportion of measles cases in the vaccination-targeted population decreased during 2007–2010 after the SIAs. More than 60% of measles cases were in adults or infants, especially in the coastal and eastern provinces during 2009 and 2010. A total 567 isolates of measles virus were obtained from clinical specimens from 27 of 31 provinces in mainland China during 2009 and 2010. Except for two vaccine-associated cases, one genotype D4 strain, two genotype D9 strains, and four genotype D11 strains, the other 558 strains were genotype H1 cluster H1a. Genotype H1 has been the only endemic genotype detected in China since surveillance began in 1993. Only genotype H1 was found in mainland China during 1993–2008, except for one detection of genotype H2. More recently, multiple genotypes of imported measles were detected even with the background of endemic genotype H1 viruses. Analysis of the 450-nucleotide sequencing window of the measles virus N gene showed that the overall genetic diversity of the recent genotype H1 strains decreased between 2008 and 2010. The lower genetic diversity of H1 strains suggested that enhanced vaccination may have reduced the co-circulating lineages of endemic genotype H1 strains in mainland China.

Epidemiology of viral respiratory infections in a tertiary care centre in the era of molecular diagnosis, Geneva, Switzerland, 2011–2012

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Abstract

Few studies have examined the epidemiology of respiratory viral infections in large tertiary centres over more than one season in the era of molecular diagnosis. Respiratory clinical specimens received between 1 January 2011 and 31 December 2012 were analysed. Respiratory virus testing was performed using a large panel of real-time PCR or RT-PCR. Results were analysed according to sample type (upper versus lower respiratory tract) and age group. In all, 2996 (2469 (82.4%) upper; 527 (17.6%) lower) specimens were analysed. Overall positivity rate was 47.4% and 23.7% for upper and lower respiratory samples, respectively. The highest positivity rate was observed in patients under 18 years old (p <0.001); picornaviruses were the most frequent viruses detected over the year. Influenza virus, respiratory syncytial virus, human metapneumovirus and coronaviruses showed a seasonal peak during the winter season, while picornaviruses and adenoviruses were less frequently detected in these periods. Multiple viral infections were identified in 12% of positive cases and were significantly more frequent in children (p <0.001). In conclusion, we observed significant differences in viral infection rates and virus types among age groups, clinical sample types and seasons. Follow-up of viral detection over several seasons allows a better understanding of respiratory viral epidemiology.