1-S10-4

Symposium

Dynamics of host chromatin 3D response to virus infection

Yumiko Imai¹, Yu Ichida¹, Masami Shiimori¹

¹*Laboratory of Regulation for Intractable Infectious Diseases, National Institutes of Biomedical Innovation, Health and Nutrition (NIBIOHN)*

Influenza viruses cause worldwide epidemics and pandemics, and sometimes trigger critical illness especially among humans with high risk factors, including obesity, diabetes, and cancers, of which population is increasing with the aging of society. To date no effective preemptive medicine or treatment of severe influenza has been established. Influenza virus is a single stranded RNA virus, and transcription and replication of the virus genome occur in the nucleus. Since viral infection is generally associated with virus-driven hijack of the host cellular machineries, influenza virus may utilize and/or affect nuclear system. Recent high-resolution chromatin interaction maps using chromosome conformation capture (3C) techniques such as 4C and Hi-C have defined units of chromatin that are 3D, termed topologically associated domains (TADs). In the present study, using 4C-seq and ChIP-seq we examined how host chromatin 3D structure and epigenetic modification were changed to influenza virus infection, and how they were involved in the pathology of severe influenza. Our data suggest that host chromatin 3D dynamics could be a novel target of prevention and/or treatment for severe influenza virus infection.