

SURVEYING THE STRUCTURE AND ANTIGENICITY OF EMERGING STRAINS OF THE INFLUENZA VIRUS BY MASS SPECTROMETRY

Paul E. Smith, Bethny Morissey, Kevin M. Downard

School of Molecular & Microbial Biosciences, University of Sydney, NSW 2006

Influenza is a leading cause of death in Australia with over 5000 attributed to the virus annually. The surface antigens hemagglutinin and neuraminidase are the viral coat antigens responsible for the initial stages of infection and onset of symptoms. The rapid rates of antigenic change in the determinants of these antigens results in the inability of antibodies raised to similar strains of the virus to interact with and neutralise emerging forms. Rapid monitoring of this antigenic variation forms the basis of influenza surveillance and treatment.

Previous studies in our laboratory resulted in the development and application of a MALDI-MS based immunoassay to identify both the structural and antigenic identity of protein antigens associated with the virus in complex biological mixtures. In these studies, we demonstrated that it is possible to preserve (Kiselar & Downard, 1999) and directly analyse specific solution-state associations (Kiselar & Downard, 2000) on a MALDI sample surface throughout the deposition and ionization process. We have subsequently developed efficient methods to recover proteins from native gels prior to their treatment with antibodies or other binding partners (Mackun and Downard, 2003) to advance a proteomics based approach to study protein interactions with high sample throughput.

Here we demonstrate the separation, recovery and analysis of influenza antigens of emerging type A strains in terms of their structure and antigenicity by electrophoresis and MALDI-MS.

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Mackun K., Downard K.M. (2003) Strategy for the Study of Protein-Protein Interactions of Gel-Separated Proteins by Mass Spectrometry, *Anal. Biochem.*, 318: 60-70.