[PS2.35]

Golgi vesicle trafficking machinery is exploited by Chlamydia pathogen

Vladimir Lupashin*, Irina Pokrovskaya, Uma Nagarajan
University of Arkansas for Medical Sciences, United States

Chlamydia trachomatis is a major cause of pelvic inflammatory disease, ectopic pregnancy, and infertility among women; and also the leading cause of preventable blindness in the world. Gram negative *Chlamydia sp.* are obligate intracellular pathogens with a unique developmental cycle. Throughout their entire time in the host cell, chlamydiae remain within the confinements of the cytoplasmic membrane compartment termed inclusion, which very early during infection becomes fusiogenic with a subset of exocytic vesicles originating from the Golgi region.

To uncover the communication mechanism between the Chlamydia inclusion and the host cell Golgi apparatus we employed immunofluorescent confocal microscopy with the set of affinity purified antibodies to different components of Golgi trafficking machinery, which include vesicle coat proteins, Rabs, SNAREs, coiled-coil and oligomeric vesicle tethering factors. This approach allowed us to determine if the endogenous components of Golgi trafficking machinery are associated with Chlamydia inclusions. Our results indicated that COG8 subunit of the Conserved Oligomeric Golgi complex, Rab6 GTPase and v-SNARE GS15 are associated with *C. trachomatis* inclusion at the different stages in the infection cycle. Further, siRNA mediated knockdown of COG8, GS15 or Rab6 significantly affects infectious chlamydial yields.

Our approach allows discovering and validating new biomarkers for chlamydial infection and ultimately will lead to a better understanding of host-pathogen interaction. Targeting these interactions can lead to development of specific topical microbicides for both genital and ocular chlamydial infection.

Keywords: Chlamidya, inclusion, Golgi, vesicular trafficking