101. The Fermi-SETI Paradox: When Should We Expect ET to call?

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If habitable planets on which other spacefaring civilizations could evolve are common, the galaxy should be teeming with life. But there is no sign of this whatsoever, so where are they?This is the famous Fermi Paradox, named after physicist and Nobel laureate Enrico Fermi, who posed the question in 1950. Today it remains one of the most intriguing unanswered questions that greatly affect our view of our place in the universe. More explictly, the Fermi Paradox can be stated as follows: "If there were extraterrestrial civilizations, they should have reached Earth long ago. The lack of any serious evidence for such visits (UFOs and Erich von Daniken don't count), one should conclude we are alone". But are we? The book " Where is everybody" lists some serious solutions (along with many less serious but nevertheless amusing ones) to the Fermi Paradox.
(http://www.nss.org/resources/books/non_fiction/NF_023_whereiseverybody.html)

During 10 years of teaching "Astrophysics and Life in the Universe" at the Hebrew University and at UCLA, astrophysicist Amri Wandel has developped a new approach to the fameous paradox – considering it from the SETI point of view. He presents some convincing solutions to the classical Fermi Paradox, but on the other hand puts up a new approach, which could be dubbed "the Sagan Paradox" after Carl Sagan's famous science-fiction novel (and movie) "Contact".

102. The definition of Genes

Sonja Prohaska
Leipzig University, Germany

103. Identification of the prebiotic translation apparatus within the contemporary ribosome

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Evolution of translation is a key question in understanding the emergence of life. Contemporary translation is a complex process by which the genetic information is converted into proteins. This process takes place at the ribosome, a large, universal ribonucleoprotein catalytic machine that is, correspondingly, most complicated, thus unlikely to emerge as if by chance. Peptide bond is formed at the peptidyl transferase center (PTC), the active site of the ribosomal large subunit. The PTC is confined within a conserved symmetrical region of about 180 nucleotides, which exists in all known structures of the ribosome. The symmetry relates two RNA elements, the A- and the P- sub-regions, having matching 3D folds and nucleotide conformations but nearly unrelated sequences. The reactants are accommodated at the ribosomal A- and

P- sites, being related by an approximate 2-fold symmetry, in a stereochemistry favorable for peptide bond formation.

A structural element that could have existed independently in the prebiotic era and is suggested to be the vestige of the proto-ribosome was identified as being part of the symmetrical region. This simple apparatus, constructed from a dimer of small L-shaped, stable RNA molecules, could have assembled spontaneously under prebiotic conditions. Its structure enabled the catalysis of peptide bond formation in the same manner the contemporary ribosome does and permitted simple elongation. Structural details of this apparatus will be presented and its significance to the evolution of translation and to the origin of life will be discussed.

104. Simulating the Origins of Metabolism

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Computational models of metabolic evolution have demanding pre-requisites. One component is an Artificial Chemistry model as substrate on which a metabolism can be selected. This component must have the sufficient complexity to mimic the complexity of a modern metabolic network, without restricting the possibly chemistry to the 'known' extant end results. In addition, a genetic system that expresses (metabolic) enzymes and a non-trivial map from enzyme or ribosome sequence/structure to catalytic activity must be implemented. Finally, a fitness function must be implemented that evaluates metabolic efficiency. In my presentation I will sketch such a setup and present first results obtained in collaboration with Christoph Flamm and Alexander Ulrich.

201. Rooting the Ribosomal Tree of Life using the early Expansion of the Genetic Code

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The origin of the genetic code and the rooting of the tree of life are two challenging problems in the study of life’s early evolution. Although both have been the focus of numerous investigations utilizing a variety of methods, until now each problem has been addressed independently. Typically, attempts to root the tree of life have relied on phylogenies of genes with ancient duplications, which are subject to artifacts of tree reconstruction and horizontal gene transfer, or specific physiological characters believed to be primitive, which are often based on subjective criteria. Here, we demonstrate a unique method for rooting based on the identification of amino acid usage biases comprising the residual signature of a more primitive genetic code. We find that for a phylogenetic tree of concatenated ribosomal proteins, the branch leading to the bacterial domain contains a strong and unique signal of amino acid bias identifying it as containing the root of the translation machinery.

202. Insert, Fracture, Break and Scatter - Gene Fission by Inteins and Homing Endonucleases

Shmuel Pietrokovski
Dept. of Molecular Genetics, The Weizmann Institute of Science

203. Bacteria Guided Reflections on Water Complexity

Eshel Ben-Jacob
School of Physics and Astronomy, Tel Aviv University

301. Chemical Evolution - The Case of Beta-Galactosidase

Akiva Bar-Nun and Gideon Fleminger
Tel Aviv University

Several years ago we showed that a simple mini-enzyme, consisting of Cys-Cys(Fe+2), is capable of hydrolyzing beta-galactose and also of condensing the two sugars back to beta-galactose under anhydrous conditions. Moreover, it was formed when two Cystein molecules, in the presence of Fe(+2), arranged themselves around the beta-galactose. Our mini-enzyme will be compared with the present day beta-galactoside; a tetramer of 4 identical subunits, each consisting of 1023 amino acids. This huge and very complex molecule is only 1000 times faster than our mini-enzyme in hydrolysing beta-galactose.

302. Self-Assembling Short Peptides: Significance for Prebiotic Molecular Evolution

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Molecular self-assembly is a process by which molecules interact with each other to form supra-molecular structures. Aromatic staking plays a major role in the association of such structures and is known to take part in the formation of amyloid fibrils, which are highly-ordered protein aggregates that are involved in the etiology of various degenerative diseases. Recent studies of aromatic peptides revealed their ability to self-assemble into ordered amyloid-like structures.

The unique physical and chemical characteristics of these peptide assemblies point out their possible role in the origin of life. We have demonstrated the spontaneous formation of self-assembling peptides under prebiotic conditions, which possess the ability to bind and stabilize ribonucleotides. The formation of these peptide

assemblies is dependent on the homochirality of the peptide monomers, a characteristic which consist with the homochirality of all living matter. Based on these findings, we propose a model for the role of short self-assembling peptides in the prebiotic molecular evolution and the origin of life.

303. Replication of Short and Simple Peptides and its Relevancy to the Origin of Life

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Non enzymatic molecular replication has been the subject of intense research over the past two decades, and several different replicating systems have been prepared and analyzed, including nucleic acids, fatty acids, peptides, and organic molecules.[1] Several research groups including the authors have studied in the past ?-helix forming sequences that self assemble to coiled-coil tertiary structures. In these systems, monomeric or dimeric peptides, twenty five to forty amino acids in length, served as templates for substrate binding and thus for enhanced condensation and replication. However, it has been postulated that shorter peptides with simpler sequences may serve as templates for self replication, provided that they are able to arrange themselves into unique and well defined structures. We will discuss here the design, kinetic analysis and relevance to the origin of life of rather simple peptides, close analogs of the synthetic amphiphilic Glu-(Phe-Glu)n peptides that can form soluble one-dimensional ?-sheet aggregates in water, and serve to significantly accelerate their ligation and self replication.[2]

[1] Dadon, Wagner, Ashkenasy "The Road to Non-enzymatic Molecular Networks", Angew. Chem. Int. Ed. 2008, 47, 6128 – 6136.
[2] Rubinov, Wagner, Rapaport, Ashkenasy "Self Replicating Amphiphilic ?-Sheet Peptides" Angew. Chem. Int. Ed. 2009, 48, 6683-6686.

401. Vesicles as Model Compartments for the Study of Minimal Cells and Origin of Life

Tereza Pereira de Souza and Pier Luigi Luisi
Friedrich-Schiller-Universität Jena, Germany

Liposomes and micelles are systems used to study properties of cellular structures. These systems, mimetizing cellular proprieties, have been used to analyze chemical reactions occurring in biological processes, as well to study the putative routes in origin of life. Here we will present some experimental and theoretical studies concerning vesicles self-reproduction (in particular the so-called matrix effect); the interaction between vesicle and RNA, where RNA appears capable of discriminating between vesicles differing slightly in size; also the green fluorescent protein expression inside 200-nm extruded vesicles; some aspects of local concentration inside vesicles; and a theoretical approach for pH and ionic concentration in

membrane neighborhoods.

403. Diploidy and the Selective Advantage for Sexual Reproduction in Unicellular Organisms

Maya Kleiman and Emmanuel Tannenbaum
Ben-Gurion University

The existence of sex is among the most intensively studied problems in evolutionary biology. The current predominant theories for the existence suffer from a number of drawbacks, making the question of the evolution and maintenance of sex an open problem in biology. The various theories either require what may be overly restrictive assumptions to obtain a selective advantage for sex, or assumptions that are not realistic. Here, we develop mathematical models comparing asexual and sexual reproduction strategies based on the asexual and sexual pathways in Saccharomyces cerevisiae (Baker's yeast), a diploid, unicellular organism that engages in a form of sexual reproduction when stressed. Our modeling assumes semi-conservatively replicating, diploid genomes. We find that the explicit consideration of diploidy, a feature lacking in previous models comparing asexual and sexual reproduction, leads to a selective advantage for sexual reproduction under far less restrictive conditions than previous models. We also find an intimate connection between diploidy, sex, and recombination. That is, diploidy only has a selective advantage over haploidy with sex, and sex only has a selective advantage under relatively relaxed conditions when the genome is diploid. Furthermore, sex in a diploid organism is only advantageous with meiotic recombination. These results suggest a plausible explanation for the ubiquity of diploidy and its association with sex in biology, as well as for the existence of meiosis in sexually reproducing organisms.