

KINETICS OF ANTIBODY-ANTIGEN INTERACTIONS USING A MASS SPECTROMETRY BASED IMMUNOASSAY

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The development of a MALDI mass spectrometry based immunoassay capable of characterising the structure and antigenicity of protein antigens without the need to immobilise, isolate or purify either antigen or antibody was first reported in 1999 [1]. The approach was subsequently applied to determine the antigenicity of strains of the influenza virus using whole virus [2] and gel-resolved antigen [3]. We report here the ability of the assay to characterise the relative rates of antibody binding [4] from time-course experiments in which digested antigen is treated with monoclonal antibody and monitored by mass spectrometry over a 24 hour period. The reduction in the relative area of ions of peptides representing different segments within common and across different determinants is measured by mass spectrometry as a function of incubation time. Relative rates of antibody binding are subsequently determined providing information important in the design of vaccines and anti-viral drugs.

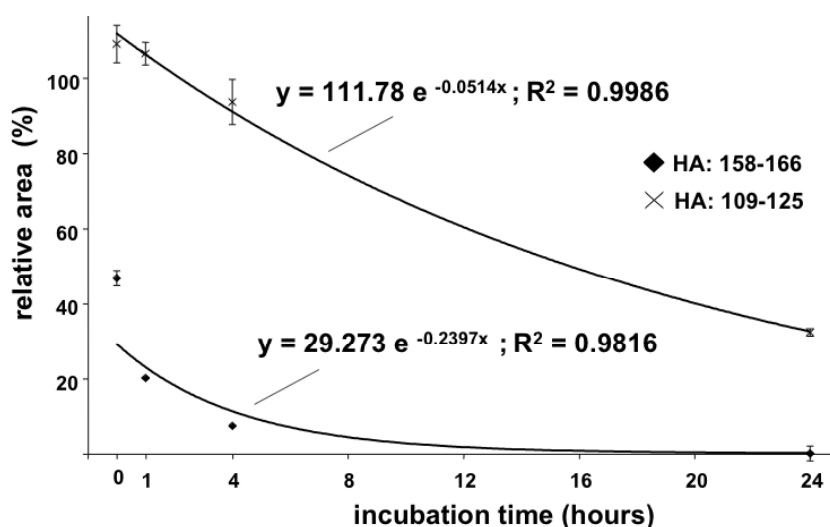


Figure: Reduction in the relative area of the ions for peptide segments of the hemagglutinin antigen of a type H3N2 strain of the influenza virus as a function of antibody incubation time over 1-24 hours.

References:

- [1] Kiselar JG, Downard KM (1999) *Anal. Chem.*, 17: 1792-1801.
- [2] Kiselar JG, Downard KM (1999) *Biochemistry*, 43: 14185-14191.
- [3] Morrissey B, Downard KM (2006) *Proteomics*, 6: 2034-2041.
- [4] Morrissey B, Downard KM (2006) in publication.