Identification of Two Functional SUMO Interacting Motifs (SIMs) in the Non-structural Protein of Influenza A Virus NS1A

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Identification of Two Functional SUMO Interacting Motifs (SIMs) in the Non-structural Protein of Influenza A Virus NS1A

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We have previously shown that the non-structural protein of Influenza A virus NS1A is post-translationally modified by conjugation of the Small Ubiquitin-like MOdifier (SUMO). Our functional studies have also demonstrated that SUMO conjugation (SUMOylation) affects NS1A's ability to neutralize the cellular interferon response of the host cell and other functions associated to NS1A. Importantly, we have also shown that influenza infections trigger a global increase in cellular SUMOylation and have recently demonstrated that such an increase is mediated by NS1A. This observation led us to investigate the molecular mechanism endowing NS1A with the ability to increase global cellular SUMOylation. Sequence analyses of NS1A revealed the presence of two putative SUMO Interacting Motifs (SIMs) in NS1A, located at positions 144-147 (SIM1) and 178-181 (SIM2). Here, we demonstrate through the use of various pull down analyses that NS1 is capable of interacting with SUMO via non-covalent interactions likely mediated by the two putative SIMs. Ongoing site-directed mutagenesis studies will confirm whether the SIMs constitute the sites mediating the confirmed interaction between NS1A and SUMO1. If so, recombinant viruses expressing a mutant NS1A lacking the SIMs will be developed to evaluate the relevance of the SIMs in NS1 and evaluate whether this affects the global increase in cellular SUMOylation and viral multiplication. Ultimately, these studies will provide important new insight on the host-pathogen interactions occurring during influenza infections of potential relevance for the future development of novel anti-influenza therapies.