ACS SyntheticBiology

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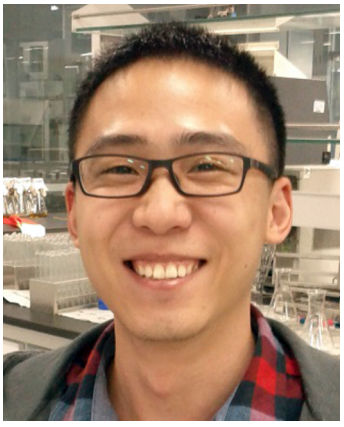
YIFAN LI



Jing Fu

Current Position. Ph.D. Candidate, Department of Biochemical Engineering, School of Chemical Engineering and Technology, Tianjin University, Tianjin, China. Advisor: Prof. Xueming Zhao.

Education. B.S. in Biochemical Engineering, East China University of Science and Technology, China.

Nonscientific Interests. Music, reading, and computer games.

I regard myself as an engineer. I love making new stuff, building new things, and solving problems. I'm generally interested in the development of novel tools and methods for the engineering of biological systems. In this work, we used recombineering to develop Multiplex Iterative Plasmid Engineering (MIPE), which is a highly efficient and flexible method for diversification of plasmid sequences. To demonstrate this approach, we applied MIPE to fine-tune gene expression level in the 5-gene riboflavin biosynthetic pathway and successfully isolated a clone with 2.67-fold improved production in less than a week. We also showed the ability of MIPE to simultaneously target 41 nucleotides (23 codons) scattered along the 750 bp protein coding sequence, which was an extremely difficult task to be implemented with other site directed mutagenesis techniques (OE-PCR or QuikChange) (read Li's article; DOI: 10.1021/sb400051t).

TSUNG-YI LIN (STEVEN)

Tsung-Yi Lin

Current Position. Ph.D. Candidate, Department of Chemistry, University of Massachusetts—Amherst, MA, U.S.A. Advisor: Prof. Nathan A. Schnarr.

Education. M.S. in Anatomy and Cell Biology, National Taiwan University, Taiwan. Advisor: Chung-Liang Chien. B.S. in Medical Technology, National Taiwan University, Taiwan.

Nonscientific Interests. Hiking, kayaking, reading, and watching sci-fi movies.

Our research, which focuses on the most prominent class of small molecules in modern pharmaceuticals, polyketides, aims to create an arsenal of promising drug candidates by using environmentally benign bacteria as programmable, microscopic factories. In this work, we unearthed a new polyketide synthase not only to diversify the polyketide engineering repertoire but also to open a new avenue for understanding the evolving relationship between polyketide synthase and fatty acid synthase. Currently, I am working on examining the substrate specificity on each ketosynthase and the key elements for controlling it. Furthermore, I am also using various methods to reconstitute Fluvirucine in *E. coli* with the gene cluster that we discovered (read Lin's article; DOI: 10.1021/sb4000355).

ZHENQUAN LIN

Jing Fu

Current Position. Ph.D. Candidate, Department of Biochemical Engineering, School of Chemical Engineering and Technology, Tianjin University, Tianjin, China. Advisor: Prof. Xueming Zhao.

Education. B.S. in Biological Sciences, East China University of Science and Technology, China.

Nonscientific Interests. Music and reading.

My research is focused on rational metabolic engineering and synthetic biology for riboflavin production. In this paper, we use λ-red recombination to develop Multiplex Iterative Plasmid Engineering (MIPE), which is a highly efficient and optimized method for modifying the sequence of plasmids. As a proof-of-principle experiment, we first employed MIPE for combined tuning the genes of the riboflavin biosynthetic pathway, successfully isolated a clone with 2.67-fold improved production. We also used MIPE to target several sites simultaneously and generated libraries of up to 107 rfp sequences in one reaction (read Lin's article; DOI: 10.1021/sb400051t).

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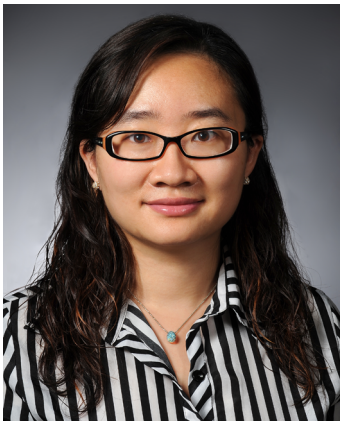
ZENGYI SHAO



Zengyi Shao

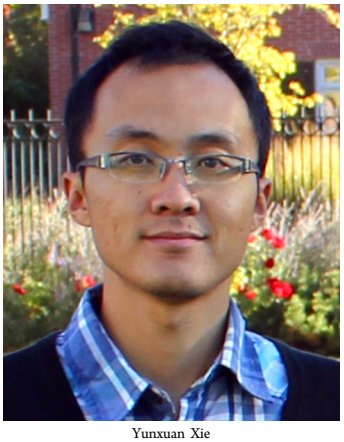
Current Position. Assistant Professor, Department of Chemical and Biological Engineering, NSF-Center for Biorenewable Chemicals, Iowa State University, Ames, Iowa.

Education. Postdoctoral Fellow at the University of Illinois, Urbana−Champaign. Advisor: Dr. Huimin Zhao. Ph.D. in Chemical and Biomolecular Engineering. Advisor: Dr. Huimin Zhao. B.S. in Biochemistry, Nankai University, China.

Nonscientific Interests. Travel and music.

I have been fascinated by the power of synthetic biology since I was a graduate student. In the research I conducted in Illinois, we targeted a daunting challenge in the natural product field: how to elicit pathway expression in a generally applicable manner. Traditional methods are mostly cluster-specific and suffer from laborious process. Here, we applied a "refactoring" strategy to replace the sophisticated regulations embedded in individual natural product gene clusters with a set of characterized promoters in a plug-and-play scaffold. The strategy offers a potential solution for activating vast amount of cryptic pathways identified through genome mining for novel natural product discovery. My current research group at Iowa State University mainly focuses on engineering individual microorganisms and microbial consortia to address critical issues in energy sustainability and chemical production. My group is very interested in using synthetic biology to achieve high throughput strain optimization (read Shao's article; DOI: 10.1021/sb400058n).

YAN WANG



Yunxuan Xie

Current Position. Postdoctoral fellow, Department of Chemistry, University of Nebraska—Lincoln, Nebraska, U.S.A. Advisor: Dr. Liangcheng Du.

Education. Ph.D., Microbiology, State Key Laboratory of Microbial Technology, Shandong University, China (2012). Advisor: Dr. Yuezhong Li and Dr. Liangcheng Du.

Nonscientific Interests. Travel, cycling, and photography.

My Ph.D. candidate work was mainly on genetic and biochemical characterization of two copies of groEL gene in *Myxococcus xanthumonus*. My current research focuses on the molecular mechanism and genetic engineering for the biosynthesis of novel bioactive natural products from *Lysobacter*. This paper describes a facile method for site-specific gene integration in *Lysobacter enzymogenes* for yield improvement of two promising antibiotics. Using black-yellow color switch as a novel selection marker, we constructed a series of broadly adaptable vectors for gene expression. As a proof of principle study, a positive regulator gene for antibiotic biosynthesis in *Lysobacter* was selected. The yields of Anti-MRSA WAP-8294A and the antifungal antibiotic HSAF were improved by 7 times and 2 times, respectively, in the resulting mutant. This work represents the first successful metabolic engineering of *Lysobacter* and provides a clue toward manipulating secondary metabolites production in largely unexplored sources (read Wang's article; DOI: 10.1021/sb4000806).

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