Pattern-based differential sensing strategy for Avian influenza (AI) virus characterization

Jun-Seok Lee
Senior Research Scientist, Molecular Recognition Research Center, KIST, South Korea
junseoklee@kist.re.kr

Recently avian influenza (AI) emerged a serious pandemic disease since previously undescribed influenza A virus was identified in 2009. Influenza A viruses are divided into subtypes based on two surface proteins, hemagglutinin (HA, H1-H16) and neuraminidase (NA, N1-N9). Among those subtypes, some strains, such as H5 and H7 viruses, are categorized as highly pathogenic avian influenza (HPAI) viruses and cause high mortality. Due to their high pathogenicity, it causes huge economic losses in the poultry industry once it out-break. Particularly, H5 type HPAI viruses (firstly reported in Guangdong, China in 1996) have caused continuous outbreaks in East Asia in these days. Although stamping-out or vaccination strategies were actively implemented for rapid eradication of HPAI viruses as surveillance protocols, development of quick and accurate diagnostic methods have been highly demanded.

Differential sensing has become an important concept in the field of chemosensors, supramolecular chemistry, and phonemic profiling. Especially, inspired from early 1990's initiatives for drug screening against NCI-60 human tumor cell lines, phenotypic profiling approaches have been demonstrated its practical usage for identifications for cancer cell type, organ origin of cancer cells, bacterial strains. As an extend of previous works, we have applied pattern-based differential sensing approach for avian influenza (AI) virus. Influenza virus infects host cell by recognition of surface glycan structures, and their target species were determined depending on two factors: (i) the stereochemistry of sialic acid (SA)-galactose on host cell surface (e.g. α(2,3): avian, α(2,6): human), (ii) hemagglutinin sub-types of AI. We envisioned that infection efficiency profile against various mammalian cell lines could be an unique profiling parameter for AI subtype, and demonstrated proof-of-concept study in image-based screening platform. Some of mammalian cell lines exhibited notable infectivity preference to specific AI subtypes. Currently, we are further investigating mammalian cell surface glycan/glycoproteins to unveil molecular mechanism of AI infection.