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MARÍA-EUGENIA GUAZZARONI

María-Eugenia Guazzaroni

Current Position. Postdoctoral fellow, Department of Biochemistry, FCLRP-USP Ribeirão Preto, São Paulo, Brazil.

Education. Ph.D. in Molecular Biology and Biochemistry at the Universidad de Granada, Spain (2007), Advisor: Juan Luis Ramos Martín. B.S. in Microbiology at the Universidad Nacional de Río Cuarto, Argentina (2001).

Nonscientific Interests. Traveling, culinary tourism, good books, good movies, sharing time with loved ones.

During my Ph.D. studies, I studied transcriptional regulation in bacteria using different biochemical and molecular techniques. As a postdoctoral fellow, I performed several studies in the field of metagenomics, with a strong focus on functional metagenomics of extreme environments. Working with the bases of transcriptional regulation and activity screening of genes with potential interest in biotechnology gave me the ability to combine understanding in basic science with applied approaches. Results presented in the current work provide new strategies for the engineering of synthetic regulatory circuits in bacteria with potential use in biotechnology applications. (Read Guazzaroni's article; DOI: 10.1021/sb500084f).

KANA ISHIMATSU

Kana Ishimatsu

Current Position. Postdoctoral fellow, Department of Systems Biology, Harvard Medical School. Advisor: Dr. Sean Megason.

Education. Postdoctoral fellow, Department of Computational Intelligence and Systems Science, Tokyo Institute of Technology, Advisor: Daisuke Kiga. Ph.D. Biology, The University of Tokyo (2010), Advisor: Hiroyuki Takeda. M.S. The University of Tokyo (2007), Advisor: Hiroyuki Takeda. B.S. The University of Tokyo (2005), Advisor: Hiroyuki Takeda.

Nonscientific Interests. Eating. Any team sports. I started practicing volleyball this summer. I also like snowboarding.

My basic research interest is in finding a simple logic to explain the development of multicellular organisms. Although genomic and epigenomic information have been accumulated in past research, how a single cell becomes a complex, organized biological form is still an understudied subject. Differentiation/reprogramming is a primary topic in developmental biology, and this study, using a synthetic biology approach, proposes a new and simple mechanism explaining differentiation/reprogramming—reprogramming driven by gene-overexpression. I believe that this kind of reprogramming underlies the establishment process of induced pluripotent stem cells (iPSCs). My long-standing goal is to implement synthetic gene networks in multicellular organisms in order to facilitate understanding and, furthermore, to control their developmental systems. (Read Ishimatsu's article; DOI: 10.1021/sb400102w).

JASON G. LOMNITZ

Ann E. Savageau

Current Position. Ph.D. Candidate, Biomedical Engineering Graduate Group, University of California, Davis. Advisor: Michael A. Savageau.

Education. B.Sc. in Genomic Sciences, National Autonomous University of Mexico (UNAM). Advisors: Julio Collado-Vides and Michael A. Savageau.

Nonscientific Interests. Reading, board games, family, and friends.

My Ph.D. work includes the development of enabling technologies for the analysis of complex systems, and its application to the study of genetic regulatory circuits with the goal of identifying design principles that govern their operation. The technology that I am currently developing is in the form of

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new software that includes new theory in the field of nonlinear dynamics. This paper shows an application of our methods, where we identify generic differences between unique oscillator designs. We discovered a set of design principles regarding different mechanisms for feedback control and modes of transcriptional regulation that contribute to the global robustness of the distinct designs. Currently, I am working on new methods to explore the complete phenotypic repertoire of nonlinear models and to discriminate models based on their potential to generate specific patterns of behavior. (Read Lomnitz's article; DOI: 10.1021/sb500236e).

DAVID L. SHIS

David L. Shis

Current Position. Ph.D. Candidate in the Department of Biochemistry and Cell Biology at Rice University, Advisor: Dr. Matthew Bennett.

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

Nonscientific Interests. Ballroom dancing, running, swimming, and cooking.

My research is on developing scalable transcriptional networks. While the ability to construct synthetic genetic systems has improved dramatically, the ability to implement large-scale synthetic gene circuits remains limited. One obstacle to this is the ability to implement multi-input transcriptional regulation. In our paper, we explore one strategy to facilitate multi-input AND transcriptional logic by coexpressing multiple LacI/GalR transcriptional repressors. By coexpressing multiple LacI/GalR chimeric repressors, one can specify the ligands that derepress a promoter containing the lac operator site. Furthermore, by applying novel DNA binding domains that bind orthogonal operators, simultaneous multi-input transcriptional regulation can be achieved. By applying these principles, we implement expression systems regulated by as many as four ligands. Altogether, our work enables the implementation of synthetic gene circuits with increased computational capacity. (Read Shis' article; DOI: 10.1021/sb500262f).