

from malignancy and a higher incidence of comorbidities than the general population without CP. This study was supported by grants from the Ministry of Science and Technology, Taiwan (MOST 107-2634-F-002-015 and 106-2628-E-002-004-MY3).

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Epidemic intelligence activities during major international incidents involving emerging infections

C. O'Connor, J. Wilburn*, A. Walsh, D. Morgan

Public Health England, Emerging Infections and Zoonoses, London/UK



Purpose: To review and describe sources of information used by Public Health England's epidemic intelligence (EI) system during the Ebola virus disease (EVD) outbreak in West Africa, and Zika virus outbreak in the Americas. Outputs from this analysis will be used to refine EI practices to inform risk assessments and policy during future major incidents.

Methods & Materials: Since 2003, Public Health England has maintained a manual event-based surveillance system of mostly open source data for detecting and monitoring incidents involving emerging infectious diseases. Where possible, initial alerting sources for data (eg media) are validated by obtaining a definitive information source (eg national authorities). Data collated during the West African EVD and the Americas Zika virus outbreaks were analysed to assess the relative importance of different sources for information gathering.

Results: EI activities during these two incidents resulted in the collection of 5,072 and 2,631 entries for EVD and Zika virus respectively, comprising 41% and 18% of total EI entries recorded during their respective outbreak periods.

For EVD and Zika virus, 51% and 33% of entries respectively had different initial alerting sources compared to definitive information sources. Of these, aggregate open-source surveillance websites (eg ProMED) were the principal sources of initial alerts (40% for EVD and 46% for Zika virus).

For EVD, 41% of definitive information came from media outlets, 19% from the World Health Organization (WHO), 12% each from scientific journals and national authorities. For Zika virus, 33% of definitive information came from scientific journals, 29% from media outlets, 21% from national authorities, and 13% from WHO.

Conclusion: Although resource intensive, EI activities are an important feature of national preparedness to inform risk assessments, policy and guidance during major infectious disease incidents.

While national and international authorities are recognised as principal sources of EI, aggregate surveillance systems, traditional media outlets, and scientific journals remain essential sources of information during international incidents.

This analysis highlights the importance of comprehensive but flexible EI systems, particularly for incidents caused by emerging infectious agents. In particular, it emphasises the utility of manual EI systems readily adaptable to the specific requirements of individual incidents.

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Viral etiology of community-acquired infection in Vietnam: unraveling the unknown by next-generation sequencing analysis

A.T. Nguyen^{1,*}, N. Le², H. Nguyen², T. Tran², C. Anscombe², C.-Y. Lau³, D. Limmathurotsakul⁴, C. Nguyen⁵, R. van Doorn⁶, X. Deng⁷, M. Rahman², E. Delwart⁸, G. Thwaites⁹, T. Le²

¹ Oxford University Clinical Research Unit, Emerging Infectious, Ho Chi Minh/VN

² Oxford University Clinical Research Unit, Ho Chi Minh/VN

³ National Institutes of Health, Bethesda/US

⁴ Mahidol Oxford Tropical Research Unit, Bangkok/TH

⁵ Hospital for Tropical Diseases, Ho Chi Minh/VN

⁶ Hospital for Tropical Diseases, Ho Chi Minh City/VN

⁷ Blood Systems Research Institute, San Francisco/US

⁸ University of California at San Francisco, Blood Systems Research Institute and Department of Laboratory Medicine, San Francisco, CA/US

⁹ Oxford University Clinical Research Unit, Ho Chi Minh City/VN

Purpose: Community-acquired (CA) infection is a major public-health problem worldwide. Yet despite extensive laboratory diagnosis, the etiology remains unknown in >50% of the patients. Improving our knowledge of the causative agents is essential for improving disease burden.

Methods & Materials: A deep-sequencing based viral metagenomics approach was employed to analyze 493 clinical samples (384 plasma, 92 pooled nasal- and throat swabs, 10 stools and 7 CSF) from 386 CA infected patients with unknown origin (children and adults) recruited from 6 hospitals cross Vietnam in 2014–2015. Sensitive specific PCRs were used to confirm deep sequencing results.

Results: 22 viruses were detected in 54/493 samples (including 11 viruses in 32 plasma samples), corresponding to a detection rate of 14% (54/386). The detected viruses included enteroviruses (n=14), hepatitis B virus (10), rhinovirus (5), rotavirus A (3), measles virus, respiratory syncytial virus, parainfluenza virus, adenovirus, hepatitis C virus, dengue virus, influenza A/B virus, parechovirus 1/6 (2 each), metapneumovirus, human immunodeficiency virus, coronavirus, WU-polyomavirus, scaffold virus, salivirus (1 each) and recently described viruses including human pegivirus 2 and gemycircularvirus (1 each).

Conclusion: Multiple viral pathogens were detected by deep sequencing in 54/386 (14%) CA infected patients with unknown origin. Metagenomics can be a sensitive pan-pathogen assay for unbiased/sequence-independent detection of known/unknown pathogens in clinical samples. The results warrant further active surveillance for novel pathogens in Asia where there is a high risk of emerging infections.

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