Department of Chemical Engineering Seminar Series

From Yeast to Man: Systems Analyses Advance Therapeutic Development & Drug Discovery in Complex Diseases



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Abstract

Current challenges in therapeutic development, biopharmaceutical production, and limitations of human disease models motivate our pursuit to understand how cellular processes and molecular interactions perform under systemic perturbations. Systems biology approaches - with their integration of computational, experimental, and observational inquiries - guide the rigorous assessment of regulation at multiple scales. We employ a systems-level understanding to characterize biological networks underlying complex cell behavior including (i) cell stress response pathways of a single-cell organism such as yeast, and (ii) communication networks within 3-D tissues that recapitulate human physiology and disease progression. As arguably the most well-characterized cellular response promoting homeostasis, the Unfolded Protein Response (UPR) is defined by a coordinated program of transcription that up-regulates genes within the early secretory pathway. In contrast to this classical description, our investigations in S. cerevisiae further indicate that an extensive program of global repression exists, highly enriched in protein synthesis and metabolic functions. DNA recombination strategies combined with high-resolution imaging techniques determined that protein redistribution, resultant spatial effects, and organelle modifications are diverse consequences of UPR activation. The elucidation of these pathways has become of growing importance in therapeutic development, as the UPR has been intimately linked to Alzheimer's disease, Parkinson's disease, diabetes, cancer, and inflammation. Clearly, the complexity of human physiology must be assessed in a more complex environment that accounts for interacting cell types coexisting in a hierarchical 3-D structure. The emergence of organ-on-a-chip microfabricated devices facilitates the study of human physiology in vitro, enabling the development and validation of predictive models in drug discovery. The integration of tissue engineering, primary cell sources, emerging biomaterial strategies, and computational models promoted novel experiments to investigate breast cancer metastasis. As a result, we have identified plausible signatures of human-specific cross-talk between the tumor and hepatic tissues. Ultimately, these results will directly impact clinical prognosis of early metastatic disease while improving drug efficacy and toxicity models of chemotherapies.

Speaker Biography

Carissa Young is a postdoctoral associate at MIT in the Department of Biological Engineering leading integrated systems approaches in biomarker discovery of breast cancer metastasis, liver and lung inflammation. She earned her PhD in Chemical and Biomolecular Engineering at the University of Delaware in 2012 with an emphasis in cellular and protein engineering, and a BS in Chemical Engineering from Georgia Tech in 2002. Carissa has 19 publications in the field of biotechnology and is the recipient of a NIH Development award, NSF ADVANCE award, Recombinant DNA Technology award, and Academic and Civic Excellence award. Notably, Carissa has held six teaching appointments in academia and worked within the pharmaceutical industry.

