ACS SyntheticBiology
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RYAN E. COBB

Sun Min Kim

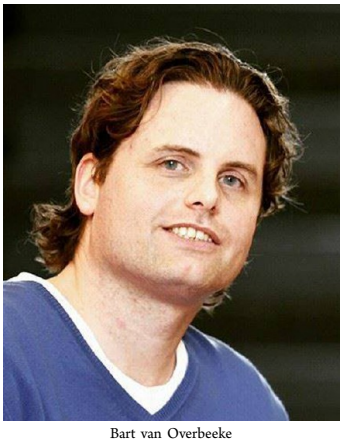
Current Position. Senior Metabolic Engineer, Dow AgroSciences, Indianapolis, IN.

Education. Ph.D. Chemical Engineering, University of Illinois at Urbana−Champaign, Urbana, IL (2015). Advisor: Huimin Zhao. B.S. Chemical Engineering, The Ohio State University, Columbus, OH (2008).

Nonscientific Interests. Baking; hiking; classic films; music; exploring new restaurants.

Streptomyces are fascinatingly complex bacteria that have contributed immeasurably to human health and well-being. Encoded in their genomes are the blueprints for a wealth of chemically diverse natural products with a wide range of interesting and useful bioactivities. The traditional tools to read and write these blueprints, however, often require a significant investment of time and labor, limiting the scope of genetic manipulations that can be performed. In this paper, we sought to bring *Streptomyces* genetics into the modern era by adapting the versatile CRISPR/Cas9 system of genome engineering to *Streptomyces* hosts. We demonstrate that high efficiency genome editing can be performed in three *Streptomyces* species using a single customizable basis plasmid. Moving forward, we envision numerous applications for this tool in both homologous and heterologous strain engineering. (Read Cobb's article; DOI: 10.1021/sb500351f).

TOM DE GREEF



Bart van Overbeeke

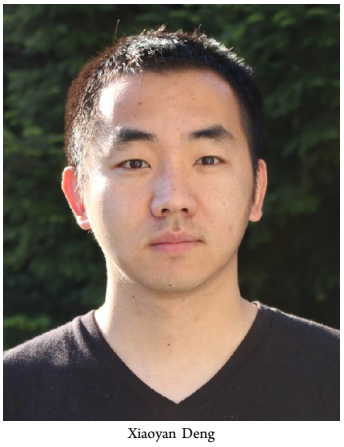
Current Position. Assistant Professor, Department of Biomedical Engineering, Eindhoven University of Technology, Netherlands.

Education. Visiting scholar, Harvard School of Engineering and Applied Sciences, Harvard, USA. Advisor: D. Weitz; Ph.D. in Chemistry, Eindhoven University of Technology, Netherlands. Advisors: E. W. Meijer and R. P. Sijbesma; B.S. in Biomedical Engineering, Eindhoven University of Technology, Netherlands.

Nonscientific Interests. I enjoy cycling, reading fantasy books and popular scientific literature, watching soccer games with friends and spending time with my (growing) family.

Our research is focused on understanding the molecular logic and design principles of regulatory networks in the living cell trough a bottom-up, *in vitro* synthetic biology approach. By combining modular biochemical systems with microfluidics and computational approaches our goal is to engineer a wide variety of dissipative biochemical reaction networks (BRNs) that display higher-order regulatory behavior. In addition, we also explore diagnostic and medical applications of these programmable biomolecular systems. Given the enormous computational power of cellular signaling pathways, I believe that progress in information processing biochemical networks will fundamentally change the biomedical sciences. (Read de Greef's article; DOI: 10.1021/sb500300d).

YI-LING DU



Xiaoyan Deng

Current Position. Michael Smith Foundation for Health Research Postdoctoral Fellow, Department of Chemistry, University of British Columbia. Advisor: Katherine S. Ryan.

Education. Ph.D. Biochemistry and Molecular Biology, Zhejiang University, China (2011). Advisor: Yong-Quan Li. B.S. Biotechnology, Zhejiang University, China (2006).

Nonscientific Interests. Traveling, hiking, sports.

I am interested in understanding the biology and chemistry of microbial secondary metabolism, and the application of the above knowledge for metabolic engineering and synthetic biology studies. The biosynthetic pathways of microbial natural products are shaped by long evolutionary processes. Dissection of

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biosynthetic pathways sharing the same ancestor has given insights into the naturally occurring modes of structural diversification, and provided a molecular toolbox for genetic manipulation. In this work, we artificially accelerate the evolution of bisindole biosynthesis by mixing and matching components from different bisindole biosynthetic pathways. This work not only generates a series of novel biologically active compounds, but also gives information about the substrate specificities of a number of enzymes. (Read Du's article; DOI: 10.1021/sb5003218).

RACHIT JAIN

Rachit Jain

Current Position. Advisor for iGEM activities at University of Georgia.

Education. Ph.D. Biological and Agricultural Engineering, University of Georgia, Athens, GA, USA (2015). Advisor: Dr. Yajun Yan; B.S. Biotechnology (2009) Visvesvaraya Technological University, Dharwad, India.

Nonscientific Interests. Swimming, tennis, poetry writing, cooking, travel.

My doctoral research encompassed using metabolic and protein engineering tools to establish efficient biological platforms for the production of chemicals. These chemicals are generally produced *via* processes that are harmful to the environment. By engineering *Escherichia coli*, my research has provided an alternative platform for the manufacture of 1,2-propanediol, 1-propanol using simple carbon sources such as glucose. The establishment of efficient biological processes often requires manipulations of cell's metabolism as well as engineering protein activity. My current interests lie in developing technologies with this outlook. (Read Jain's article; DOI: 10.1021/sb500345t).

AMI KABADI

Ami Kabadi

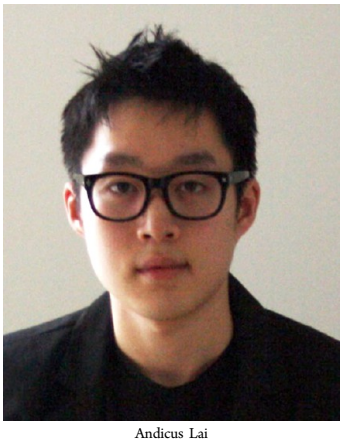
Current Position. Research Associate, Duke University, Department of Biomedical Engineering.

Education. Ph.D. in Biomedical Engineering at Duke University (2015) Advisor: Charles A. Gersbach, B.S. in Biology and minor in Chemistry at Duke University (2009).

Nonscientific Interests. Reading, cooking (currently working on mastering the grill), traveling, and crafting.

My graduate research has been focused on developing protein engineering techniques for controlling cell fate decisions. Conventional genetic reprogramming approaches make use of naturally occurring transcription factors that stimulate specific genetic networks and induce a coordinated change in differentiation state. Although there have been successful studies using naturally occurring transcription factors, these transcription factors are often inadequate for generating efficient, fast, and homogeneous cellular responses. One promising route to overcome these obstacles is to engineer new proteins with enhanced capabilities compared to their natural counterparts. Therefore, in this work, we engineered a reprogramming transcription factor that induces more efficient and robust differentiation compared to the natural counterpart. In the future, I plan to use my protein engineering skills to develop genome engineering techniques for correcting the genetic basis of human diseases. (Read Kabadi's article; DOI: 10.1021/sb500322u).

ANDICUS LAI



Andicus Lai

Current Position. Undergraduate Student, Department of Civil Engineering at Ryerson University.

Education. B.S. in Biochemistry and Health and Disease at University of Toronto. Advisor: Sergio Peisajovich.

Nonscientific Interests. Cooking, technology, and sci-fi movies.

My research was focused on engineering chimeric scaffolds using endogenous components to develop a new method to engineer novel spatiotemporal regulation in signaling pathways. Scaffolds are composed of modular interaction domains that allow tethering of multiple partner proteins. By recruiting specific signaling proteins, scaffolds insulate signals between pathways, determine the localization of the assembled complex, and become a target for pathway regulation. In this work, we created a library of chimeric scaffolds by shuffling modular interaction domains within the yeast mating pathway. From this library, a variety of scaffold architectures were shown to recover pathway activity in a pathway deficient in the native scaffold protein. Elucidating fundamental principles of information transfer within a cell can potentially lead to useful biotechnologies and improve our understanding of mechanisms of disease. (Read Lai's article; DOI: 10.1021/sb5003482).

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ANDREJA MAJERLE

Martina Mohorcic

Current Position. Researcher, Laboratory of Biotechnology, National Institute of Chemistry, Ljubljana, Slovenia.

Education. Ph.D. in Biochemistry and Molecular Biology, University of Ljubljana, Slovenia (2001). Advisor: Roman Jerala.

Nonscientific Interests. Family and friends, outdoor summer and winter activities, arts.

My research interests are focused on the application of synthetic biology to problems, which have potential application in fields such as medicine or biotechnology. We demonstrated the applicability of modular DNA-binding proteins for the design of complex biological devices for processing information such as logic circuits (*Nature Chemical Biology*, 2014) or switches (*Nature Communications*, 2014). This principle could be used for applications ranging from reprogramming cells to building digital biological memory. My co-workers and I also developed a sensor for HIV-1 protease in living cells (*Sensors*, 2013) and a signaling device for the detection of infection with HIV-1 in human cells (*ACS Synthetic Biology*, 2014), where we engineered a genetically encoded sensor composed of a fused membrane anchor, viral protease target site and an orthogonal transcriptional activator into a human cell line. In this way the devised sensor is based on the detection of an essential viral function, which makes it less sensitive to mutations that make virus resistant to chemical inhibitors, and the device was really activated also by clinically relevant protease mutants that are resistant to protease inhibitors. This principle could also be implemented for other viral proteases or adopted to target other viral functions. (Read Majerlés article; DOI: 10.1021/sb5002483).

LENNY MEIJER

Vincent van den Hoogen

Current Position. Ph.D. Candidate, Department of Chemical Biology and Computational Biology, Eindhoven University of Technology, The Netherlands. Advisor: Dr. T. F. A. de Greef.

Education. M.Sc. degree in Biomedical Engineering (2014) at Eindhoven University of Technology. Advisor: Dr. T. F. A. de Greef.

Nonscientific Interests. Cycling, hiking and traveling.

My research interests are in the field of *in vitro* synthetic biology. Specifically, I focus on the engineering of biochemical reaction networks of arbitrary complexity using a bottom-up approach. Theoretical and experimental studies of these molecular networks gain a deeper understanding of the cellular complexity. Moreover, biochemical reaction networks executing logic gate operations can be used for biosensing purposes. In this paper an *in silico* method is described that can be used to design biochemical reaction networks with parameters for which the networks execute the desired behavior robustly. In this way, the chance of successful implementation of biochemical networks *in vitro* will be increased. (Read Meijer's article; DOI: 10.1021/sb500300d).

ERNST OBERORTNER

Ernst Oberortner

Current Position. Software Developer at Joint Genome Institute (JGI) of Lawrence Berkeley National Laboratories (LBNL).

Education. Postdoc at Boston University, Prof. Dr. Douglas Densmore; Ph.D. in Computer Science at Vienna University of Technology, Prof. Dr. Schahram Dustdar and Prof. Dr. Uwe Zdun; M.Sc. in Computer Science at Vienna University of Technology, Prof. Dr. Schahram Dustdar.

Nonscientific Interests. Jogging, hockey, hiking, rock climbing.

Synthetic biology is an attractive and challenging application domain of computer science. Specifically, I work on specification languages (1) to automate design workflows based on state-of-the-art distributed computing principles and (2) to describe and learn well-established solutions to commonly recurring problems in engineering biological systems. In this work, we present a language to specify biological systems based on constraints, which describe the structural compositions of the system's building blocks. That is, constraints encapsulate knowledge about valid and invalid structural compositions. The language and its applicability may or may not be immediately intuitive to a scientist. To further push the development of novel technologies, however, (synthetic) biology requires standardized languages to communicate biological knowledge. (Read Oberortner's article; DOI: 10.1021/sb500352b).

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EUN JOONG OH

Eun Joong Oh

Current Position. Ph.D. candidate, University of Illinois. Advisor: Prof. Yong-Su Jin.

Education. M.S. Food Science and Biotechnology, Seoul National University, Seoul, Korea, Advisor: Prof. Jin-Ho Seo.; B.S. Food Science and Biotechnology, Seoul National University, Seoul, Korea.

Nonscientific Interests. Playing soccer, playing the piano.

My research is focused on designing and constructing engineered yeast to convert sugars from cellulosic biomass to biofuels and value-added chemicals. I am interested in elucidating the relationship between determined genotypes and phenotypes of interest in engineered yeast, because it is a prerequisite to designing optimal microbial platforms. On the basis of an understanding of cell metabolism and genetics, I am also interested in investigating regulation of the desired phenotypes using advanced genome engineering techniques such as the CRISPR-Cas9 system. Efficient utilization of sugars from cellulosic biomass is essential for the cost-effective production of value-added chemicals using microorganisms. Here, we developed an optimal yeast strain capable of simultaneous utilization of mixed substrates derived from cellulosic biomass by synthetic biological approaches. I am working on expanding the cofermentation strategy to make other value-added products in engineered yeast. (Read Oh's article; DOI: 10.1021/sb500364q).

SERGIO PEISAJOVICH

Sergio Peisajovich

Current Position. Assistant Professor, Department of Cell and Systems Biology, University of Toronto, Canada.

Education. B.Sc. University of Buenos Aires, Argentina; Ph.D. Weizmann Institute of Science, Israel, Advisor: Yechiel Shai; Postdoctoral Advisors: Dan Tawfik (Weizmann Institute of Science, Israel) and Wendell Lim (UCSF).

Nonscientific Interests. Playing with my kids.

My lab is interested in understanding how cellular processes mediated by complex networks of interactions evolve. Yeast signaling networks provide us with a great model system, as they possess much of the complexity of networks found in human cells, yet because yeast are microorganisms, their evolution can be studied in real time in the lab. In this paper, we have explored the extent of modularity of Ste5, a well-characterized scaffold protein in the yeast MAPK-mediated signaling pathway. To our surprise, we found that Ste5 modular domains can be arranged in several orders without affecting pathway function. Together with a recent article that we published in PLoS Biology (Sato *et al. PLoS Biol.* **2014**, *12* (12), e1002012), this work suggests that signaling complexes do not possess rigid structures but are rather flexible and dynamic ensembles. (Read Peisajovich's article; DOI: 10.1021/sb5003482).

YANNICK RONDELEZ

Takuya Shigeta

Current Position. CNRS researcher (France) and Project Associate Professor at the University of Tokyo.

Education. Postdoc, University of Tokyo (Advisor: H. Noji); Ph.D., University Paris XI/Paris V (Advisor: O. Reinaud).

Nonscientific Interests. Long distance hiking and cycling; my longest travel is a 6 month cycling trip from Cape Town to Cairo.

My research interests focus on the relation between chemistry, information processing, and life. I have a physico-chemical background, with a biological focus developed through a Ph.D. spent on synthesizing bioionorganic models of enzymes. I am now working for the French National Research Center (CNRS) leading a project on molecular programing. My goal is to understand the molecular principles of biological information processing and to apply this knowledge to the design of smart chemical assemblies with complex dynamic behaviors and responses *ex vivo*. To that goal, I use synthetic informational polymers, such as DNA, as small pieces of molecular software. (Read Rondelez's article; DOI: 10.1021/sb500300d).

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PALOMA M. SATO

Paloma M. Sato

Current Position. Young researcher at Institute of Biomedical Sciences at University of São Paulo.

Education. Postdoctoral Fellow, Department of Cell and Systems Biology, University of Toronto, Canada. Supervisor: Sergio G. Peisajovich; Ph.D. Sciences, University of São Paulo, Brazil. Advisor: Glaucia Souza; B.S. Biological Sciences, University of São Paulo State, Brazil.

Nonscientific Interests. Bodybuilding, healthy lifestyle, cooking, traveling, dogs and family.

My current research is focused on producing mutated promoters to search for phenotype diversity related to the filamentation pathway in yeast. This paper represented an important beginning for my scientific career in synthetic biology. Using a direct evolution approach, we selected from a large library variants with shuffled protein domains that rescue the Ste5 activity in the mating pathway of *Saccharomyces cerevisiae*. Our results showed that the scaffold protein is modular, which allows us to argue that signaling transduction has relaxed geometric constrains, thus facilitating the evolution of networks. In the future, we hope to build synthetic networks with specific connections that can give cells new functions. (Read Sato's article; DOI: 10.1021/sb5003482).

HENDRIK W. H. VAN ROEKEL

Hendrik W. H. van Roekel

Current Position. Ph.D. candidate, Department of Biomedical Engineering, Eindhoven University of Technology, The Netherlands. Advisors: Dr. Tom F. A. de Greef and Prof. Peter A. J. Hilbers.

Education. M.Sc. in Biomedical Engineering, Eindhoven University of Technology, The Netherlands (2011).

Nonscientific Interests. Cooking, retro and arcade video gaming, traveling (cities, country-sides and resorts), fishing.

My Ph.D. work encompasses the field of synthetic biology with a focus on computational strategies. It has become apparent that it is imperative that synthetic biology is aided by computational modeling. Taking this notion a step further, the aim is to use *in silico* strategies for rationally designing and engineering cell-free out-of-equilibrium synthetic network motifs from the bottom up that are capable of displaying predefined high-order temporal dynamics. This paper is a thorough description of a successful application of such an *in silico* design strategy on the bottom-up engineering of biomolecular circuits based on the DNA polymerase-exonuclease-nickase toolbox. In the future, I hope to use my skills and knowledge to improve diagnostic procedures and therapeutic interventions. (Read van Roekel's article; DOI: 10.1021/sb500300d).

XIAOLI XUE

Cheng Fan

Current Position. Associate Professor, Key Laboratory of Synthetic Biology, Institute of Plant Physiology and Ecology, Chinese Academy of Science, Shanghai, China. Advisor: Prof. Dr. Zhongjun Qin.

Education. Ph.D. in Microbiology, Department of Cell Biology, Helmholtz Center for Infection Research, Germany. Advisors: Prof. Dr. Irene Wagner Doebler, and Dr. Helena Sztajer.

Nonscientific Interests. Travels, movies, and delicious foods.

I am interested in microbial synthetic biology, and my current research is focused on the reduction and reconstruction of the *Escherichia coli* genome. To accelerate the genome reduction progress, we developed a new method named MEGA (multiple essential genes assembling) deletion and replacement. By assembling essential genes in a BAC (bacterial artificial chromosome) and complementing them in trans, we can remove a large chromosomal fragment containing essential genes through one round of deletion. This method also allowed us to locate growth important genes in a large region, which would provide useful information for our genome reduction research. We are in the progress of constructing *E. coli* strains with smaller genome by using this method. Moreover, we are interested in the construction of a reduced *E. coli* genome using the bottom-up synthetic approach. (Read Xue's article; DOI: 10.1021/sb500324p).

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LI-BANG ZHOU

Li-Bang Zhou

Current Position. Ph.D. Candidate, Institute of Bioprocess and Biosystems Engineering, Hamburg University of Technology, Hamburg, Germany. Advisor: Prof. Dr. An-Ping Zeng.

Education. B.S. in Plant Biology, Nanjing Agricultural University, China.

Nonscientific Interests. Music, badminton, reading, and travel.

I am interested in developing molecular tools that can be used for engineering industrial microorganisms. An effective tool for controlling gene expression, the riboswitch is attractive for engineering biological systems. In this work, we demonstrated the use of natural lysine riboswitches and intracellular L-lysine as a signal to control the competing but essential metabolic pathways of lysine biosynthesis. This riboswitch-based system can be easily adapted to enhance the fluxes of desired metabolic pathways. Currently, I am working on altering a natural lysine-OFF riboswitch to a synthetic lysine-ON riboswitch. In the future I hope to combine the riboswitch with other novel biomolecular tools and concepts, to develop hyper-producing microorganisms. (Read Zhou's article; DOI: 10.1021/sb500332c).

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