The 22nd annual meeting of The Israel Society for Astrobiology and the Study of the Origin of Life (ILASOL)

28 December 2008, Botnar Hall, Weimzann Institute of Science

- ABSTRACTS -

Thermodynamic and kinetic control of replication processes in peptide networks

Gonen Ashkenasy, Zehavit Dadon and Nathaniel Wagner

Department of Chemistry, Ben Gurion University of the Negev
Beer Sheva, Israel
Tel: +972-8-6461637 Fax: +972-8-6472943
Email: gonenash@bgu.ac.il

Non enzymatic replication has been demonstrated in various different molecular systems including DNA, RNA, peptides and organic molecules. In almost all of these systems the auto catalytic processes result in the ***covalent*** attachment of shorter fragments when forming the new full length molecule. Peptide based replication systems, as well as other systems, have been used to construct networks of replicating molecules, in which replication takes place via auto or cross catalytic reactions. However, the formation of strongly-held replication products allowed utilizing these networks only for demonstration of competition or mutual behaviour under kinetic control. I will discuss here a new system, in which the peptide templates and products contain weaker peptide surrogate bonds. As a result, the kinetics of networks of such peptides is governed both by kinetic control, when replication processes are dominant, and/or by thermodynamic control, where stability of the products is the dominant.

Symmetry and Order in Catalytic Networks

Nathaniel Wagner and Gonen Ashkenasy
Dept. of Chemistry, Ben Gurion University of the Negev, Beer Sheva 84105, Israel

It has been postulated that the building blocks of life and molecular evolution originated with minimal self-replication via simple auto and cross catalytic reactions, which evolved over time into small networks of reactants and templates. Several candidate systems have been proposed for which reactants were originally involved. Furthermore, the level of complexity of these basic catalytic pathways has been a matter of speculation. We show, due to symmetry constraints and reasonable chemical assumptions, that the construction of these networks requires higher order catalytic reactions. Unlike first order catalysis, second order catalysis is inherently both asymmetric and cooperative, allowing for the construction of both asymmetric and cooperative network elements. This strongly suggests that early molecular evolution, self-organization and complexification actually proceeded via higher order reactions.

In this talk we will show mathematically how the construction of these more complex network elements requires higher order catalysis, by analyzing the symmetries and chemical kinetics of cross catalytic template reactions. Then we will discuss the implications of our results on some of the open questions regarding the origin of life, including at which stages of evolution did complexification emerge, and the ongoing debate between the "metabolism first" and "replication first" schools.

Evolving RNA machine for protein biosynthesis

Ilana Agmon, Chen Davidovich, Anat Bashan, and Ada Yonath
Dept of Structural Biology, Weizmann Institute, Rehovot 76100, Israel

Ribosomes are the universal cellular nano-machines that translate the genetic code into proteins. The ribosome’s active site, the peptidyl transferase center (PTC), resides within a highly conserved region of the contemporary large ribosomal subunit. Comprised of 180 nucleotides arranged as a pseudo symmetrical two-fold region in all known ribosome structures, this region confines a void that provides the space required for the production of the nascent proteins. Particularly, the elaborate architecture of this region is capable of positioning both tRNA substrates: (the aminoacylated and the peptidyl tRNA molecules) in stereochemistry required for peptide bond formation and for substrate-mediated catalysis, as well as for substrate translocation, hence enabling the repetition of peptide bond formation and facilitating amino acid polymerization. Consistent with comprehensive mutagenesis experiments and quantum mechanical calculations, nucleotides positioned at the rims of this region appear to navigate this motion and their interactions with the translocating tRNA seem to stabilize the transition state of peptide bond formation.

As the symmetry of this region relates the backbone fold and nucleotides orientation, but not nucleotide sequence, it emphasizes the superiority of functional requirements

over sequence considerations. Furthermore, the overall fold of the RNA backbone of this region resembles motifs identified in “ancient” as well as “modern” RNA molecules of comparable size. Consistently, the extremely high conservation of this region throughout all known kingdoms of life implies its existence irrespective of environmental conditions. The universality of the three dimensional structure of this region, its central location within the ribosome, and the inherent tendency of RNA segment of comparable size to dimerize, indicate that this region may represent the proto-ribosome and support the hypothesis that the proto-ribosome evolved by gene duplication or gene fusion.

Preliminary experimental results and conceptual issues will be presented and discussed.

Two-way interaction between the biota and climate

Hezi Gildor

Dept. of Dept. of Environmental Sciences and Energy Research Weizmann Institute of Science

There is a coupling between the biota and climate on a wide range of spatial and temporal scales. For example, oceanic biological activity is influenced by ocean circulation and mixing processes which regulate the availability of nutrients and light for photosynthesis. In turn, phytoplankton modulate the penetration of solar radiation in the upper ocean controlling, to some extent, the local stratification and sea surface temperature (SST). In addition, oceanic biological activity acts to sequester carbon in the ocean and away from the atmosphere, influencing the radiative balance of the atmosphere. Hence there is a capacity for two-way interactions, or feedback loops, between the biota and climate. As suggested by proxy records extracted from ice and ocean cores, by recent measurements, and by numerical models, such two-way interactions were likely major players in past climate variability, and may act to amplify or moderate an anthropogenically induced climate change in the near future.

In this lecture I shall describe two examples of feedbacks between the biota and climate. In the first example I will demonstrate using a simple coupled physical-biochemical box model of the climate system the amplification of the glacial-interglacial variability of the physical climate system by ocean biogeochemistry. Such an amplifying role of the ocean biogeochemistry may play a role in future climate change. In the second example, I will discuss the "The lightning–biota climatic feedback" which involves an increase in deposition oflightning-produced nitrogen compounds into ecosystems as a response to a global-temperature rise. This increases primary production on both land and ocean, whichreduces atmospheric carbon dioxide (CO2), and consequently global temperature inreturn.

From vesicles to protocells: early transitions in the origins of life.

Kepa Ruiz-Mirazo

Department of Logic and Philosophy of Science, University of the Basque Country

In this talk I will focus on three main issues. First, I will reason why compartmentation is necessarily an early step in the long and complex sequence of transitions from physical-chemical self-organization phenomena towards biological systems. Then, I will explore different compartment-first models (both theoretical and experimental), paying special attention to Szostak's recent contribution to a better understanding of the properties of hypothetically very primitive (fatty acid) membranes. Finally, I will indicate which is, from my point of view, the most promising avenue of research to move beyond these vesicle models and get closer to protocellular (still infra-biological) systems.

In that respect, our idea of 'minimal lipid-peptide cell' will be briefly introduced and compared with other proposals (like the so-called 'ribo-cell'). As a general conclusion, I will present a picture that acknowledges progress being made in the field, but also the big difficulties remaining in order to achieve a bottom-up synthesis of autonomous systems with open-ended evolutionary capacities, i.e., of full-fledged living systems. hools.

Translation efficiency: mechanism and involvement in phenotypic divergence

Orna Dahan, Ran Kafri and Yitzhak Pilpel .

Molecular Genetics, Weizmann Institute.

The utilization of sequence data to gain functional insights into the mechanisms underlying the biology of organisms is a challenging task. We show that phenotypic differences between species may be reflected in translational signals embedded within the coding sequences of the genes underlying the phenotype. By analyzing the coding sequence and the copy number of each tRNA gene in the genome of several yeast species, we have generated profiles of predicted translation efficiency across species. We then examined the functions of gene groups exhibiting similar profiles. Our results demonstrate that translational control signals are correlated with, and perhaps even causative of, life style differences among related species. Although translation efficiency has been extensively researched, there are still many open questions. I will end my talk by presenting our plans to address some of these questions.