Molecular basis on the sialyl-linkages recognition by human respiroviruses

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Human respiroviruses (parainfluenza virus type 1 and 3) are one of the most frequent pathogens for respiratory tract diseases. Human parainfluenza viruses (hPIVs) have two spike glycoproteins, hemagglutinin-neuraminidase (HN) and fusion (F) glycoprotein. hPIVs infection is initiated by binding of the HN glycoprotein to sialosugar chains. The receptor recognition of HN glycoprotein is suggested to be one of the factors associated with tissue tropism of hPIVs. We found that the sialyl-linkages recognition of human parainfluenza virus type 3 (hPIV-3) was different from that of human parainfluenza virus type 1 (hPIV-1). Concretely, hPIV-3 binds to both α2, 3- and α2, 6-linked sialosugar chains, but hPIV-1 binds to only α2, 3-linked sialosugar chains.

Amino acids contributing to sialyl-linkages recognition of hPIV-3 HN glycoprotein were estimated by comparison of amino acid residues within the receptor pocket of HN glycoproteins between hPIV-1 and hPIV-3. Then, we generated the expression plasmids containing wild type gene or mutanted genes of hPIV-3 HN glycoprotein. The sialyl-linkages recognition of HN glycoproteins expressed on the surface of COS7 were determined by hemadsorption assay. The hemadsorption activities of HN glycoproteins-expressed cells were quantified by the amount of hemoglobin in erythrocytes bound to the cells.

In this study, we suggested that two amino acid residues of hPIV-3 HN glycoprotein played an important role for the sialyl-linkages recognition of hPIVs.