



UNIVERSITY of CALIFORNIA, SAN DIEGO

SCHOOL OF MEDICINE

MASS SPECTROMETRY AND MICROBIOLOGY TOOL DEVELOPMENT

We focus on developing/testing mass spectrometry and microbiology tools to improve the study of the host-microbe interaction. One such tool, Biomimetic Virulomics, was pioneered by the Gonzalez lab and its further development was **awarded an NIH R21 (2020-2022 funding period)**. This tool allows for the capture and identification of cell-type specific effector proteins (*Lapek et al, ACS Nano 2017; Distler et al. 2017*). We have utilized this tool to study proteins of unknown function in the context of their host cell specificity in the top 10 human pathogen, Group A Streptococcus (*Weirzbicki and Campeau et al., Cell Reports 2019*).

More recently, we have started to develop protocols in the lab to perform deep and multi-omics layered clinical proteomics, which include posttranslational modification (PTM) analysis. Using these developing tools, we constructed an expansive resource of bacteremia prognostic biomarkers. Integrating contemporary proteomic and metabolomic techniques enabled the identification of > 10,000 features from > 200 serum samples collected upon clinical presentation. We interrogated the complexity of serum using multiple computational strategies, which provided a more comprehensive view of the early host response to infection. Notably, our biomarkers exceed the predictive capabilities of those previously reported, particularly when used in combination. Lastly, we validated the biological contribution of a subset of mortality-associated pathways using a murine model of bacteremia. Together, our findings represent a starting point for the development of a rapid prognostic test for identifying high-risk patients at a time early enough to trigger intensive monitoring and interventions. We have published this work (*Wozniak et al., Cell Sept. 2020*).

Looking forward, we plan to establish a robust single cell proteomics platform at UCSD to allow the research community to assess their biological systems in new and powerful manners. The single cell proteomics project has **received funding through the Chan-Zuckerberg Initiative (2020-2022 funding period)**.