BP 20: Posters - Physics of the Genesis of Life (Focus Session)

Time: Tuesday 14:00–16:00 Location: P1A

BP 20.1 Tue 14:00 P1A

Chemically Driven Ligation Chain Reaction - Towards Protein-free Hypercycles in Sequence Space? — •Stefanie Leiner, Evgeniia Edeleva, and Dieter Braun — Systems Biophysics, Physics Department, LMU Munich, Germany

Which mechanism could have fostered the stable emergence of functional sequences for an RNA world? Eigen's hypercycles suggests that cooperating replication leads to hyperexponential selection.

Hypercycle dynamics can be implemented via competitive oligonucleotide ligation in long-term experiments. Under serial dilution, to mimic molecule degradation, this process enhances the replication of majority sequences and allows their emergence from a random sequence pool. Hyperexponential replication arises from the competitive binding kinetics of ligation: oligonucleotides with long-range sequence correlations ligate faster by cooperative hybridization. The mechanism requires thermal cycling - a non-equilibrium boundary condition that could be provided together with accumulation by heat flow across pores of rock [1].

Our investigations show that EDC can be used in an in-situ activated ligation reaction with 80 % yield for temperatures below ~40 °C [2][3]. We show preliminary results towards protein-free hypercycles in sequence space.

[1] S. Toyabe, D. Braun, under review. [2] M. Jauker et al. Angew. Chem. Int. Ed. 2015, 54, 14559-14563. [3] Taran et al. J. Sys. Chem. 2010, 1:9, 1-16.

BP 20.2 Tue 14:00 P1A

Replicating codon sequences only with tRNA — Simon Lanzmich, Thomas Rind, and •Dieter Braun — Faculty of Physics and Center for Nanoscience, LMU Munich, Germany

The origins of biological information replication constitute a major challenge for understanding the origins of life. Modern life employs a complex tRNA/RNA/protein machinery to build proteins and replicate DNA [1,2,3]. We present a purely thermally driven replication mechanism that selectively replicates sequences of short codons. It does not depend on a particular base-by-base replication chemistry, but only requires the hybridization of short complementary domains. Codons are carried by molecules very similar to tRNA [4]. Upon a few point mutations, the latter adopt secondary structures where the anticodon is framed by two stem-loops [5]. The stem-loops of different molecules are pairwise complementary, such that sequences of strands can form supramolecular chains. Replication of a template succession of these proto-tRNAs is facilitated by temperature oscillations and implements (1) binding of strands with matching anticodons to the template (2) fluctuations in the bound strands' hairpins hybridize to neighboring tRNA and (3) heating splits the replicate from the template. Experiments show that this purely physical ligation chain reaction proceeds exponentially and amplifies the template codons severalfold within a few temperature cycles.

[1] IUBMB Life 61, 99 (2009) [2] Science 244, 673 (1989) [3] RNA 16, 1469 (2010) [4] J.Comput.Chem. 32, 170 (2010) [5] PRL 108, 238104 (2012)

BP 20.3 Tue 14:00 P1A

The efficiency of driving chemical reactions by a physical non-equilibrium is kinetically controlled — •Tobias Göppel, Vladimir V. Palyulin, and Ulrich Gerland — Physics of Complex Biosystems, Physics Department, Technical University of Munich, James-Franck-Strasse 1, D-85748 Garching, Germany

An out-of-equilibrium physical environment can drive chemical reactions into thermodynamically unfavorable regimes. Under prebiotic conditions such a coupling between physical and chemical non-equilibria may have enabled the spontaneous emergence of primitive evolutionary processes. Here, we study the coupling efficiency within a theoretical model and focuses on generic effects arising whenever reactant and product molecules have different transport coefficients in a flow-through system.The physical non-equilibrium is represented by a drift-diffusion process, which is a coarse-grained description for the interplay between thermophoresis and convection, as well as for many other molecular transport processes. As a simple chemical reaction, we consider a reversible dimerization process, which is coupled to the transport process by different drift velocities for monomers and dimers. Within this minimal model, the coupling efficiency between the non-equilibrium transport process and the chemical reaction can be analyzed in all parameter regimes. The analysis shows that the efficiency depends strongly on the Damköhler number, a parameter that measures the relative timescales associated with the transport and reaction kinetics.

BP 20.4 Tue 14:00 P1A

Spatial organization of encapsulated circuits — •Aurore Dupin, Berta Tinao, and Friedrich C. Simmel — Systems Biophysics and Bionanotechnology - E14, Physics Department and ZNN, Technische Universität München, am Coulombwall 4a, 85748 Garching, Germany

Compartmentalization is at the origin of cellular life as we know it today, although the selective advantage of porous or tight membranes for early cells is debated. The compartmentalization of metabolic circuits can reduce cross-talk by isolating parts of the circuits, and increase the efficiency of the metabolic processes by co-localizing reagents. The effect of compartmentalization on synthetic gene circuits has been studied in isolated water-in-emulsion droplets, where communication was mediated by non-specific diffusion. In contrast, our goal is to build large biomimetic networks exhibiting controlled communication and topology. Such a spatial organization should allow for more complex circuit dynamic behaviors.

To this end, we employ the droplet-interface-bilayer technique to construct spatially organized networks of defined composition. In these networks, protein pores exhibiting chemical selectivity incorporate in lipid bilayer interfaces to mediate the communication between droplets, similarly to natural cell membranes. We implement a variety of RNA-based circuits where the pore-mediated translocation of chemicals is used to induce dynamical behavior. In the future, we envision the implementation of more complex circuits within such networks, including in vitro protein expression systems.

BP 20.5 Tue 14:00 P1A

Elucidating signatures of the genetic code with binding assays — •Evgeniia Edeleva, Philipp Schwintek, and Dieter Braun — LMU Munich, AG Braun, Amalienstrasse 54, 80799 Munich, Germany

What defined specific assignment of amino acids to their cognate codons during the emergence of the genetic code? According to the stereochemical theory, the assignments were established based on affinity interactions between amino acids and their codons/anticodons. In the structure of the modern tRNA molecule, the acceptor stem with the amino acid and the anticodon loop with the anticodon triplet are separated by 6 nm in space, making direct interaction impossible. However, two alternative primal tRNA structures have been proposed that bring together in space the amino acid and the codon determinant [1, 2]. Both structures contain tetraloop-like geometries - simple structures that were recently shown to possess enzymatic activity such as ligation, cleavage, and terminal recombination [3].

In this project, we experimentally study the binding of stable AMP activated amino acid analogs to RNA motifs of AMP-binding aptamers as a testbed or to the above mentioned tetraloop-like structures containing corresponding coding triplets using microscale thermophoresis. We aim to elucidate patterns of anticodon-amino acid correlations for the emergence of the genetic code.

[1] J.J. Hopfield, Proc. Natl. Acad. Sci. U. S. A. 75, 4334-8 (1978)
[2] A.S. Rodin et al., Biology Direct 4, 4 (2009)
[3] P. Stadlbauer et al., Chemistry 21, 3596-604 (2015)

BP 20.6 Tue 14:00 P1A

Peptide-based vesicles as precursors to protocells — •Kilian Vogele, Marisa Götzfried, Elisabeth Falgenhauer, Friedrich C. Simmel, and Tobias Pirzer — Systems Biophysics and Bionanotechnology E14, Physics-Department and ZNN, TU Muenchen, 85748 Garching, Germany

Commonly stated requirements for protocells are the maintenance of a metabolism, sensing and responding to the environment, the capability for self-reproduction and Darwinian evolution. In order to meet these requirements compartmentalization is often regarded as an essential aspect. In the lab, protocellular compartmentalization is typically modelled with self-assembled vesicles, for which various molecular com-

ponents such as fatty acids, lipids or amphiphilic peptides have been utilized. Here we use synthetic elastin-like polypeptides (ELP) to create self-assembled peptide vesicle structures. Among their advantages are tunability in size, permeability and stimuli-responsiveness. The ELP vesicles are fabricated by rehydration from glass beads and have a size of about 200 nm, as observed by DLS and TEM. Using flow cytometry and spectroscopy, we demonstrate successful encapsulation of GFP and fluorescent DNA in the polymersomes, and we also show transcription of the fluorescent RNA aptamer dBroccoli inside of the vesicles. On the long run, we aim at the self-reproduction of ELP vesicles by expression of ELP encoding genes in an artificial transcription-translation (TX-TL) system.

BP 20.7 Tue 14:00 P1A

Phospholipids and the prebiotic formation of vesicles — •Maria Tsanakopoulou, Cecile Caumes, Claudia Percivalle, Bhavesh Patel, Colm Duffy, and John Sutherland — MRC Laboratory of Molecular Biology, Francis Crick Avenue, Cambridge Biomedical Campus, CB2 0QH, UK

Glycerol-2-phosphate, which, along with the 1-phosphate, can readily be synthesised by phosphorylation of glycerol, was used as the substrate for the prebiotically plausible formation of alkyl chain phospholipids (1,3-bisacylated and 1-monoacylated glycerol-2-phosphate esters). All the alkyl chain acids were produced selectively in two steps from the aldol reaction of acetaldehyde and reduction by macroporous nickel and hypophosphite - known corrosion products of iron-nickel meteorites. The corresponding acyl imidazolides were used as activated forms of the acids for the formation of the phospholipids. Solutions of different concentrations of the phospholipids bearing the longer chain acyl groups were studied and were found to form vesicles, which could have played a role in the origins of the prokaryotic cells. If the mixture of the phospholipids contains a lot of the shorter chain derivatives, vesicles are not formed. In this case, it was found that recycling - iterative partial selective hydrolysis and reacylation - changes the composition of the mixture in favour of the longer chain derivatives with the result that vesicles can then be observed.

BP 20.8 Tue 14:00 P1A

High-resolving chemical analysis of products formed under hydrothermal vent conditions — •Jessica Sobotta[1], Alexander Ruf[2,3], Wolfgang Eisenreich[1], Philippe Schmitt-Kopplin[2,3], and Claudia Huber[1] — [1]Biochemistry, Technische Universität München, Garching Germany — [2]Analytical BioGeoChemistry, Helmholtz Zentrum München, Munich Germany — [3]Analytical Food Chemistry, Technische Universität München, Munich Germany

Hydrothermal vents offer a continuous supply of reactive nutrients which react with transition metal minerals. The combination of high pressure, a temperature gradient and a nearly neutral pH can lead to a high diversity of organic molecules including amino acids, hydroxy acids, fatty acids and small peptides [1-3]. In depth analysis of these complex reaction mixtures requires high-resolving analytical tools [4,5] and sophisticated approaches [6]. The combination of FT-ICR-MS, GC-MS and NMR methods have provided a complementary profile of the products for both low and high molecular weight compounds, including an unexpected variety of CHOS derivatives. In summary, high-resolving analytical methods expand our view into the fascinating chemistry of a potential origin of life scenario under hydrothermal vent conditions. [1] C. Huber, G. Wächtershäuser, Science (2006) 314:630-632. [2] C. Huber, W. Eisenreich et al. (2003) Science 301:938-940. [3] C. Scheidler, J. Sobotta et al. (2016) Sci. Rep. 6. [4] Schmitt-Kopplin et al. (2010) PNAS 107:2763-2768. [5] Popova et al. (2013) Science 342:1069-1073. [6] Tziotis et al. (2011) EJMS 17.4: 415-421

BP 20.9 Tue 14:00 P1A

Modeling a mechanism for pre-biotic selection and organization — •Varun Giri[1] and Sanjay Jain[2,3] — [1]Department of Biological Experimental Physics, Saarland University, Saarbrücken, Germany — [2]Department of Physics and Astrophysics, University of Delhi, Delhi, India — [3]Santa Fe Institute, Santa Fe, New Mexico, United States of America

Large molecules such as proteins are crucial for life. Production of these molecules requires good catalysts, and the only good catalysts known today are themselves large molecules. For the origin of life this presents a chicken-and-egg problem in chemistry. We use a mathematical model based on an artificial but pre-biotically plausible chemistry to investigate how certain specific chemical species can be selected out of a large set of possible combinations. We further describe a cascading mechanism by which large and improbable molecules are formed relatively easily in our system, thereby making more plausible the appearance of macromolecules like proteins, RNAs, etc., in pre-biotic settings. We start by considering a set of small molecules and construct a network of chemical reactions amongst these molecules and their reaction products. We find that under certain circumstances, autocatalytic sets (ACSs) come to dominate the chemistry in that the concentrations of the molecules belonging to an ACS are much higher than the background. We study the conditions under which large catalysts can appear starting from chemistries comprising of small molecules and later dominate the system.

BP 20.10 Tue 14:00 P1A

Spatial fractionation of RNA in an inhomogeneous temperature gradient — •Prasanna Padmanaban, Juan Iglesias Artola, and Moritz Kreysing — MPI of Molecular Cell Biology and Genetics, Dresden

Thermal gradients across small pores are able to accumulate nucleic acids from dilute aqueous solutions, e.g. a pre-biological ocean, pond, or puddle [1]. More recently it was found that an open pore of this kind can even act as length selective filter for nucleic acids that are delivered by a steady hydrodynamic flow through this pore. This results in the deposition of long, rare and potentially functional nucleic acids inside this small porous compartment [2]. It was shown that this selection pressure towards increasing molecular complexity is capable of stabilizing long replicators in the presence of short parasites.

Here, we investigate the accumulation characteristics of spatially varying, rather than homogenous, temperature gradients. We present simulation results that indicate distinct, RNA-length dependent accumulation zones. We interpret this as a spatially varying fitness landscape and present an experimental strategy to map it. Our finding implies the possibility of a continuous evolutionary process over multiple levels of innovation in a single compartment, and without the need for temporal changes of the system.

[1] Baaske et al., PNAS 104(22), 9346*9351 (2007)
[2] Kreysing et al., Nat Chem, 7(3), 203*208 (2015)

BP 20.11 Tue 14:00 P1A

Strong accumulation in a 3D printed thermal trap — •Matthias Morasch, Jonathan Liu, Christof B. Mast, and Dieter Braun — Systems Biophysics, Physics Department, Ludwig-Maximilians-Universität München, Amalienstrasse 54, 80799 München, Germany

Thermogravitational traps were shown to be a plausible solution for the concentration problem of the origin of life (1,2,3). In order to simulate the conditions in porous rock more closely, we developed a new microfluidic chamber in which we can accumulate molecules with full optical readout and a wide range of geometries.

Using this technique, we could show a strong accumulation of DNA at water-air interfaces (4). A combination of capillary flow and continuous evaporation-condensation cycles of water pushes the molecules towards the meniscus of the interface, reaching up to 1000-fold accumulation. This robust mechanism may be common for many naturally occurring fluid systems and therefore lead to an accumulation of various kinds of molecules.

In addition, we use the technique to grow crystals from RNA precursor materials inside the chamber. Our goal is to grow a small amount of single, pure crystals from a racemic mixture and measure the chirality of these crystals inside the chamber. We hereby aim to show a plausible scenario for a symmetry breaking process in water-filled porous rocks.

(1) Braun & Libchaber, PRL 89, 188103 (2002) (2) C. B. Mast et al., PNAS 110, 8030-8035 (2013) (3) M. Kreysing et al., Nat. Chem. 7, 203-208 (2015) (4) J. Liu et al., under review

BP 20.12 Tue 14:00 P1A

Microthermal Approaches to the Origin of Life — •Lorenz Keil[1], David Horning[2], Friederike Möller[1], and Dieter Braun[1] — [1]Systems Biophysics, LMU Munich, Amalienstrasse 54, 80799 Munich, Germany — [2]Department of Chemistry, The Scripps Research Institute, La Jolla, CA 92037

All known living systems are built around information stored in RNA and DNA. To protect this information against molecular degradation and diffusion, the second law of thermodynamics imposes the need for a non-equilibrium driving force. We have shown that heat gradi-

ents in millimeter sized pores can drive an accumulation, replication, and selection of ever longer molecules, implementing all the necessary parts for Darwinian evolution. Here, we show that heat gradients can also form pH gradients of at least 1-2 units. Thermophoresis accumulates individual species of a buffer solution differentially at the bottom. Since the accumulation of the proton acceptor is mostly stronger compared to the proton donor, the pH increases towards the bottom of the trap. The result is the formation of a pH gradient facilitated by a temperature difference. This finding opens the door for various reaction pathways to the origin of life that involves pH oscillations. We also found that laminar thermal convection can efficiently drive an ribozyme-based form of polymerase chain reaction. The RNA polymerase ribozyme replicates short RNA strands up to 10 nucleic acids, enabling the propagation of information in a natural environment and the absence of proteins.

BP 20.13 Tue 14:00 P1A

Reversible cooperation of molecular replicators — •Georg Urtel[1,2], Thomas Rind[2], and Dieter Braun[2] — [1]Universite Pierre et Marie Curie, Laboratoire Jean Perrin, 4 place Jussieu, 75005 Paris, France. — [2]Braun Lab, LMU Munich, Amalienstraße 54, 80799 München, Germany.

For evolution to occur, information-carrying molecules have to replicate their information into new molecules before their own degradation. One class of prebiotically plausible molecules capable of carrying information are oligonucleotides. In random sequences, hairpin molecules are ubiquitous [1]. Replication mechanisms typically require an initiation site on the template to start replication (e.g. [2]). Due to their self-complementarity, hairpins replicate exponentially using only one primer. But, the secondary structure inhibits the initiation site and the hairpin replicators grow slow and go extinct even when degradation is weak. Our experiments show how two hairpin species with similar loop sequence can overcome this problem by a reversible cooperation termed 'crossbreeding'. In this mechanism, new species emerge which lose the secondary structure, but keep the sequence information. These crossbreeds replicate more efficient, outgrow the hairpins and survive strong dilutions. The mechanism can be reversed and hairpins can regrow under changed conditions, showing that their information is preserved in the process. [1] B. Obermayer et al., PRL, 107, 018101 (2011). [2] D. P. Horning et al., PNAS, 21, 9786 (2016).

BP 20.14 Tue 14:00 P1A

Globular Protein Design from Ancestral Supersecondary Structures — •Mohammad ElGamacy, Murray Coles, and Andrei Lupas — Max Planck Institute for Developmental Biology, Tuebingen, Germany

Combinatorial reshuffling of subdomain-sized peptides may have provided a very economic means for sequence space navigation and thus protein fold evolution. Previously, through a bioinformatic study we identified a set of highly conserved, subdomain-sized motifs recurring across distant folds, a cue that such motifs may have predated the existing pedigree of folds. This has led to the hypothesis that these ancestral fragments may have provided the basic building blocks for modern protein folds. We also demonstrated repetition of these fragments as a mechanism in creating new folds. The aim of this work was to investigate an alternative mechanism via recombination of heterologous fragments, especially that we were unable to detect any such recombination incidents between the ancestral fragments in modern proteins. To provide an exemplar, we attempted to reconstruct a polymerase-beta N-terminal domain out of two conserved supersecondary structures derived from two unrelated folds. We have done so using a computational strategy that introduces a minimal number of mutations to the constituting fragments. The resulting NMR structure agreed with the designed coordinates with atomic accuracy, demonstrating that a recombination event and a few mutation are sufficient to evolve a new domain.

BP 20.15 Tue 14:00 P1A

On the Physical Origin of Biological Communication — •Matthias F. Schneider — Medical and Biological Physics, Otto Hahn Str. 4, Dortmund, Germany

Life is full of hydrated interface that all have to obey the 2nd Law. The enormous power of this approach was first pointed out by K. Kaufmann starting in the late 80ties when following Einstein's approach to thermodynamics. This work is strongly inspired by his theory.

From a thermodynamic state to (biological) function. With Einstein's approach one finds, that state and state changes regulate morphological transitions, interface conductivity, catalytic rates etc..

On communication. Pulses that propagate in interfaces can modulate the state and hence the aformentioned functions, especially the activity of enzymes. This is in striking contrast to all known biological communication models where diffusion is the key element for transport.

The waves observed can be driven into a non-linear regime, where excitation only occurs over a critical threshold. The striking similarity with the nervous impulse is in support of Kaufmann and Heimburg's work.

Specificity. Finally I present a model where specificity arises naturally from physics and does NOT need to be introduced by structural compatibilities (lock & key).

In conclusion: Excitation, Propagation and Fluctuations arising from physics and lead to phenomnena we ultimately name "function". Importantly, this mind set is in strong contrast to the molecular/structural approach.

BP 20.16 Tue 14:00 P1A

Reactivity of ribonucleotides in hydrothermal prebiotic conditions: an approach from ab-initio molecular dynamics and NMR experiments — •Andrea Pérez-Villa[1], Thomas Georgelin[2], Jean-François Lambert[2], Baptiste Rigaud[2], Marie-Christine Maurel[3], François Guyot[1,3], Marco Saitta[1], and Fabio Pietrucci[1] — [1]IMPMC/UPMC (Paris, France) — [2]LRS/UPMC (Paris, France) — [3]UPMC/MNHN (Paris, France)

The "RNA world" is one of the most accepted hypothesis of origins of life, due to the versatility of RNA in several chemical processes. Previous studies have investigated the RNA formation in different prebiotic scenarios, like the exposure to drying/wetting cycles and the role of mineral surfaces. However, the spontaneous synthesis of RNA monomers (ribonucleotides), in the primitive Earth is still a key question in the prebiotic chemistry field. In this work, we model the reactions involved in ribonucleotide formation/breakdown under hydrothermal prebiotic conditions, by means of ab initio molecular dynamics in explicit water. We exploit free-energy methods combined with a topological approach developed in our group able to accurately describe variations of chemical bonds. From this framework, we explore different reaction pathways for the nucleotide synthesis/degradation as well as quantitatively reconstruct the free energy surface. We also present a series of NMR experiments for the nucleotide to characterize the different substrates and products and determine the kinetics of the reaction, providing complementary information to the simulations and validating the predicted values from the free-energy calculations.

BP 20.17 Tue 14:00 P1A

Driving early biochemical reactions by the thermal accumulation of ATP over ADP/AMP? — •Alexandra Kühnlein[1], Christof B. Mast[1], Amelie Benk[2], Joachim P. Spatz[2], and Dieter Braun[1] — [1]Systems Biophysics and Center for NanoScience, LMU Munich — [2]MPI for Intelligent Systems, Stuttgart

Life is in non-equilibrium. And all prevalent biochemical reactions use ATP as energy source. Can this chemical driving be accomplished from prebiotic gradients? Interestingly, a simple thermal gradient is capable to accumulate ATP over ADP/AMP due to its difference in charge. This mechanism provides a modern energy source with prebiotic mechanisms. With this hypothesis, we can allow previously studied thermal replication and selection systems [1,2] to use ATP as the energy currency of its biochemical reactions. No highly evolved and complex ATP synthase would be necessary for life in its first steps.

Experimentally, we feed the thermal trap with an equilibrium concentration ratio of ATP and ADP. The local accumulation of the energy-rich species is monitored by the fluorescent protein PercevalHR [3] that was generously provided by the Spatz lab.

[1] PRL (2010) doi:10.1103/PhysRevLett.104.188102; [2] Nat. Chem. (2015) doi:10.1038/nchem.2155; [3] Nat. Comm. (2013) doi:10.1038/ncomms3550

BP 20.18 Tue 14:00 P1A

Temporal climatic fluctuations frozen into chemical non-equilibrium: appearance of high-energy biomolecules — •Jean-Francois Lambert[1], Maguy Jaber[2], Thomas Georgelin[1], Mariame Akouche[1], Yuriy Sakhno[1], and Marie-Christine Maurel[3] — [1]Sorbonne Universités, UPMC Univ Paris 06, LRS (UMR7197) Case Courrier 178, 4 Place Jussieu, 75005 Paris, France — [2]Sorbonne Universités, UPMC Univ Paris 06, LAMS (UMR8220) Case Courrier 225, 4 Place Jussieu, 75005 Paris, France — [3]Sorbonne

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Life relies on metastable molecules: prebiotic biopolymers synthesis was thermodynamically upfield in water. Chemical energy had to be extracted from the environment and stored in the system to synthesize them. This can be done by adsorbing precursor molecules on mineral surfaces and submitting them to drying-wetting cycles. When water activity is low, anabolic condensation reactions become favorable and complex biomolecules are formed. We evidenced the generation of peptides from single amino acids, and of nucleotides from ribose, nucleobases, inorganic phosphate, using in - and ex situ analysis techniques. When higher water activity is restored, complex biomolecules become thermodynamically metastable, but for kinetic reasons are not necessarily degraded. One must study the catalytic effect of surface sites on both condensation and hydrolysis, and maintain a clear distinction between thermodynamics and kinetics. In many cases macroscopic fluctuations of water activity can result in chemical energy storage.

BP 20.19 Tue 14:00 P1A

Bridging the RNA and lipid worlds — •James Saenz — B CUBE, Technical University Dresden, Arnoldstrasse 18, 01307 Dresden

How did the first cells arise? Primitive life would have relied on simple systems that could self-assemble from prebiotic molecules and segregate biomolecules through compartmentalization. It is clear that membranes can self-assemble to form compartments. But what selective advantage would membranes have provided to reaction networks of primitive biomolecules? Prebiotic lipid membranes may have been crucial for the emergence of early cells by providing a surface to concentrate and enhance the catalytic activity of primitive ribozymes. To this end, we are exploring how membrane-RNA interactions can lead to an RNA-lipid world on the path to life.