ACS SyntheticBiology

Introducing Our Authors

pubs.acs.org/synthbio

ERIC ARCHER

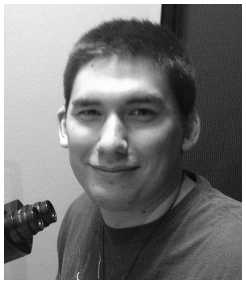

Image courtesy of Tolga Cagatay.

Current position: Ph.D. student in the lab of Dr. Gürol Süel at The University of Texas Southwestern Medical Center, Dallas, TX

Education: B.S. in Biology, New Mexico State University; advisor: Dr. Graciela Unguez

Nonscientific interests: Knife-making, gun collecting, Pekiti-Tirsia Kali, Shorin Ryu Karate, reading science fiction, and studying politics

My research explores the possibility of using bacteria in medicine as biological sensors of inflammation. The motivation for this project is the eventual construction of an engineered organism that detects and treats inflammation in inflammatory bowel disease. I made use of the *E. coli* nitric oxide sensor NorR to detect the upregulation of inducible nitric oxide synthase (iNOS) in inflamed gut epithelial cells. Upon the detection of nitric oxide, my engineered *E. coli* strain activates a DNA recombinase switch, permanently reorienting a constitutive promoter and altering the expression of fluorescent reporters. In the future, this strain will be used as the foundation for further work to construct a bacterial device capable of sensing active inflammatory bowel disease in patients and responding by producing anti-inflammatory molecules directly within the gut lumen. (Read Archer's article; DOI: 10.1021/sb3000595)

TAL DANINO

Image courtesy of Tal Danino.

Current position: Postdoctoral scientist at the Koch Institute for Integrative Cancer Research, Massachusetts Institute of Technology, Cambridge, MA; advisor: Dr. Sangeeta Bhatia

Education: Ph.D. in Bioengineering from the University of California, San Diego; advisor: Dr. Jeff Hasty. B.S. in Physics, Chemistry, Math from the University of California, Los Angeles

Nonscientific interests: Painting, videography, and traveling

My research is focused on the design of engineered bacteria in the context of applications such as energy and medicine. Utilizing techniques from synthetic biology, we develop the design criteria for genetic circuits and bacterial functions directly tied to the application. This provides insight for further design and allows for improvement of existing technologies. The manuscript in this issue focuses on cancer drug delivery and highlights how bacteria can be designed as transient drug-delivery systems for cancer therapy. With the use of time-lapse imaging and mathematical modeling of bacteria in tumor environments, we characterize how the dynamics of population growth and plasmid-loss can be engineered to create different drug release profiles. (Read Danino's article; DOI: 10.1021/sb3000639)

TRUONG D. NGUYEN-HUU

Image courtesy of Dan Duong.

Current position: Ph.D. student in the lab of Dr. Matthew Bennett at the Department of Biochemistry and Cell Biology, Rice University, Houston, TX

Education: M.Sc., Master of Biotechnology at the University of Queensland, Australia, 2009; advisor: Dr. Fred Meunier. B.Eng. in Biotechnology at Nong Lam University, Vietnam, 2005; advisors: Dr. Don D. Le and Thuy T. Nguyen.

Nonscientific interests: Reading, traveling, and spending time with my family

My graduate research focuses on how gene networks allow cells to respond to changes in environmental conditions. In *S. cerevisiae*, activity of the galactose-metabolic pathway (the GAL network) allows yeast cells to metabolize galactose in the absence of glucose. However, this network is strictly repressed when both glucose and galactose are available in the environment. Thus, the network is only activated when glucose is depleted from the environment. Using a custom-made microfluidic device, I investigate how different rates of glucose depletion affect the induction of the GAL network. Our goal is to understand how the dynamics of environmental factors determine the phenotypic outcome at both the single cell and population levels. (Read Nguyen-Huu's article; DOI: 10.1021/sb3000589)

Received: September 24, 2012
Published: October 19, 2012

ROBERT PENCHOVSKY

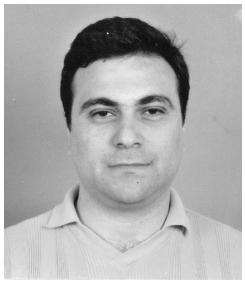

Image courtesy of Robert Penchovsky.

Current position: Assistant Professor of Genetics at the Faculty of Biology, Sofia University, "St. Kliment Ohridski" in Bulgaria

Education: Postdoctoral Researcher at Yale University, New Haven, CT; advisor: Ronald R. Breaker. Ph.D. in Genetics, University of Cologne, Germany in the laboratory of John S. McCaskill at the former National Institute of Germany for Mathematics and Informatics (*Gesellschaft für Mathematik and Datenverarbeitung* mbH - GMD), later part of Fraunhofer-Gesellschaft (FhG), at Schloss Birlinghoven, Sankt Augustin, Germany. M.Sc. in Biochemistry and Microbiology with specialization of genetics and an Associate degree in applied computer sciences from Sofia University, "St. Kliment Ohridski", Bulgaria

Nonscientific interests: Playing chess and tennis, swimming, boxing, cycling and many other sports. I am a fan of F1 motor racing and also like to watch so-called independent films from USA, Germany, Bulgaria, and Russia in their native languages

RNA is a unique biopolymer because it plays very diverse roles in nature. RNA is much more than a messenger between genomic DNA and proteins; it is also a powerful catalytic biopolymer that is directly responsible for the peptide bond formation during protein synthesis in the most advanced cellular machine, the ribosome. These findings inspired us to engineer functional RNA assemblies. We use computational modeling of secondary RNA structures to design catalytic RNAs that can sense the length of their substrate molecules and response to specific nucleic acid sequences. As a result, we have built multiple RNA assemblies with the functionality of integrated digital circuits. Our findings demonstrate that research within the framework of RNA synthetic biology can be used to build *de novo* complex molecular machines. (Read Penchovsky's article; DOI: 10.1021/sb300053s)

ARTHUR PRINDLE

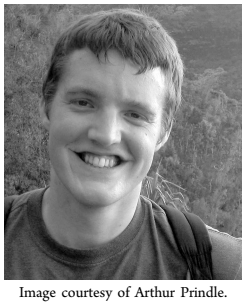

Image courtesy of Arthur Prindle.

Current position: Ph.D. student at the University of California, San Diego. Advisor: Jeff Hasty

Education: B.S. in Chemical Engineering, Caltech, Pasadena, CA

Nonscientific interests: Keeping my wife happy, playing with our parrotlet Widget

For me, bacteria are the ideal platform for exploring and engineering biology. They are small, extremely hardy, inexpensive to maintain, reproduce quickly, and comprise a vast array of species with unique properties. The majority of synthetic biology efforts have utilized *E. coli* out of tradition, ease of genetic manipulation, and a prevalence of available tools and methods. A next generation of *integrated* synthetic biology will utilize the native networks of diverse microbial species in concert with engineered gene circuits. Achieving this vision will require the development of microbial "shopping catalogues" complete with strain-specific pros, cons, and lists of parameters that define their circuit compatibility. And, of course, a willingness to accept that most will not work as intended the first time. (Read Prindle's article; DOI: 10.1021/sb300060e)

ARUN STEPHEN RAJKUMAR

Image courtesy of Henrike Niederholtmeyer.

Current position: Ph.D. student in the Laboratory of Biological Network Characterization, Institute of Bioengineering, École Polytechnique Fédérale de Lausanne, Switzerland; advisor: Prof. Sebastian J. Maerkl

Education: M.S. (by research) in Biophysics from Anna University, Chennai, India

Nonscientific interests: Literature, scale modeling, and popular science

My research focuses on studying transcriptional regulation through synthetic biology. The work involved is a hybrid and collaborative endeavor involving standard molecular cloning, synthetic biology, microfluidics and mathematical modeling. The published article describes some of the groundwork required. I want to understand how eukaryotic promoters are designed, and have been doing so by synthesizing variants of a known promoter and inferring the role of each regulatory element in the promoter of interest from observed changes in regulatory function. I hope to understand how regulatory elements which can be studied *in vitro*, such as transcription factor binding sites or nucleosome-disfavoring sequences, are integrated into promoters *in vivo*, ultimately providing us with "rules" of promoter construction and culminating in robust, quantitative models of transcriptional regulation. (Read Rajkumar's aticle; DOI: 10.1021/sb300045j)

CALVIN SCHMIDT

Current position: Undergraduate student at Rice University, Houston, TX, majoring in Biochemistry and Cell Biology; advisor: Dr. Matthew Bennett

Education: J.K. Mullen High School, Denver, Colorado

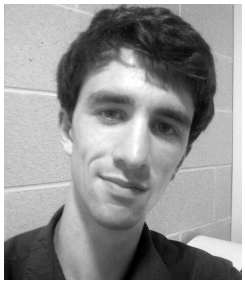

Image courtesy of Calvin Schmidt.

Nonscientific interests: Cycling, basketball, technology, entrepreneurship, finance

I am interested in making synthetic biology and genetic modification simpler for researchers and industry. This field will be coming into its own as our understanding of genetics matures. The ability to customize what cells produce will lead to transformations in the fields of medicine and biofuels production, making the manufacturing process more efficient. In this paper we detail a genetic circuit that will make working with multiple plasmids easier by reducing the number of antibiotics needed for plasmid maintenance. This will allow multiplasmid networks to be used in batch reactors without the expense of extra antibiotics. This will be needed as genetic circuits grow larger and more complex. My current work is focused on developing circuits that function across organisms. (Read Schmidt's article; DOI: 10.1021/sb3000589)

■ DAVID SHIS

Image courtesy of Faiza Hussain.

Current position: Ph.D. Candidate in the Department of Biochemistry and Cell Biology at Rice University in Houston, TX; advisor: Dr. Matthew Bennett

Education: Bachelors of Science in Bioengineering, University of California, Berkeley

Nonscientific interests: Ballroom dancing, running, swimming, and cooking

My graduate research is focused on the development of scalable synthetic gene networks. While the ability to construct synthetic genetic systems has improved dramatically, the ability to implement high order synthetic genetic circuits remains impaired. Multiplasmid systems require the use of multiple selectable markers, which can impose a large metabolic burden on the host. By utilizing split selectable marker in an expression system that works in trans, it becomes possible to select for multiple plasmids with one selectable marker. This reduces the metabolic load and complexity of multiplasmid systems. This will simplify the implementation of high order synthetic gene circuits as researchers develop larger and more complex synthetic gene networks for applications in bioengineering and synthetic biology. (Read Shis' article; DOI: 10.1021/sb3000589)