Applications Of Anti-Non-Structural Protein 1 Antibody In Against The Growth Of H5N1 Avian Influenza Virus

Mok Chee Keng

Abstract
A new strategy to prevent the infection of H5N1 avian influenza A viruses is needed due to the emergence of drug resistant mutants. Our group identified several monoclonal antibodies (mAb) targeting the viral non-structural protein 1 (NS1), which is a highly conserved and indispensable component of viral replication. 1G1, one of the mAb, has been identified targeting the H5N1 NS1 effector domain (ED) and found being capable of inhibiting viral growth. A single chain variable fragment (scFv) of 1G1 would be used for further characterizations. Epitope mapping of mAb-1G1 was performed through mutagenesis screening assay. The 1G1-scFv was cloned into a CMV vector and transiently transfected in H1299, 293T, and A549 cells. The localization of NS1 co-transfecting with 1G1-scFv was validated using immunofluorescence assay. For further examination, a recombinant H5N1 NS1 virus was generated and used in viral inhibition assay. Our findings demonstrated that 1G1-scFv binds to the nuclear localization sequence at C-terminal end of ED, subsequently inhibiting viral growth. When combined with the known 2H6-scFv, the multi-targeting neutralization of H5N1 was better than using single-targeting neutralization through inhibiting the functions of viral NS1 protein.

Biography
Chee Keng received his PhD in Biomedical Sciences, Chang Gung University, Taiwan, under the supervision of Prof. SHIH Shin-Ru in 2013. He previous study is focused on the influenza virology as well as genomic analysis and functional study of neuraminidase. He also worked closely with the Taiwan CDC contracted Diagnostic Virology Lab and Biosafety Level 3 Lab during the 2003 SARS, 2009 H1N1 pandemic, and 2013 H7N9 outbreak, to establish several molecular diagnostic platforms. In 2014, he moved to NUS to undertake a postdoctoral Research Fellow with A/Prof. TAN Yee Joo. Their on-going projects focus on the alternative approach of anti-avian influenza research using monoclonal antibody.

Understanding The Role Of Linker Histone H1 And Its Subtypes In Nuclear Structure

Chen Junjie

Abstract
Linker histone H1 is one of the five main histone protein (H1, H2A, H2B, H3 and H4) families which are components of chromatin in eukaryotic cells. Unlike the other histones which make up the nucleosome, H1 binds to the nucleosome and the "linker DNA" region between nucleosomes. Linker histones H1 are thus involved in chromatin condensation and the formation of higher order chromatin structure, and they also act as transcriptional repressors, modulating the local accessibility of transcriptional factors, regulatory proteins, chromatin remodeling factors and histone modification enzymes to their target sites. Linker histones H1 are highly abundant nuclear proteins and its functional diversity are attracting increasing investigations. The basic structure of linker histone H1 has been determined, but its functions appear to involve its networking in the nuclei with multiple interfaces including DNA sequences, epigenetic marks and other nuclear proteins. Its functional diversity in organizing mitotic chromatin condensation and interphase chromatin orientation is likely to result from the temporal and spatial integration of its multiple interactions. Complexity also originates from the presence of 11 different H1 variants with six such variants being broadly expressed in somatic cells. My project involves the identification of specific H1 binding partners and how these interactions modulate chromatin arrangements.

Biography
Chen Junjie received his Bachelor’s degree with Honours in Chemical and Bio-molecular Engineering, NUS in 2014. Since his graduation, he has been working in A/Prof Lu Jinhua’s lab as a research assistant. He is currently pursuing his part-time graduate studies.