00343 Combinatorial Bioinformatics Approach for High Definition Lipidomics of Pseudomonas Aeruginosa

Tan An Sen (1), See Ye King Clarence (2), Pandiyan P S (2), Lee Li Xian Megan (2), Lee Siwen Julianne (2), Guan Xue Li (2)

Singapore General Hospital (1), Nanyang Technological University (2)

Aims: Multidrug resistant Pseudomonas aeruginosa poses one of the greatest challenges to global public health today and there is an urgent need for new agents against similar panresistant organisms. Lipids have been found to serve key metabolic functions in bacteria and with significant alterations in bacterial lipid composition noted in antibiotic-resistant strains. As such, lipidomics is an emerging field that has shown immense promise to open novel avenues for new drug and biomarker discovery. However, to date an important limitation of this relatively new technique lies in that it currently lacks community-wide agreement concerning the best approach for accurate and comprehensive identification of lipids. Therefore, this first-of-its-kind study chiefly aims to address this research gap, potentially advancing the search for the optimal bioinformatics approach to perform lipidomics.

Methodology: We performed high definition characterization of P. aeruginosa strain PAO1 using time-offlight mass spectrometry (TOF-MS) with information dependent acquisition (IDA) and examined the relative performance of 6 popular bioinformatics approaches: Progenesis QI, Lipid View, Lipid Match, NIST MS Search, XCMS, as well as manual inspection for lipidomics compound discovery, comparing these in terms of accuracy, throughput, and coverage across 5 major phospholipids classes – phosphatidylglycerol (PG), phosphatidylethanolamine (PE), lyso-phosphatidylethanolamine (LPE), cardiolipin (CL) and phosphatidic acid (PA).

Result: In this novel study, we found remarkable differences in performance between the approaches with no approach demonstrating categorical superiority over others. The merging of unique identifications from all 6 tested bioinformatics approaches resulted in a total number of lipid identifications that was 85.9% more than, or almost double that of the number found by the single best approach.

Conclusion: We conclude that no single best approach presently exists and the integration of various approaches may be required for comprehensive lipidome characterization. Future work may include further validation in additional bacterial strains and species.