LMU LUDWIG-MAXIMILIANS-UNIVERSITÄT MÜNCHEN GRK2062

WHAT'S GOING ON

in the Research Training Group Molecular Principles of Synthetic Biology

NEWSLETTER #3 2017

FOCUS ON RESEARCH

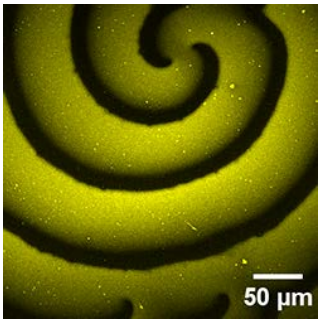

Figure 1. *In vitro reconstitution of the MinDE system from* Escherichia coli

Two proteins, MinD (labelled with 30% Venus-MinD) and MinE, self-organize into planar surface waves and spirals on a lipid support.

Prof. Dr. Petra Schwille

C1 / Area C Synthetic Systems

Bottom-up synthetic biology

"What I cannot create, I do not understand." - This famous quote by Physicist Richard Feynman summarizes our motivation for taking the bottom-up approach to understanding life. Instead of following the classical biology strategy of observing and modifying a living organism, we reconstitute small subsystems from defined, purified or even fully synthetic components (e.g. proteins, lipids, nucleic acids, DNA-origami). This enables us on the one hand to take quantitative biophysical measurements at drastically reduced system complexity. On the other hand, this approach hands us the possibility to freely combine components, and alter concentrations and measurement conditions. The ultimate goal of bottom-up synthetic biology is to one day combine multiple of these well-characterized units to once again form a living organism or protocell that is then fully understood and programmable.

Due to our group's strong foundation in membrane biophysics our main focus is on processes that happen on or involve biological membranes. To advance the current understanding of cell division, we have reconstituted the Min system of *Escherichia coli*, which positions the crucial division factor FtsZ in the cell middle. FtsZ, as well as a division machinery found in Archaea (CdvABC) are also under investigation using our minimalist approach. Looking more towards eukaryotes, we are dissecting the interactions of a minimal actin cortex and the membrane, as well as the role of actin in endocytosis.

The field of bottom-up synthetic biology is still a long way from building a living cell, but so many fascinating discoveries have already been and will still be made on the way there.

GRK2062 PUBLICATION

RNA 2017. 23: 762-769

Gene expression control by *Bacillus anthracis* purine riboswitches

Marion Kirchner and Sabine Schneider

Abstract

In all kingdoms of life, cellular replication relies on the presence of nucleosides and nucleotides, the building blocks of nucleic acids and the main source of energy. In bacteria, the availability of metabolites sometimes directly regulates the expression of enzymes and proteins involved in purine salvage, biosynthesis, and uptake through riboswitches. Riboswitches are located in bacterial mRNAs and can control gene expression by conformational changes in response to ligand binding. We have established an inverse reporter gene system in *Bacillus subtilis* that allows us to monitor riboswitch-controlled gene expression. We used it to investigate the activity of five potential purine riboswitches from *Bacillus anthracis* in response to different purines and pyrimidines. Furthermore, in vitro studies on the aptamer domains of the riboswitches reveal their variation in guanine binding affinity ranging from namomolar to micromolar. These data do not only provide insight into metabolite sensing but can also aid in engineering artificial cell regulatory systems.

Full text http://dx.doi.org/10.1261/rna.058792.116

NEW MEMBERS

PIs

We welcome **Thorben Cordes** as new PI of the GRK2062. He will start in July at the LMU faculty of biology as a W2 professor for "Physical and Synthetic Biology". His research project within the research training group will focus on "Sensitive fluorescence monitoring of ATP turnover and small molecule transport".

EVENTS

Joint Retreat 2017 - ICMSE Pre-conference and ICMSE main conference

Date: August 26-27, 2017 and August 27-29, 2017
Location: Uni Basel, Switzerland
Deadline for registration is extended till May 31, 2017. After that four GRK2062 junior researchers will be elected to present a talk at the Pre-conference. GRK2062 Junior Researchers Committee and Kirsten Jung will care for this.
Accommodation in Hotel Spalentor is already booked for all junior researchers (about 4 min to walk to the conference location). There will be a **bus transfer** from Munich to Basel on August 25, 2017 and back to Munich in the evening of August 29, 2017.

GRK2062 General Meeting 2017

Our meeting will take place on May 29, 2017 at 6 pm in room G00.031 at the LMU Biocenter.

Upcoming Transferable Skills Courses

For women only: **Führungswerkstatt** Dr. Brigitte Winkler
The course will run on October 17, 2017 at LMU Biocenter.
Please note: the course is held in German, but contributions in English are welcome.
For details of the program and registration please contact grk2062@bio.lmu.de

Scientific Writing, Science Craft
This course will run on the 22nd and 23rd of February 2018 at LMU Biocenter. For a full description please click here.

iGEM 2017

Aurore Dupin and Lukas Aufinger (both Simmel group) have taken on responsibility for the current iGEM team. This year's team consists of 17 students from LMU and TU Munich. Their goal is to create a novel paper-based microfluidic device for the detection of specific RNA sequences as a point-of-care testing (POCT).

Background: Nowadays, there is a trend among medical practitioners to prescribe antibiotics when bacterial infections are suspected without a laboratory confirmation as a way for speeding up recovery (Van Heirstraeten et al., 2014). This has led to an increase in antibiotic-resistant bacteria, which cannot be fought with commonly prescribed antibiotics,

requiring the development of new strategies. Because of this, there has already been antibiotic resistance-related deaths, which are expected to increase in the future. However, new antibiotic discovery takes a lot of time and monetary investment.

Current bacterial tests take around 48 hours while virus detection methods can take several days. However, nucleic acid-based detection methods could allow for faster diagnosis. Therefore, the iGEM team seeks to develop a method that allows to report the presence of a specific pathogen within hours. For this reason, we will use the CRISPR effector Cas13a, which is able to target specific single-stranded RNA (East-Seletsky et al., 2016; Abudayyeh et al.). This system allows for simple and fast design of new sequence targets, being an ideal tool for detecting fast mutating pathogens. Also, it has been shown to detect attomolar (1 molecule in a cubic millimeter) concentrations of viral RNA (2016; Gootenberg et al., 2017).

In order to provide a fully integrated ‘sample-to-answer’ solution for POCT, they will construct a reusable device that includes a module for sample processing and RNA extraction, as well as a detection module. They will develop their system specific for saliva samples and upper respiratory tract pathogens. The test itself will be conducted on low-cost disposable paper-based test strips to avoid cross-contamination.

In the long term, this device could be an easy and fast diagnostic tool in developing countries as well as an instrument in developed countries for discerning between bacterial and viral infections, that could help reducing antibiotics prescription.

JOURNAL CLUB

Science 355, 1283 (2017) 24 March 2017

Article

Self-assembly of genetically encoded DNA-protein hybrid nanoscale shapes

Florian Praetorius and Hendrik Dietz

Abstract

We describe an approach to bottom-up fabrication that allows integration of the functional diversity of proteins into designed three-dimensional structural frameworks. A set of custom staple proteins based on transcription activator-like effector proteins folds a double-stranded DNA template into

a user-defined shape. Each staple protein is designed to recognize and closely link two distinct double-helical DNA sequences at separate positions on the template. We present design rules for constructing megadalton-scale DNA-protein hybrid shapes; introduce various structural motifs, such as custom curvature, corners, and vertices; and describe principles for creating multilayer DNA-protein objects with enhanced rigidity. We demonstrate self-assembly of our hybrid nanostructures in one-pot mixtures that include the genetic information for the designed proteins, the template DNA, RNA polymerase, ribosomes, and cofactors for transcription and translation.

Full text: http://dx.doi.org/10.1126/science.aam5488

MISCELLANEOUS

Responsible Research - July 20, 2017

All researchers are obliged to conform to rules of Good Scientific Practice. These rules are implicit, but the border between acceptable and unacceptable practice is often unclear. What is responsible research conduct? How can I present data accurately? What exactly is plagiarism? What are the pros and cons of open science? What is an ombudsperson?

Open to students, doctoral candidates, postdocs - scientists of all levels
Thursday, July 20, 2017 from 13:00 - 19:00 in the BMC Munich and the LMU Biocenter, Martinsried

Program:

- **Keynote Lectures:**
  Prof. Dr. Joachim Heberle, DFG: The German Research Ombudsman: An instrument dealing with scientific misconduct
  Prof. Dr. Marcus Munafò, University of Bristol: Scientific ecosystems and research reproducibility
  Prof. Dr. Debora Weber-Wulff, HTW Berlin: Plagiarism and the scientific process
- **Breakout Sessions:**
  Avoiding Plagiarism, Animal Research, Clinical Trials, Experimental Design and Statistics, Image Analysis, Open Science
  Participation is free of charge. Online registration is mandatory, and will be open from May 15 - June 30, 2017. Early registration is recommended. For program details and registration see www.lifescience-munich.de.

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