

16.049

An Annual Epidemic of Influenza in Japan Analyzed with Network Analysis

Y. Takahashi*, K. Omata, T. Shimbo

International Medical Center of Japan, Tokyo, Japan

Background: In this decade, several countries have suffered from infection of humans with highly pathogenic H5N1 influenza, provoking the threat of a worldwide pandemic. Information about a spread pattern of infectious diseases such as influenza of the currently ordinary types H3N2 and H1N1 is thought to be useful for taking preventative measures against this misgiving pandemic. This study aimed to analyze annual epidemics of the ordinary influenza in Japan with network analysis and to explore spread patterns.

Methods: The analyzed data was the cases of influenza-like-illness during these 20 years. We constructed the vectors of the increasing rates of the reported cases for each prefecture at each week, and calculated the matrices of the space-time correlation which was defined for all pairs of prefectures. As each correlation was treated as each tie, a valued-network was depicted, and was analyzed with network analysis. All prefectures were also classified with cluster analysis.

Results: In 2007, the ties between prefectures were strong in the south-east region of Japan, and the strongest tie was that between Miyazaki and Kagoshima. Relatively strong ties could be that between geographically neighboring prefectures. On the other hand, the ties were relatively weak for a prefecture isolated from the others by seas (Hokkaido or Okinawa). The trend seemed almost similar during analyzed years.

Conclusion: An epidemic could be spread within geographically neighboring prefectures connected with a strong tie. These prefectures should be targeted to organize preventative measures of pandemic of H5N1 intensively.

doi:10.1016/j.ijid.2008.05.259

16.050

Detection of Infectious Pathogenic Viruses in Untreated and Treated Wastewater Samples from An Urbanised AreaA. Filipidou¹, T. Parasidis¹, I. Alexandropoulou¹, E. Stavrou², K. Karlou², A. Vantarakis^{2,*}¹ *Democritus University of Thrace, Patras, Greece*² *University of Patras, Patras, Greece*

Background: Processed sewage waste often contain residual pathogenic viruses, bacteria, cysts of protozoa but most sewage-related disease outbreaks have been attributed to re-use of raw sewage waste water, raw sludge, or night soils on food crops consumed raw, to contamination of drinking water from septic tanks, to consumption of raw shellfish from sewage-polluted waters or to use of contaminated recreational water. Regardless of the improvement in sanitary conditions in urbanised areas, infectious diseases caused by pathogenic viruses in water have been reported from year to year. In this study, infectious enteroviruses, adenoviruses and HAV in untreated and treated wastewater samples from an urbanised area were investigated.

Methods: Fifty treated and untreated sewage samples were collected weekly for six months from the inlet and outlet of a major urban sewage treatment plant and investigated for the presence of enteroviruses, adenoviruses and Hepatitis A viruses. For the detection of these viruses, RT-PCR and nested PCR were used. Positive PCR products were sequenced in order to identify the virus types circulating in the community.

Results: Fifty samples of untreated and treated sewage samples were processed. All types of viruses were detected in inlet and outlet samples. Pathogenic viruses were detected in 60% of the raw sewage samples and in 52% of the treated wastewater. Enteroviruses, adenoviruses and HAV were detected in ten, ten and one sample from the inlet wastewater accordingly. In outlet treated wastewater, eleven samples were found positive for adenoviruses and three samples were found positive for enteroviruses. Also, in one case, there was no detection of virus in the inlet but there was detection in the outlet sample. Adenoviruses type 3, type 10 and type 41 were identified. For enteroviruses, coxsackie A2, echovirus type 27 and 30 were detected. For HAV, strain H2 was isolated.

Conclusion: It was the first time to screen the virological quality of the treated wastewater in Greece. The presence of high amount of pathogenic viruses in sewage and their possible survival after the sewage treatment is a possible problem for public health.

doi:10.1016/j.ijid.2008.05.260

16.051

Outbreak of Gastroenteritis Occurred in North-Eastern Greece Associated with Several Waterborne Strains of NorovirusesT. Parasidis¹, E. Vorou², Mellou², G. Theodoropoulou-Rodiou³, G. Katsantridou³, G. Stamatopoulou³, A. Vantarakis^{1,*}¹ *Democritus University of Thrace, Alexandroupolis, Greece*² *Hellenic Center for Infectious Diseases Control, Athens, Greece*³ *Microbiology Laboratory, General Hospital of Xanthi, Greece, Xanthi, Greece*

Background: Noroviruses (NLVs) are recognized as a worldwide cause of nonbacterial gastroenteritis. In Europe, a study on viral gastroenteritis showed that NLVs are responsible for >85% of all non bacterial outbreaks of gastroenteritis reported from 1995–2000. NLVs can be classified into 5 genogroups, GI - V. The present study focused on reported increase of gastroenteritis cases during May, June, July and August 2006 in a prefecture of NE Greece. An epidemiological study was performed to study the cause of epidemics.

Method: Laboratory investigation.

Fecal samples from patients with gastroenteritis who visited the hospital with characteristic symptoms of acute gastroenteritis (diarrhea, vomiting, nausea, fever) were received for further bacteriological analysis (*Salmonella*, *Shigella*, *Campylobacter*, Enteropathogenic *E. coli* O157:H7, *Yersinia*), parasitologic (including *Cryptosporidium*) and virological analysis (*Rota*-viruses, *Adenoviruses* and

Noroviruses). For the bacteriological and parasitological analysis standard culture techniques were performed. For the detection of the presence of Noro-viruses (genotypes I and II) nested RT-PCR was used. Positive samples were confirmed by sequencing. In parallel, water samples were analyzed.

Outbreak investigation: A questionnaire was developed to gather information on patient's gender, age, symptoms, dates of onset symptoms, laboratory tests and hospitalization for the performance of epidemiological analysis.

Results: Of the patients, 92% had diarrhea, 48% vomiting, 40% nausea and 50% fever. 50% of the patients was hospitalized in pathology and paediatrician unit of general Hospital for 1 or 2 days. From 98 fecal samples analyzed in six, *S. typhimurium* was detected, in two 2, *S. enteritidis*, in four, *C. jejuni*, in one rota-viruses. In eight Noro-viruses type 1 and in 25 Noro-viruses type 2 were detected. 38% of the cases were from Xanthi city with wide presence. 39.7% of the patients were under 4 years old, 32,3% was from 5 up to 24 years old, 11,3% was from 25 up to 44 years old, 8,1% was between 45 and 64 years old, 8,5% was > to 65 years old. Water analysis although showed *E.coli* contamination, no noroviruses was detected.

Conclusions: During epidemiological investigation of the increased number of cases, all criteria for Noro epidemics, were confirmed.

doi:10.1016/j.ijid.2008.05.261

16.052

A Cohort Study to Assess the New WHO Japanese Encephalitis Surveillance Standards

T. Solomon^{1,*}, T. Thu Thao², P. Lewthwaite¹, M.H. Ooi³, R. Kneen⁴, N. Minh Dung², N. White⁵

¹ University of Liverpool, Liverpool, United Kingdom

² The Hospital for Tropical Diseases, Ho Chi Minh City, Vietnam

³ Institute of Health and Community Medicine, Universiti Malaysia Sarawak, Kota Samarahan, Sarawak, Malaysia

⁴ Royal Liverpool Children's NHS Trust, Liverpool, United Kingdom

⁵ The University of Oxford-Wellcome Trust Clinical Research Unit, The Hospital for Tropical Diseases, Ho Chi Minh City, Vietnam

Background: Approximately half the world's population lives in areas affected by Japanese encephalitis (JE). JE can be controlled through vaccination, but disease surveillance is needed to support countries in their decisions on vaccine implementation. New surveillance standards for JE have been produced by the WHO, but it is unclear how good they are. In this study we assessed the field test version of the new WHO JE surveillance standards.

Methods: We applied the clinical case definition of acute encephalitis syndrome (AES), laboratory diagnostic criteria and case classifications to patients with suspected central nervous system (CNS) infections in southern Vietnam.

Findings: 380 patients (149 children) with suspected CNS infections were recruited and evaluable, of whom 296 (96 children) met the AES case definition. 54 children were infected with JE virus (JEV), of whom 35 (65%) had AES, giv-

ing a sensitivity of 65% (95%CI 56–73%), and specificity 39% (30–48%). 9 adults with JEV all presented with AES. The 19 JEV-infected children missed by the surveillance included 10 with acute flaccid paralysis, 2 with a flaccid hemiparesis, and 6 with meningism only. Altering the case definition to include limb paralysis and meningism improved the sensitivity to 89% (83–95), whilst reducing the specificity to 23% (15–30). An acute serum sample diagnosed 41(68%) of 60 JEV positive patients; an admission CSF diagnosed 33 (72%) of 46 patients with this sample, including 7 that were serum negative. Examining a 2nd sample at day 10 diagnosed 61 of 62 patients. 5 patients with neurological manifestations of dengue infection had JEV antibodies in serum, and would have been misdiagnosed had we not tested for dengue antibodies in parallel.

Conclusion: The case definitions detected about two thirds of the children infected with JE virus, missing those presenting with acute flaccid paralysis. A modified case definition which included acute paralysis and meningism detected nearly 90% of children. An acute CSF sample is more sensitive and specific than an acute serum sample. This formal evaluation of surveillance standards during their development provides an evidence base to support their recommendation, and should be encouraged for future WHO standards.

doi:10.1016/j.ijid.2008.05.262

16.053

Laboratory Surveillance for Influenza in Cuba

B. Acosta*, A. Piñon, O. Valdes, C. Savon, G. Gonzalez, A. Goyenechea, G. Gonzalez-Baez, B. Hernandez, S. Oropesa

Tropical Medicine Institute Pedro Kouri, Havana city, Cuba

Background: Influenza epidemics are caused by rapid evolution of the viral genome and continue to play a significant role in the annual frequency of mortality and morbidity as a result of respiratory tract infection. World Health Organization created more than 50 years ago the World Influenza Surveillance System, which has contributed to the knowledge and the understanding of the epidemiology of these viruses. However, it still is necessary to improve and strengthen the surveillance and control of this disease all over the world.

Method: During the 2005–2006 influenza season, the totality of respiratory samples were analyzed using two multiplex RT nested-RCP multiplex for the detection of 14 respiratory virus and an third RT nested PCR assay (L gen) was used for detection of hMPV. Recently, we introduce two RT nested-RCP for the typing and subtyping of hemagglutinin and neuraminidase of influenza A virus, including the subtype A (H5N1).

Results: Virological surveillance highlighted the predominant circulation of B viruses (32% of isolates) in Cuba, in contrast to many other countries in Europe and North America where AH3N2 viruses were isolated most frequently, and in contrast to the infrequent isolation of B viruses in Cuba during the previous years. Influenza A(H1N1) viruses were not identified. However, the surveillance through serum pair studies showed a predominant positively to influenza A (H3N2) and the circulation studies using monoserum of