Solving riddles in human pharmacology with single cell proteomics

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Human response to drug treatment is highly variable at the level of individual patient, organ, and cell type. For decades, molecular pharmacology has sought increasing granularity to better understand heterogeneity in drug response at all these levels. Single cell proteomics promises absolute granularity by measuring phenotypic response at the smallest complete unit of human biology. In this talk I will describe our progress toward developing high throughput single cell proteomics approaches to address the most pressing challenges in human pharmacology today. One early success has been in identifying response markers that appears meaningful when thousands of cancer cells are homogenized for analysis that we find are driven by just a few cells making dramatic, but ultimately unsuccessful, efforts to survive treatment. While many challenges exist in this newly emerging field, these results hint that the possible applications of single cell proteomics may include helping to refine choices for combinatorial drug therapies in the clinic.

Ben Orsburn has made a career of developing new mass spectrometry methods to address biological problems. A dozen years in industry positions landed him in well over 150 labs around the world helping other scientists meet their goals with their LCMS systems. He is best known for attempting to make today's newest proteomic advances approachable through the blog "News in Proteomics Research." He recently returned to academic research as a member of the faculty at the Johns Hopkins Medical School, in the Department of Pharmacology and Molecular Sciences. His research is primarily focused on the use of single cell proteomics to study the mechanisms of action, toxicity, and development of resistance to drugs in human systems.