known about the specific membrane protein binding of actinoporins when attacking human cells. Therefore, a comprehensive proteomic analysis was performed using SILAC approach in conjunction with the combination of pull-down assay and shotgun mass spectrometry to identify protein(s) from mammalian HeLa cells that interact with HALT-1. As a result, a total of 21 putative mammalian proteins were identified for the first time. In bioinformatics analysis, 19 putative proteins were identified to play an important role in protein synthesis, glycolysis mechanism, cytoskeleton, cell proliferation and cell survival whereby any modification, activation or inactivation may lead to cell disruption and apoptosis. While the remaining putative proteins may play an important role in cellular defense and survival via the activation of the immune system and transportation of newly synthesized proteins. This study provides a preliminary screening of protein(s) interacting with HALT-1, and the protein-protein interaction could be a critical step in the cytolytic mechanism and hence triggering the response of host cell for cellular survival and defense.

**PP-15**

**The population structure of Salmonella Typhi is highly homogeneous: Evidence from MLST and Phylogenomic Analyses**

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Salmonella Typhi (S. Typhi), the etiologic agent of typhoid fever, has caused 21.7 million cases with 200,000 deaths annually worldwide. Multilocus sequence typing (MLST), a universal subtyping method has been used for many bacterial species but it is less discriminative for S. Typhi. Hence, a newer method, phylogenomic analyses that based on whole genome sequencing was further employed to investigate the population structure of S. Typhi. Here, we performed MLST on 19 S. Typhi strains from endemic localities of Malaysia, Chile and Papua New Guinea as well as in-silico MLST on 20 global S. Typhi strains using WGS data. The sequence types (STs) of the strains were determined and used for phylogenetic tree construction. Further, a high resolution phylogenomic tree was generated from the WGS to determine the genetic relatedness and population structure of the strains. We found only two STs (ST1 and ST2) in both local and global strains, further reiterates the genetic homogeneity of S. Typhi. The dn/dS ratio, Fu and Li’s test and Tajima neutrality analyses of the MLST found very little evidence of diversifying, neutral mutations or purifying selection. Recombination test showed no signals of loci recombination. Taken together, the S. Typhi demonstrated a high level of temporal stability with limited evidence of geographical structuring. The nsSNP analyses of the most diverse housekeeping gene (hemD) of S. Typhi revealed that the gene may potentially be applied for S. Typhi identification through gene sequencing. This was supported by the alignment of 333 hemD genes from Salmonella enterica spp.