UNIVERSITY OF DELAWARE
ENGINEERING
DEPARTMENT OF CHEMICAL & BIOMOLECULAR ENGINEERING

DEPARTMENTAL SEMINAR

MARK BLENNER

McQueen-Quattlebaum Associate Professor

Clemson University

Friday | March 6, 2020 | 9:00 AM

102 Colburn Lab

Dr. Blenner is the McQueen Quattlebaum Associate Professor of Chemical and Biomolecular Engineering at Clemson University, and Director of the Molecular Engineering for Sustainability and Health GAANN. He received his PhD in Chemical Engineering from Columbia University in 2009 and completed three years of postdoctoral training as an American Heart Association Postdoctoral Fellow and an NIH NRSA Postdoctoral Fellow at Harvard Medical School and Children's Hospital Boston. Dr. Blenner has won Presidential Early Career Award for Scientists and Engineers (PECASE), the 2019 Clemson University Junior Researcher of the Year, the NIH Outstanding Investigator Award, the Dean's Professorship Award, the Air Force Office of Scientific Research Young Investigator Award, and the NASA Early Career Faculty Award. His research is broadly focused on engineering biomolecular and cellular systems for the production of fuels, chemicals, enzymes, biopharmaceuticals and biosensors. Recently his group has started to focus on understanding and leveraging cellular stress response for diagnosing problems and improving bioproduction platforms and as biosensors.

TAPPING INTO THE POTENTIAL FOR BIOCHEMICAL PRODUCTION USING NON-CONVENTIONAL YEAST

Biochemical production has been practiced for centuries; however recent advances in genomics and synthetic biology have enabled exploitation of a wide array of microbes engineered to produce an unprecedented number of molecules with greater than natural efficiency. Specifically, these advances are enabled by an increasing catalog of biocatalysts (microorganisms) with properties well suited for production of certain classes of products. The engineering challenge is to improve these biocatalysts to perform non-native reactions and to increase productivities and yields to levels of economic viability. Since these biocatalysts are produced by the genes encoded in microbial genomes, genetic engineering tools and a better understanding of genetics and cellular metabolism are needed. Until recently, our group has mainly focused on oleaginous yeast – that use a variety of feedstocks and are able to naturally accumulate a large amount of lipids. This seminar describes our development of genetic engineering tools for Yarrowia lipolytica and their application to better understanding and engineering of cellular metabolism. We have built synthetic promoters that control both the strength and the dynamics of gene transcription. To increase the speed of strain engineering, we developed a CRISPR-Cas9 system for efficient genome editing, compatible standard integration sites were identified, and a novel form of targeted integration was developed. Using these tools, we've elucidated a cryptic xylose metabolism pathway. More recently established pathways to produce oleochemicals by taking advantage of naturally high flux pathways and improving titer and specificity by controlling the cell physiology. Finally, we have started applying these tools to improve production of secondary metabolites that draw on the same high flux precursors.