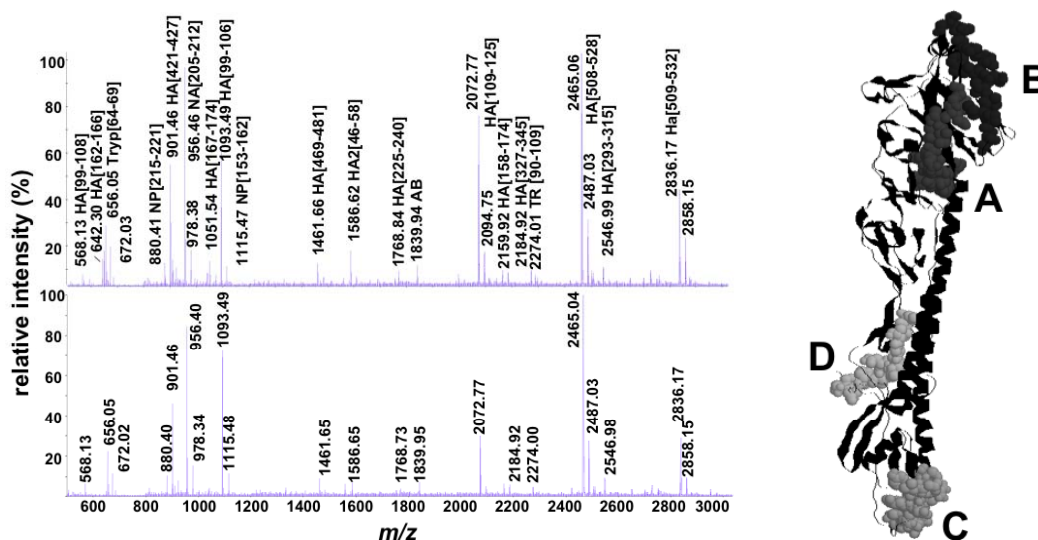


ANTIGENICITY OF H3N2 SUBTYPES OF THE INFLUENZA VIRUS BY MASS SPECTROMETRY

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The most common strain of the influenza virus identified within infected individuals for the latest flu season in Australia, Europe and the U.S.A was of the H3N2 subtype. Characterising the structure and antigenicity of this and other subtypes is central to a global surveillance strategy to design and prepare effective vaccines against the virus. We first reported in 1999 [1] on the use of mass spectrometry to survey both the structure and antigenicity of the virus from a single pair of mass spectra recorded for digested whole virus before and after treatment with a monoclonal antibody to a target antigen. We have subsequently advanced the approach to gel-resolved antigens [2] to improve sequence coverage and as such the successful identification of determinants. We describe here the ability of this proteomics method to characterise multiple determinants of the hemagglutinin H3 antigen across three diverged strains of the H3N2 subtype in a single analysis [3].



Figures: MALDI mass spectra of gel-recovered hemagglutinin after tryptic digestion of the Panama2007/99 type A strain (top) without antibody, and (bottom) after 24 hours incubation with monoclonal antibody raised to a H3N2 serotype (left); Ribbon representation of the partial structure of the hemagglutinin H3 antigen of the Panama 2007/99 strain in which determinants identified (A-D) are shown in space-filled format (right).

References:

- [1] Kiselar JG, Downard KM (1999) *Biochemistry*, 43: 14185-14191.
- [2] Morrissey B, Downard KM (2006) *Proteomics*, 6: 2034-2041.
- [3] Morrissey B, Streamer M, Downard KM (2006) in publication.