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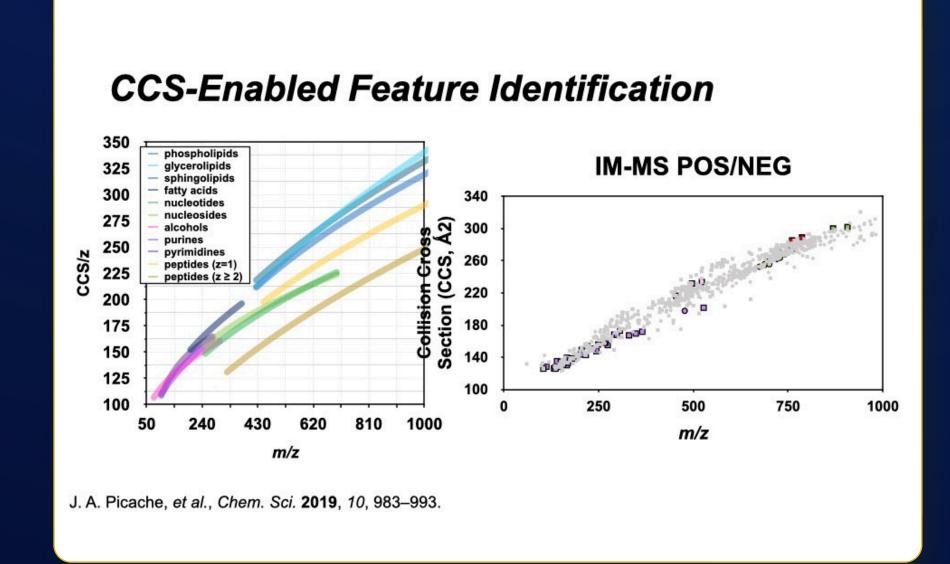
A multi-omics approach for microorganism identification using HILIC-IM-MS/MS

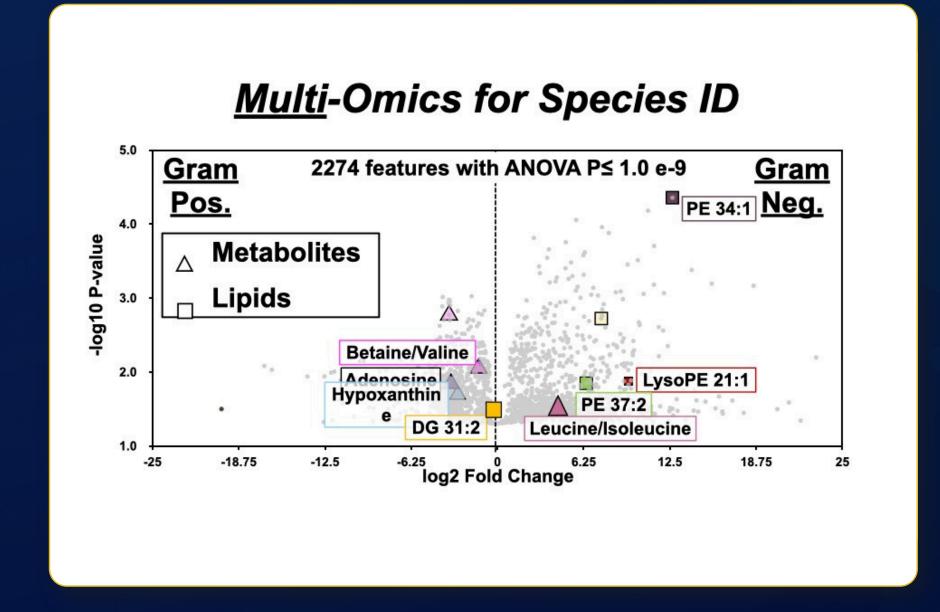
The emergence of multi-omics approaches has empowered scientists to answer complex systems biology questions. The genomic and proteomic information of *Staphylococcus aureus*, *Acinetobacter baumanii*, *Enterococcus faecium*, and *Pseudomonas aeruginosa*, has been thoroughly explored.

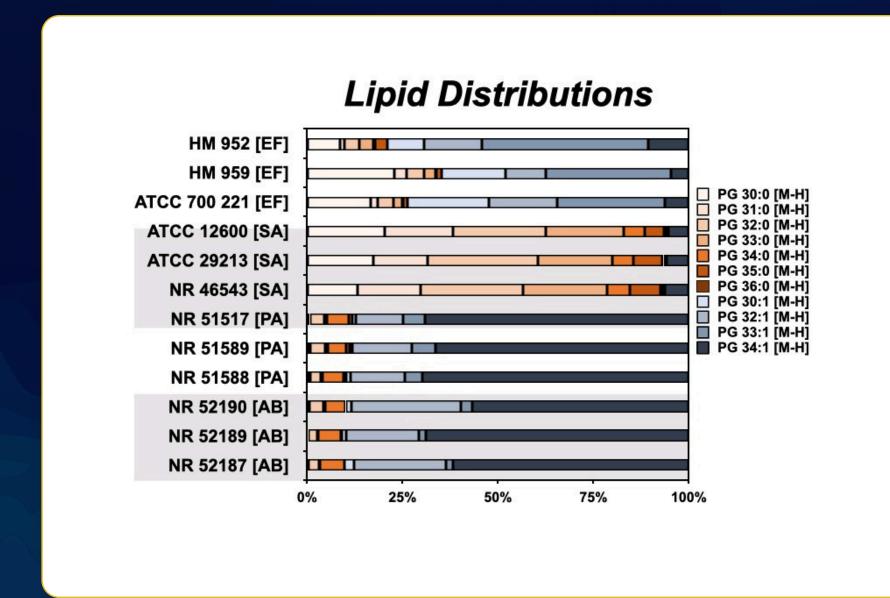
However, there remains a significant lack of knowledge of the downstream metabolomic and lipidomic profiles of these small organisms. Here, we have optimized a high throughput multi-omics approach that can isolate the constituent parts of the whole biological system that are not otherwise explained by the template-driven aspects of genomics and proteomics.

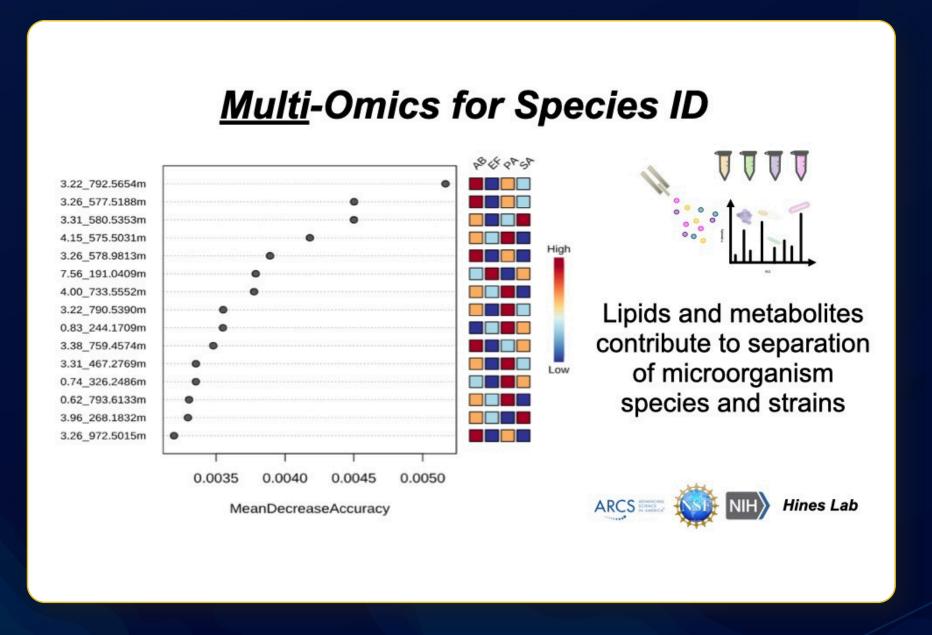
We showcase the potential for a streamlined method for managing multi-omics experiments of diverse microbe populations using an optimized workflow. We analyzed three different extraction methods for their abilities to simultaneously recover lipid and metabolites from Gram-positive and Gram-negative bacteria. Our findings indicate a new use for a well-organized extraction and quantification workflow for widespread applications within lipidomic and metabolomic endeavors in microbial research.

ESKAPE Pathogens Pose a Global Health Threat Enterococcus faecium Staphylococcus aureus Klebsiella pneumoniae Acinetobacter baumannii Pseudomonas aeruginosa Enterobacter spp.









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