ACS SyntheticBiology
Introducing Our Authors
pubs.acs.org/synthbio

DAPHNE CHE

Dung Lan Che

Current position. Associate at Montage Ventures.

Education. Ph.D. Chemistry, Stanford University (2015). Advisor: Bianxiao Cui; B.S. Chemistry, University of California, Berkeley (2008).

Nonscientific Interests. Technology, travel, and cooking.

My Ph.D. work focused on utilizing neuronal microfluidic platform and fluorescence microscopy to decipher the underlying mechanism of axonal transport in neurons, and characterizing the dual characteristics of the light-sensitive CRY2-CIB1 protein pair. CRY2-CIB1 is a powerful and popular optogenetic protein pair that allows light-inducible manipulation of various signaling pathways and cellular processes in living cells. Under blue light, CRY2 can both undergo the homo-oligomerization process (CRY2-CRY2) and the heterodimerization process with CIB1 (CRY2-CIB1), leading to complex protein interaction. My article in this issue described a quantitative characterization of how the two light-dependent responses of CRY2 interact with each other under blue light. This result can be used as a guide to establish new optogenetic strategies to probe cellular processes in a more controlled manner. (Read Che's article; DOI: 10.1021/acssynbio.5b00048.)

LITING DUAN

Liting Duan

Current position. Ph.D. candidate, Department of Chemistry, Stanford University. Advisor: Dr. Bianxiao Cui.

Education. B.S. in chemistry, Renmin University of China.

Nonscientific Interests. Music, movies, ceramics, and traveling around.

I am interested in developing optogenetic strategies that enable optical control of various intracellular activities, including molecular motors recruitment, organelle transport, and signaling pathways. Compared with traditional methods, optogenetic methods are noninvasive, fast, reversible, and able to achieve precise spatiotemporal control. Therefore, optogenetic methods can be very helpful and powerful for researchers to disentangle many problems that have been difficult to solve with traditional ways. CRY2/CIB1 pair is one of the most popular light-inducible dimerizers currently available. In this work, we systematically examined the dual characteristics of CRY2/CIB1, homo-oligomerization, and heterodimerization, which contributes to a better understanding of CRY2/CIB1. Looking forward, I hope to continue to investigate in CRY2/CIB1 dimerization and develop more optogenetic stragegies to control cellular processes. (Read Duan's article; DOI: 10.1021/acssynbio.5b00048).

ANNA PAYNE-TOBIN JOST

Adam Jost

Current position. Advanced microscopy postdoctoral fellow, Nikon Imaging Center at Harvard Medical School. Advisor: Jennifer Waters.

Education. Ph.D., cell biology, University of California San Fransicso. Advisor: Orion Weiner. B.A., biology, Vassar College.

Nonscientific Interests. Running long distances in beautiful places, honing my pizza-making skills, tasting new beers, hanging out with my cat.

I spent most of my Ph.D. working on the Phytochrome/Pif optogenetic system in yeast. This paper presents an application of the system that is a reversal of the way our lab has used it in the past, inactivating proteins by mislocalization rather than activating them via recruitment to the membrane. Using the system in this way, we were able to ask questions about cell polarity that had been impossible with previous techniques. We also found a really cool phenotype that we did not expect—greatly enlarged yeast cells—which can be a nice tool in its own way, enabling experiments on size scaling. We have only scratched the surface of what is possible with these techniques and I am hoping they will enable lots of other

Received: September 30, 2015
Published: October 16, 2015

DOI: 10.1021/acssynbio.5b00184
ACS Synth. Biol. 2015, 4, 1049−1052

discoveries. This project also reinforced my love of microscopy, which I have now turned into a full-time job as a postdoctoral fellow in the Nikon Imaging Center at Harvard Medical School. At the NIC, I am learning as much as I can about microscopes of all kinds, developing protocols for microscope quality control and trouble-shooting, and teaching in microscopy workshops and courses. (Read Jost's article; DOI: 10.1021/acssynbio.5b00053).

KORBINIAN KAPSNER

Korbinian Kapsner

Current position. Postdoctoral researcher, Physics Department, TU München, Munich, Germany.

Education. Ph.D. Physics, TU München. Advisor: Friedrich Simmel (2014); Diploma, Physics, TU München (2010).

Nonscientific Interests. In my nonscientific time I like to make music and to play board games.

Scientifically, I am interested in using microcompartmentalized reaction volumes to study the stochastic diversity in synthetic biological systems. To be able to investigate the behavior of every volume separately I developed software tools to serve the needs of my experiments. In this paper we show that apparently simple transcription reactions can show quite a diverse behavior in small reaction containers. By investigating the diversity in a population of thousands of droplets we were able to show that the reaction dynamics and its dependence on the concentration ratios cannot be explained by the statistical distribution of the molecules into the compartments alone. Especially the increase of the Fano factor with concentration requires interpretation. Probably additional physical-chemical effects take place during partitioning; we speculate that proteins may cluster during the creation of the microcompartments. (Read Kapsner's article; DOI: 10.1021/acssynbio.5b00051.)

LAURA MARTINI

Sheref Mansy

Current position. Laboratory Technician at Techno Analisys S.r.l, San Felice, Modena, Italy.

Education. Ph.D., Biomolecular Sciences, University of Trento, Italy (2015). Advisor: Sheref S. Mansy. M.S., Industrial Biotechnology, University of Modena and Reggio Emilia (2009).

Nonscientific Interests. I like outdoor activities, swing and lindy hop dancing.

My research focus is on building cellular mimics that sense and respond to the environment. Here we developed a purely *in vitro* selection method based on strand displacement to identify ligand responsive RNA sensors. The RNA library was based on a previously selected riboswitch that was responsive to thiamine pyrophosphate. Three rounds of selection allowed for the identification of a new RNA sensor with improved strand displacement ability that also retained riboswitch activity. The described methodology should be applicable to the development of new regulatory genetic elements that are responsive to small molecules. (Read Martini's article; DOI: 10.1021/acssynbio.5b00054.)

ADAM MEYER

Adam Meyer

Current position. Postdoctoral fellow, Voigt lab, MIT.

Education. UT Austin Ellington Lab. UC Berkeley.

Nonscientific Interests. If I'm not sciencing, I'm probably enjoying friends, family, baseball, history, and puns.

This work is part of an ongoing effort to enable the precise control of gene expression. Controlling complex genetic systems requires the development of compatible parts that behave optimally and predictably. When a protein with ideal properties cannot be found in nature, it is necessary to make it. This requires the efficient exploration of protein sequence and fitness landscapes in order to uncover the genotype that gives the desired phenotype. (Read Meyer's article; DOI: 10.1021/sb500299c.)

ALEXANDER PROKUP

Alexander Prokup

DOI: 10.1021/acssynbio.5b00184
ACS Synth. Biol. 2015, 4, 1049−1052

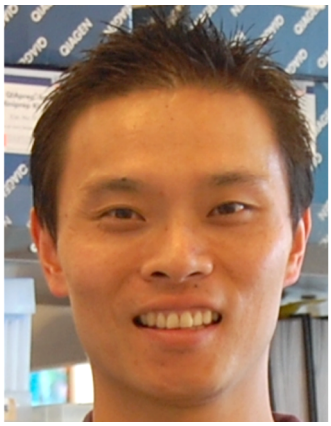
Current position. Ph.D. Graduate.

Education. Ph.D. in Chemistry at the University of Pittsburgh, B.S. Chemical Engineering at the University of Illinois Urbana−Champaign.

Nonscientific Interests. Music, hiking, camping, playing sports.

My graduate research included developing new DNA computation devices and modifying proteins with unnatural amino acids. Proteins engineered with genetically encoded with unnatural amino acids were used to investigate abasic site bypass in DNA polymerization, conduct bioconjugation reactions, and used to cross-link RNA oligonucleotides. The DNA computation devices developed by me were designed to be activated in response to different wavelengths of light as well as to directly trigger protein function. In this publication, two DNA-based signal amplification cycles were placed under optical control by modifying a single oligonucleotide with photochemical caging groups. These caging groups enabled precise ON or OFF light-switching of the cycles as well as unprecendented spatiotemporal control of DNA signal amplification. In the future, I hope to continue researching and developing chemical biology tools for biological engineering applications. (Read Prokup's article; DOI: 10.1021/sb500279w.)

STEVE SHIH



Steve Shih

Current position. Postdoctoral Scientist at the Joint BioEnergy Institute—JBEI. Advisors: Dr. Nathan Hillson and Dr. Anup Singh (will be an Assistant Professor at Concordia University in Montreal, Canada starting Jan. 2016).

Education. Ph.D in Biomedical Engineering at the University of Toronto (Advisor: Dr. Aaron Wheeler); M.Sc in Chemistry at the University of Ottawa (Advisor: Dr. Natalie Goto); B.ASc in Electrical Engineering at the University of Toronto.

Nonscientific Interests. Sports, hiking, travel, running after my toddler son.

I am interested in miniaturization. During my masters, I was constantly working at the bench−purifying proteins, transforming bacteria, and analyzing growth−the pipet was glued to my hand! Ever since, I wondered if there are easier and more efficient means of doing science. I found the answer during my Ph.D where I learned new methods for automating biology using digital microfluidics. This led me to pursue new applications for microfluidics, namely, synthetic biology. This paper represents the first microfluidic device capable of automating DNA assembly and transformation (with only a few pipet steps!). We demonstrate the utility of this method by assembling two combinatorial libraries of 16 plasmids that are transformed into bacteria or yeast. This is the first step to automate steps for synthetic biology, and I look forward to developing more novel microfluidic devices for synthetic biology in the future. (Read Shih's article; DOI: 10.1021/acssynbio.5b00062.)

FRIEDRICH SIMMEL

Friedrich Simmel

Current position. Professor, Physics Department, TU München, Munich, Germany.

Education. Diploma (1996) and Ph.D. (1999) in Physics, LMU München.

Nonscientific Interests. Playing with my children; environment and sustainability; literature about everything; alternative music.

My main research interest is the study and understanding of self-assembly and self-organization phenomena in biomolecular and biological systems, and their utilization for nanotechnology and synthetic biology. I particularly like interdisciplinary research somewhere between physics, chemistry, and biology, which is driven by theoretical concepts and ideas. My group traditionally is devoted to the development of biomolecular nanostructures and devices (mainly from DNA and RNA). Here we currently work on the integration of biological and synthetic components with structural, mechanical, and computational function into more complex systems, i.e., nanorobotic and artificial cellular systems. A major fraction of my group is now moving toward synthetic biology. Here we are interested in the biophysical and engineering aspects of synthetic biology, and also its interface with bionanotechnology. (Read Simmel's article; DOI: 10.1021/acssynbio.5b00051.)

GUOQIANG ZHANG

Qinhong Wang

Current position. Postdoctoral Research Scholar, BioTechnology Institute, University of Minnesota. Advisor: Prof. Claudia Schmidt-Dannert.

DOI: 10.1021/acssynbio.5b00184
ACS Synth. Biol. 2015, 4, 1049−1052

Education. Ph.D. Biochemistry and Molecular Biology, Tianjin Institute of Industrial Biotechnology, Chinese Academy of Sciences (2015) Advisor: Prof. Qinhong Wang. M.S. Microbiology, Henan Agricultural University, China (2011) Advisor: Prof. Liangwei Liu. B.S. Biotechnology, Shandong University, China (2008).

Nonscientific Interests. Sports and travel.

The ability to quickly generate mutations is essential in microbial evolution for improving phenotype. Although many methods have been applied for introducing mutations and modifying microbial genomes, few methods for simultaneously and massively generating multiple defined mutations and modifications are available. Transcription activator-like effector nucleases (TALENs) enable the generation of double strand break and then integrate site-specific editing into genome. TALENs have been exploited for single gene editing, but have not been used previously for multiplex editing to accelerate genome evolution and improve cellular phenotypes. Here, we describe TALENs-assisted multiplex editing and demonstrate the ability of this method for accelerating genome evolution and improving cellular phenotypes in *Sacchoromyces cerevisiae*. This method should be broadly applicable for biological and biotechnological studies. (Read Zhang's article; DOI: 10.1021/acssynbio.5b00074.)

DOI: 10.1021/acssynbio.5b00184
ACS Synth. Biol. 2015, 4, 1049−1052