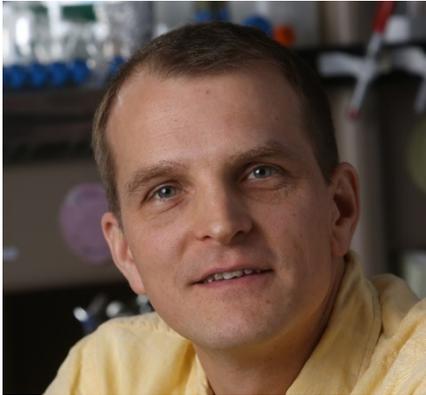


SFB 960-/BZR – Kolloquium

Dienstag, 21. Juni 2022, 15.00 Uhr

H52

SONDERTERMIN



Prof. Dr. Burckhard Seelig

University of Minnesota

Department of Biochemistry, Molecular Biology and Biophysics & BioTechnology Institute

Laboratory evolution to study the origin of functional proteins and the history of the genetic code

As the result of billions of years of evolution, modern protein enzymes catalyze a wide range of chemical reactions facilitated by their intricate three-dimensional structures. It is extremely challenging to deduce the nature of the earliest catalytic polypeptides from modern proteins. Despite the rapidly increasing wealth of information on protein structures and catalysis, we currently have only a limited understanding of how new protein folds and functions emerge in nature. Similarly, while we all recognize today's standard genetic code of twenty amino acids that supports all life, this 'universal' code is a continually evolving *work in progress* and is predicted to have originated from a smaller number of primordial amino acids. Unfortunately, molecular fossils from these earliest phases of life have not been found and may never be found due to the exceedingly long time that passed.

We study these early life processes in the laboratory by investigating potential scenarios of how the earliest primordial proteins could have originated. We implement Darwinian selection and evolution in a test tube to isolate novel proteins from vast libraries of synthetic randomized polypeptides. We have generated novel enzymes from scratch – enzymes that have not been found in nature. In contrast to their modern day counterparts, these artificial enzymes have not undergone natural evolution and can serve as a model for early proto-enzymes.

Furthermore, we are using our *in vitro* selection strategy to practically test hypotheses on the potential predecessors of our standard genetic alphabet. We are currently comparing libraries of polypeptides from different likely earlier amino acid alphabets for the ability to form structured proteins and perform simple biological functions. While we will not be able to prove a specific history of protein base life, these experiments are testing the feasibility of plausible evolutionary scenarios.

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