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### **Epidemiological and virological characterization of influenza A/H3N2 viruses during five seasons (2010/2011-2014/2015) in Korea**

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Influenza viruses have constantly changed their characteristics by antigenic shift and drift. As the most effective method to prevent influenza is vaccination with well-matched with vaccine viruses, WHO has recommended seasonal vaccine strains annually. Of seasonal influenza viruses, A/H3N2 is known to be the most variable, sometimes resulting in the vaccine mismatch. Therefore, we intended to investigate the epidemiological and virological characteristics of Korean H3N2 isolates during 2010/2011 to 2014/2015 seasons. Epidemic patterns and serological and genetic characteristics for Korean H3N2 isolates during five seasons were analyzed. For this, hemagglutination inhibition (HI) tests and sequencing on the hemagglutinin (HA) gene were used. During these periods, there were five H3N2 epidemic waves in Korea and H3N2 virus had been dominant from late of 2011 to 2015 present. Although genetically distinct determinants were not detected to differentiate seasonality, we found high frequency variation in the HA genes depending on season. From 2010/2011 to 2012/2013, Korean isolates were closely similar to the vaccine strains of corresponding years. However, isolates from 2013/2014 season started to decrease homology on the HA gene, compared with vaccine strain (A/Texas/50/2012). Furthermore these isolates had low activities to anti-vaccine sera in HI, implying that H3N2 vaccine mismatch might be started from 2013/2014 season in Korea. Taken together, it is necessary to monitor genetic evolution as well as antigenic profile of H3N2 isolates with dynamic analysis to response and prepare epidemics.

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