08.002

Use of Pseudotyped viruses for the production of reference materials as part of emerging viral outbreak preparedness

E. Bentley^{1,*}, E. Wright², M. Hassall³, S. Myhill³, P. Rigsby³, D. Wilkinson³, L. Stone³, M. Page⁴, G. Mattiuzzo⁴

 ¹ NIBSC, Division of Virology, Potters Bar, HERTFORDSHIRE/UK
² University of Sussex, Brighton/UK
³ NIBSC, Potters Bar/UK
⁴ National Institute for Biological Standards and

Control (NIBSC), Potters Bar/UK

Purpose: The recent public health emergencies of international concern (PHEIC), caused by Ebola and Zika virus, have high-lighted the lack of prophylactic treatments and need for effective diagnostics for emerging viruses. In response to this, we established International Reference Reagents for antibody detection, which enables the comparison of results from laboratories worldwide undertaking treatment/vaccine efficacy clinical trials. The requirement for high containment facilities to handle viruses with outbreak potential, such as BSL4 for Ebola virus, is a constraining challenge. We have developed serological assays using replication defective pseudotyped viruses (PV) for the evaluation of reference material to avert high containment requirements.

Methods & Materials: The preferred candidate material is a pool of plasma or sera from convalescent patients as this provides a commutable standard. For the reference material for Ebola antibody, several donations were received at NIBSC and solvent-detergent treated to ensure inactivation of virus. Characterisation is performed in-house using both PV neutralisation assays and ELISA platforms. PV is produced via plasmid transfection of 293T cells, with plasmids encoding a lentiviral core component, a reporter gene which is packaged within the core and the sequence of the envelope protein for the virus of interest. The ability of candidate material to block PV entry into target cells is measured via reporter signal reduction.

Results: Following a WHO-sponsored International Collaborative study, the 1st WHO International Standard for Ebola virus antibodies was established in 2017. Participants in the collaborative study evaluated the candidate materials using assays available in their laboratories. Data from neutralisation assays employing PV with either a lentiviral or vesiculoviral core component was correlated with the wildtype assay and showed a better correlation coefficient when the vesiculovirus PV system was used.

Conclusion: To support preparedness activities, antibody reference materials are now being established for other WHO priority pathogens such as Lassa and Nipah virus. To characterise the serological material at a low containment level, we have established assays using PV generated with both the lentiviral and vesiculovirus platforms. The two systems are currently being investigated to determine the most appropriate for each high containment virus.

https://doi.org/10.1016/j.ijid.2018.11.035



08.003

Global flu view: a platform to connect crowdsourced disease surveillance around the world

A.W. Crawley^{1,*}, D. Paolotti², C. Dalton³, J. Brownstein⁴, M. Smolinski¹

¹ Ending Pandemics, San Francisco, CA/US
² ISI Foundation, Turin, Turin/IT
³ Hunter Medical Research Institute, Newcastle/AU
⁴ Childrens Hospital, Boston, MA/US

Purpose: Participatory disease surveillance actively engages the public in reporting on symptoms of their health to provide community-level data that complements traditional healthcarebased surveillance. Participatory surveillance is timely, low-cost, can account for non-medically attended populations, and allows for direct engagement with local populations. Three examples of participatory surveillance systems – Flu Near You in North America, Influenzanet in Europe, and Flu Tracking in Australia and New Zealand – have recently collaborated to develop Global Flu View, a shared platform for aggregation and dissemination of crowdsourced data on influenza-like illness.

Methods & Materials: The collaborating surveillance systems have developed a shared application programming interface (API) for data exchange among systems. The API specifications outline specific variables that are called into a shared, cloud-based database. Data is processed via an ETL layer resulting in aggregate data at the postcode level. Key variables include reporting week, postal and country codes, user birth month and birth year, gender, vaccination status, and a series of symptom variables that include fever, cough, sore throat, headache, fatigue, and other indications of influenza-like illness. Processed data will be available to view in both graph and map formats on the website www.globalfluview. Org.

Results: The Global Flu View platform connects communitylevel influenza surveillance efforts across 15 countries on 3 continents. Tens of thousands of weekly reports are made available for users to explore through graphs, maps, and various filtering tools. The Global Flu View database also serves as a repository of influenza surveillance data that can be shared with disease modelers, researchers, and epidemiologists around the world.

Conclusion: Global Flu View can highlight the value of the participatory surveillance approach, serving as a model for other countries. The platform is poised to incorporate data from additional countries with similar tools and serves as a case study for collaborative, multi-country data sharing for global health surveillance. As of July 2018 the platform is in beta-testing mode and will be made publicly available by late August 2018.

https://doi.org/10.1016/j.ijid.2018.11.036

08.004

Novel platform (wEB) to study flu virus evolution and predict vaccine efficacy

S. Paessler^{1,*}, V. Veljkovic²

 ¹ University of Texas Medical Branch, Pathology, Galveston, TX/US
² BiomedProtection, LLC, Galveston, TX/US

Purpose: Flu epidemics and potential pandemics pose great challenges to public health institutions, scientists and vaccine producers. Creating right vaccine composition for different parts of the world is not trivial and has been historically very problematic.