

## ORAL PRESENTATION O3

### **Model of pentameric ion channel formed by transmembrane domain of small hydrophobic protein of human respiratory syncytial virus**

SiokWan Gan, Xin Lin, Jaume Torres

*School of Biological Sciences. Nanyang Technological University. Singapore*

The small hydrophobic (SH) protein is a transmembrane surface glycoprotein encoded by respiratory syncytial virus (RSV). It is ca. 64 amino acids long with one putative transmembrane domain. SH is important for viral infectivity but the mechanism is unknown. We have examined the secondary structure, orientation, oligomerization of the transmembrane domain of SH (SH-TM) in planar lipid bilayers to further understand functional significance of SH during HRSV infection. Two peptides correspond to the SH-TM were synthesized incorporating a labeled carbonyl ( $^{13}\text{C} = ^{18}\text{O}$ ) at two consecutive positions to obtain the orientation of SH-TM in the membrane. Investigation with polarized attenuated total reflection-Fourier transform infrared (PATR-FTIR) shows that the peptide is predominantly  $\alpha$ -helical with helix tilt of ca.  $21^\circ$ . Site-specific infrared dichroism (SSID) was applied to obtain the rotational orientation of SH-TM. The result is consistent with a left-handed pentameric model obtained from exhaustive molecular dynamics global search protocol using 13 homologous sequences of RSV. Perfluorooctanoate-polyacrylamide gel electrophoresis reveals that SH-TM is a homo-pentamer. These results suggest that SH-TM forms a pentameric  $\alpha$ -helical bundle with a central pore that could function as an ion channel. Conductance studies show that SH-TM has cation selectivity with a conductance of 35 pS and a reversal potential of -68 mV. Therefore, our results strongly suggest SH protein is a member of the viroporin family.