MS05-05 | Analysis of Cytomegalovirus Immune Evasion Protein UL144 Glycosylation Profile Revealed its Role in Immune Recognition

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The immune system is designed to provide protection against various pathogens, however several pathogens, including large double stranded DNA viruses have evolved multiple strategies to avoid immune recognition. This is in part achieved by removing immune activating ligands from cell surface and at the same time to express viral mimic on the cell surface to prevent killing of the infected cell by missing self-recognition. Human cytomegalovirus (HCMV) belongs to the beta herpes virus family that has co-evolved with the host immune system. UL144 is found exclusively in clinical HCMV strains and encodes a structural homologue of the herpesvirus entry mediator. UL144 plays a role in virus-mediated immune evasion by transmitting inhibitory signals to downregulate T-cell responses. Its sequence shows 10 N-linked glycosylation sites located in extracellular part. Many of them are not present in other viral species that suggest glycosylation is important only in humans and may play a role in ligand-binding recognition. Here, we present characterization of recombinant HCMV UL144 glycoprotein by liquid chromatography-tandem mass spectrometry (LC-MS/MS). Intact protein analysis determined the accurate masses of these proteins. We have also analyzed the glycan profiles and identified the most glycosylated species. The binding studies showed specific function of UL144 glycosylation in immune recognition.

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