Pei Pei Chong, J Bacteriol Parasitol 2018, Volume 9
DOI: 10.4172/2155-9597-C1-045

Pei Pei Chong
Taylor's University, Malaysia

Omics approaches to dissect host-pathogen interaction in *Staphylococcus aureus* infections

Staphylococcus aureus causes both Hospital-Acquired (HA) and Community Acquired (CA) infections. This bacterial pathogen is associated with multiple infection types including Skin and Soft Tissue Infections (SSTIs), nosocomial pneumonia and sepsis. Varied virulence factors and drug resistance phenotypes are displayed by different sequence types of *S. aureus*, with the added complexity of colonizers versus strains which cause diverse infections. Therefore there is a need to employ new strategies to study and compare different infection types and varied strains to find efficacious therapeutic and diagnostic markers. We had previously employed proteomic approaches to profile the exoproteome of strains isolated from patients with bacteremia and SSTIs as well as from healthy carriers. Genomics approach was also used to compare the host immune responses from sera collected from these patients. Our findings did not reveal any protein from bacteremia isolates that were immunogenic, but we reported for the first time the antigenicity of MetAPs and Set15 in immunoblot assays of SSTI isolates. A diverse pattern of cytokines and chemokines expression was found in the bacteremia and SSTI patients. However, several chemokines such as MIG and IP-10 were highly expressed in bacteremia versus SSTI patients and healthy carriers. MIG expression was significantly high during the early phase of bacteremia, suggesting its potential use as a diagnostic marker. Recently, another group compared the exoproteome of CA- and HA-MRSA and found some exoproteins that were unique while the abundance of several common proteins varied among the groups. Further work is warranted to investigate the feasibility of using chemokines such as MIG either as a *S. aureus*-specific bacteremia diagnostic marker or a generic sepsis marker. Future directions should be focused on development of diagnostic tools that can distinguish between mere carrier and productive infection of *S. aureus*.

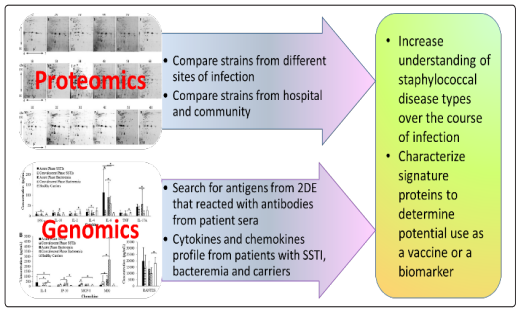

Figure-1: *Omics approaches for studying S. aureus infections.*

Recent Publications

1. Chin V K, Lee T Y, Rusliza B, Chong P P (2016) Dissecting Candida albicans Infection from the Perspective of *C. albicans* Virulence and Omics Approaches on Host-Pathogen Interaction: A Review. *International Journal of Molecular Sciences*; 17(10): E1643.
2. Liew Y K, Awang Hamat R, van Belkum A, Chong P P, Neela V (2015) Comparative Exoproteomics and Host Inflammatory Response in *Staphylococcus aureus* Skin and Soft Tissue Infections, Bacteremia, and Subclinical Colonization. *Clin Vaccine Immunol.*; 22(5): 593-603.

Biography

Pei Pei Chong is a Molecular Biologist with expertise in both infectious diseases and cancer biology. She has special interest in host-pathogen interaction particularly in candidiasis, HPV-associated pathologies, as well as drug resistance and strain typing in MRSA. She is fascinated by the vast repertoire of the Human Papillomaviruses (HPVs) and strongly feels that more studies need to be conducted to unravel at the molecular level, the strategies by which the virus adapts to different sites of infection and cause various diseases.

Peipei.Chong@taylors.edu.my