An Annual Epidemic of Influenza in Japan Analyzed with Network Analysis

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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.

16.050

Detection of Infectious Pathogenic Viruses in Untreated and Treated Wastewater Samples from An Urbanised Area

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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.

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.

16.051

Outbreak of Gastroenteritis Occurred in North-Eastern Greece Associated with Several Waterborne Strains of Noroviruses

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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 epidemiologica 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