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Surveillance of a severe A(H1N1)pdm09 dominated influenza season in N. Greece, 2015–2016

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Objects of the research: The objective was the epidemiological and virological analysis of a severe influenza A(H1N1)pdm09-dominated season, 2015–2016 in N. Greece.

Materials and methods: 686 pharyngeal swabs/washes from patients with influenza-like-illness were tested up to week 17. Influenza viruses were typed and their haemaglutinin was sequenced. (CDC and WHO protocols). All of the samples were non-sentinel, mostly originating from outpatient and inpatient hospital clinics.

Results: 246 samples were positive for influenza. A and B viruses were detected in 220 and 24 samples respectively. B viruses appeared during the first and the last weeks of the season. Out of the A viruses, 206 were H1N1pdm09 and 8 were H3N2. Molecular analysis of B viruses revealed that B-Victoria lineage viruses dominated this season. A(H1N1)pdm09 viruses were A/California/7/2009(H1N1)pdm09-like, but with accumulating variations at antigenic and other HA sites, that designated them into two distinct phylogenetic clades, 6B.1 and 6B.2.

Samples ranged between 0 and 86 years of age, with an average age 40.6 years. Sixty-seven ICU patients had an average age of 54.5 years and in all of them A(H1N1)pdm09 was detected and most suffered from underlying medical conditions, were obese or pregnant. Most common complications were ARDS and pneumonia. In total, 39 fatalities have been reported in northern Greece. All of them were attributed to A(H1N1)pdm09. Interestingly, 6 of the decedents did not suffer from any underlying medical condition, 10 of those were obese (26.%) and 25 were suffering from cardiological problems (64%). Complications and underlying medical conditions are mentioned in detail in Table 1.

Conclusions: Compared to the findings from previous studies from Greece, it seems that it was a severe A(H1N1)pdm09-dominated influenza season. This subtype seems to cause more severe influenza illness, in a younger age group, more often causing hospitalization to otherwise healthy individuals. Circulating strains are increasingly more divergent. Our findings confirmed the genetic instability of influenza type A(H1N1)pdm09 viruses and highlighted the importance of continuous surveillance for the effective management of viral epidemics. Variation observed in Greek and also in European B viruses prompted WHO to change the B vaccine component to B/Victoria.

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Enhancement of respiratory virus isolation from specimens using centrifugation and interferon inhibitors

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Virus isolation from clinical specimens is inevitable to identify the etiological agent and to investigate the epidemiological analysis. In addition, the viruses isolated are used as important sources in the fields from the basic research to the bioindustry, including therapeutics, and vaccines. However, the respiratory viruses in clinical specimens are not easily isolated in cell cultures. Thus, methods to speed or enhance virus isolation are urgently required. Many previous reports have proved that centrifugation during virus inoculation to cells increased virus yields and speeded the virus detection time. Recently, interferon inhibitors treatment has also been used to enhance virus infection by blocking the expression of interferons, modulators inhibiting virus replication in cells. We used interferon inhibitors with centrifuged cultures for the detection of metapneumovirus, human respiratory syncytial virus, and Middle East respiratory syndrome coronavirus. Combination of centrifugation and interferon inhibitor treatment significantly increased the virus replication and viruses detected earlier than the routine method. We also test and compare the virus isolation rates between the centrifugation/interferon inhibitor treatment culture and the mock-treated culture.

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Molecular characterisation of human coronaviruses from patients with respiratory disease in Slovenia

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Background: Coronaviruses (CoVs) are the largest enveloped single-strand RNA viruses and belong to the *Coronaviridae* family in the *Nidovirales* order and are divided into four genera named *Alphacoronaviruses*, *Betacoronaviruses* (divided into the four clades A to D), *Deltacoronaviruses* and *Gammacoronaviruses*, based on the phylogenetic distance of highly conserved domains. Until now six human coronaviruses have been identified and HCoV-OC43 is the most common human coronavirus and has high genetically diversity. Five genotypes of HCoV-OC43 (A to E) have been identified and genotype D has been dominant from 2004 to 2012. Until now only 90 complete genome sequences of HCoV-OC43 were available in GenBank. In this study, we investigate of the presence of different genotypes among HCoVs strains and comparison their potential similarity.

Methods: Patients hospitalized with acute respiratory tract infections were included in the study. All nasopharyngeal swabs were sent to the laboratory of the Institute of Microbiology