

OF2 Typing and hemagglutinin subtyping of influenza viruses by high resolution mass spectrometry

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typing and subtyping of influenza viruses by accurate mass identification of signature proteolytic peptide ions

Influenza viruses are classified as type A, B and C according to the nature of the nucleoprotein antigen. All three types can infect humans. Past pandemics have all been caused by type A viruses, while seasonal epidemics are associated with type A and B forms. Type A viruses are further subdivided into different serotypes based on the antibody response to these viruses. This is associated with isoforms of the two major surface antigens hemagglutinin (HA) and neuraminidase (NA) that change their structure and antigenicity due to mutations and reassortments within the genes that encode them. No such subdivision is applied for type B influenza viruses but changes in the hemagglutinin antigen have led to the occurrence of two major lineages.

Here we demonstrate that it is possible to assign the type, and either the hemagglutinin subtype or lineage, of type A and B influenza based upon the detection of characteristic signature proteolytic peptides where their mass is recorded with high accuracy. The approach obviates more labour intensive genetic and serological analysis. Such mass accuracy can be achieved routinely with high field FT-ICR mass spectrometers. The rationale behind and results for both type A and B viruses [1] will be presented in concert with the analysis of all database entries for known influenza antigens.

[1] Schwahn AB, Wong JWH, Downard KM, submitted for publication.