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"One-Test-Fits-All" approach for detection and identification of influenza virus infections using nanomicroarray and NGS assays

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Conventional methods for detection and discrimination of influenza viruses are time consuming and labor intensive. It is critical to develop accurate methods for their rapid characterization, prevention and treatment. We report a "one-test-fits-all" approach using nanomicroarray for screening, and next-generation sequencing (NGS) assays for extensive identification of influenza virus infection or co-infections. The nanomicroarray was developed to target hemagglutinin, neuraminidase, and matrix genes to identify Influenza A and B viruses. PCR mega-amplicons synthesized by using a paired set of degenerate universal primers for whole-genome of influenza viruses were detected and confirmed using NGS. Influenza infections including A (H3N2), A (pdH1N1), influenza B virus, and A (H3N2 and pdH1N1) virus co-infections were identified in nasopharyngeal swab specimens in a single test run. Bioinformatics studies reveal their comprehensive genetic composition and provide matrix reporting information for diagnosis and characterization of novel virulence and drug resistance markers in these specimens. Furthermore, analytical sensitivity studies demonstrated that the NGS sequencing-based diagnostics can achieve ultrasensitive detection of influenza genomes. The current diagnostic platform allows for extensively identifying any unknown influenza viruses in a single test, simultaneously detecting and discriminating multiple influenza virus infections in a single specimen, and effectively monitoring changes in circulating influenza viruses that may have pandemic potential, thus facilitating diagnostics and antiviral treatment in the clinical setting and protection of the public health.

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Demographic characteristics adjusted comparison of clinical presentations between severe infections with H7N9 and H1N1pdm influenza A in Jiangsu Province, China

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Influenza H7N9 and H1N1pdm can cause severe human infections. It is important to investigate the distinguishing clinical features between these two diseases. Several studies have compared the differences in general, however, age and gender adjusted comparisons may be more useful and informative to the health professionals. A total of 184 severe H1N1pdm patients and 61 severe H7N9 patients from Jiangsu Province were included in this analysis to perform age and gender adjusted comparison of clinical features. The age was significantly older (median, 56.0 vs. 27.0) and male accounted for a significantly higher proportion (70.5% vs. 48.4%) in H7N9 patients than H1N1pdm patients. Before adjusting age and gender, H7N9 patients were significantly more likely to have chronic cardiovascular disorders and their intervals from onset of illness to first medical consultation were significantly longer. However, after adjusting, both the differences became insignificant. With respect to the clinical outcome, H7N9 patients were more likely to develop ARDS, respiratory failure, heart failure, liver dysfunction, renal dysfunction and to be admitted to ICU with a significantly higher fatality, regardless of age and gender. Furthermore, H7N9 patients had significantly longer intervals from onset of illness to neuraminidase inhibitor treatment, to hospitalization and to death even after adjusting age and gender. Our results suggests that age and gender should be adjusted as important confounding factors when comparing the clinical features between severe H7N9 and H1N1pdm patients to avoid any misunderstanding regarding the differences between these two diseases. Compared with our previous results, the clinical outcomes of H7N9 patients seem getting worse, which need more data and analyses to figure out the reasons.

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