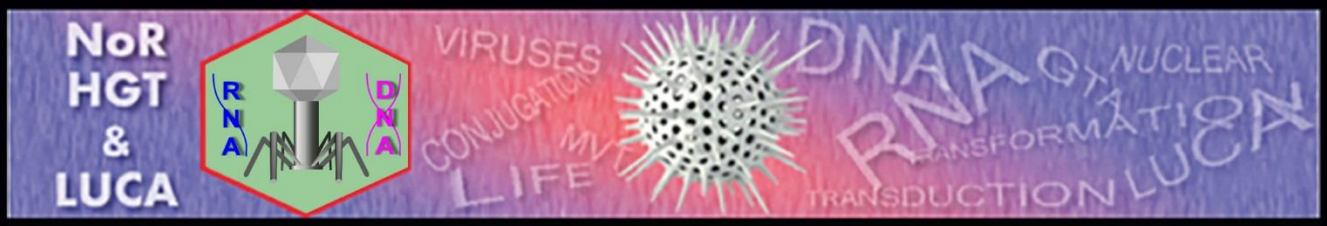
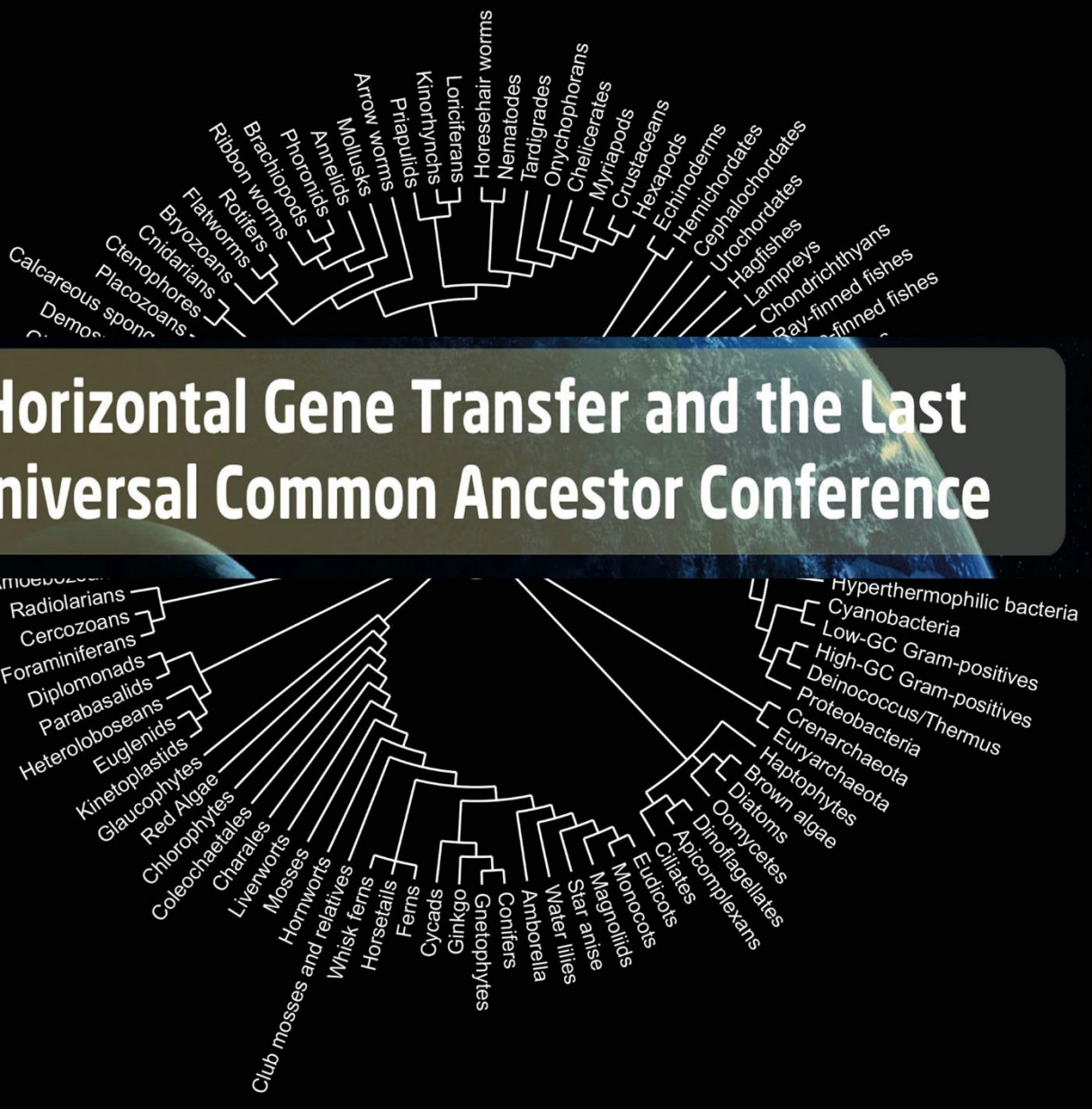
NoR HGT & LUCA





Horizontal Gene Transfer and the Last Universal Common Ancestor Conference

3rd NoR HGT & LUCA Conference

3-4 November, The Open University, Milton Keynes, UK

THE LANDSCAPE OF THE EMERGENGE OF LIFE

NoR HGT & LUCA is a member of the Society of Biology

The Open University

The landscape of the emergence of life

Most scenarios relating to the origin and early evolution of life focus, in a roundabout way, on two main hypotheses, namely the metabolism and the RNA first hypotheses. The former does not necessarily address the chemistry leading up to the point of the formation of the relevant proteins and nucleic acids in enough discernible detail for it to be labelled a 'front runner' hypothesis in the origin of life on Earth. Similarly, the latter does not convincingly explain the formation of the complex nitrogenous bases that are required for the 'knitting' of strands of RNA molecules bases. In both cases, what is required is a demonstration of a series of reactions in tandem, leading to the formation of more and more complex molecules, these being necessary for kick starting life, however what is often shown are scenarios in which hypothetical pathways and cycles are possible. For example, it can be shown that both amino acid and nucleotide oligomers can be made on the surface of clays (eg montmorillonites, (Jheeta, 2014); this is true but what is overlooked, in all cases, are the laboratory physico-chemical preparatory details of the clays required for the oligomerisation to occur, these being absent in nature.

Both metabolism and RNA first hypotheses lack sufficient solid evidence and, as such, there is no clear front runner. However, what these hypotheses have in common is that they are both in favour of life having originated on Earth in contrast to the panspermia hypothesis which broadly contends that life originated elsewhere in the Universe and then was delivered on the Earth ready-made (Hoyle 1983). Since panspermia hypothesis does not address how life originated in the Universe, it will not be considered further in this work.

How do we then unravel the origin and early evolution of life? One way is to assume that amino acids and nucleic acids, as well as their respective oligomers could have been made on the early Earth. We make this assumption so as to expedite the understanding of the emergence of life from a time of early chemistry where amino acids, nucleic acids and oligomers already existed to the point of the formation of LUCA to the subsequent emergence of the three domains of life. The mission of our Network is to examine this period in order to strengthen and expound fully the original hypotheses and ultimately better describe the route of development of the three domains of life.

(Dr Sohan Jheeta)

Jheeta, S., P. C, Joshi (2014) "Prebiotic RNA synthesis by montmorillonite catalysis." Life 4:318-330. doi:10.3390/life4030318
Hoyle, F.; Wickramasinghe, N.C. (1983). "Bacterial life in space". Nature. 306: 420

Acknowledgements: Sir John Mason Academic Trust

The NoR HGT & LUCA conference organising committee acknowledges Sir John Mason Academic Trust http://www.sirjohnmasonacademictrust.uk for its support of the conference. The Committee also acknowledges the Open University and Prof Nigel Mason for making this meeting possible.

Publications Arising from the Meeting

As we had an exceptionally high calibre of abstracts, we have been offered the opportunity by the MDPI's 'Life' Journal to produce a special issue entitled: 'The landscape of the emergence of life' on which I shall be acting as guest editor. This particular issue becomes a realistic proposition only if we submit a minimum of 8 papers, the deadline for the submission being 31st March 2017. Please note that submissions would be subject to the usual peer review criteria. I should like to encourage you all to submit either a results generated or review article and thus help promote our NoR HGT & LUCA network to the wider world.

You can find all the information including instructions for submission of your manuscript at:
http://www.mdpi.com/journal/life/special_issues/landscape_emergence_of_life

Organising Committee

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Prof Nigel J Mason (The Open University, UK - Nigel.Mason@open.ac.uk)

Conference dinner

This will take place at the Kents Hill Helton Hotel at 8.00 pm on Thursday 3rd November 2016.

Conference photo

The month of November is generally not very conducive for taking good photos in the UK, as it may be raining. So we will announce it nearer to the date after checking the weather forecast. One thing is for sure, it will be taken during a lunch break.

Inauguration of a new travel bursary for NoR HGT & LUCA

This year Dr Jheeta has initiated the Sohan Jheeta Travel Award which totals £1000, and which has enabled two postdocs and one PhD student to travel to this meeting in order to be able to participate and disseminate their scientific research at this conference. This award will be available for all future NoR HGT & LUCA conferences.

	Schedule Day 1: Thursday 3rd November
08:15-08:45	Arrival and registration
08:45-08:50	Prof Nigel Mason: The Open University, UK Welcome (5 min)
08:50-09:00	Dr Sohan Jheeta Motivation for the conference and directions for the day (10 min)
	Chair: Dr Martin Dominik: University of St Andrews, Scotland Theme: Last Universal Common Ancestor
09:00-09:45	*Keynote speaker*: Prof Peter Gogarten, University of Connecticut, USA The LUCA and Progenote Concepts – Lessons from the Study of Molecular Evolution and Phylogeny for the Early Evolution of Cellular Life (30+15)
09:45-10:15	Dr Leonardo Sorci, Università Politecnica delle Marche, Italy Bioinformatics and comparative genome analysis unveil an evolutionary conserved phage NAD metabolism (20+10)
10:15-10:45	Prof Tamir Tuller, University of Tel Aviv, Israel Deciphering modeling and engineering the regulatory codes encoded in the viral coding regions (20+10)
10:45-11:15	Coffee Break (30 min)
11:15-11:45	Prof Armen Mulkidjanian, University of Osnabruck, Germany Evolution of energy converting enzymes: Vertical hereditary transmission versus horizontal gene transfer (20+10)
11:45-12:15	Prof Sávio Torres de Farias, Universidade Federal da Paraiba, Brazil tRNAs and the emergence of the translation system (20+10)
12:15-12:45	Ms Isabela Jeronimo, Universidade Federal da Paraiba, Brazil Structural analysis of the proteome before LUCA (20+10)
12:45-13:45	Lunch (60 min)
	Chair: Prof Nigel Mason Theme: Organelles
13:45-14:30	*Keynote speaker*: Prof Helen Hansma, University of California at Santa Barbara, USA Better than Membranes at the Origin of Life (30+15)
14:30-15:00	Dr Christos Kotakis, Academy of Sciences, Hungary Why and how RNA refugeeism potentially outflees gene migrants from chloroplast to the nucleus (20+10)
15:00-15:30	Prof Michael Galperin, the National Center for Biotechnology Information, USA Likely HGT in the Evolution of Signal Transduction in Bacteria and Archaea (20+10)
15:30-16:00	Prof Claudia Lage Universidade Federal da Rio de Janeiro, Brazil The Last Unique Community Ancestors: characterising a photosymbiotic interaction among pigmented organisms from the extreme Atacama Desert (20+10)
16:00-16:30	Coffee break (30 min)
	Chair: Elias Chatzitheodoridis Theme: Prebiotic studies
16:30-17:15	*Keynote speaker*: Prof Giuseppe Battaglia, University College London, UK From Reductionism to Constructionism: Why copying Nature can help to understand (30+15)
17:15-17:45	Dr Stefan Fox, University of Hohenheim, Germany The Origin of Life on Primordial Volcanic Islands – From Prebiotic Chemistry to the First Organisms (20+10)
17:45-18:15	Mr Ryo Mizuuchi, Osaka University, Japan Adaptation, diversification, and evolution of complexity of a simple artificial RNA self-replication system (20+10)
18:15-18:45	Dr Sohan Jheeta, Independent Educator and Research Scientist, UK Hypothesis: Network of RNAs and their Influence on Life
	Close of day 1: Relax, socialise and get ready for the conference dinner
	Drink and Conference dinner

	Schedule Day 2: Friday 4th November
	Chair: Dr Sohan Jheeta Theme: evolution of simple genomes
08:30-09:15	*Keynote speaker:* Prof Andrew Pohorille, NASA Ames Research Center, USA The Origin and Early Evolution of Information Transfer in Biological Systems (30+15)
09:15-09:45	Dr Kevin Devine, London Metropolitan University, UK An Astronaut in Structure Space: Probing the structure, function and evolution of nucleic acids using synthetic organic chemistry (20+10)
09:4510:15	Dr Ole Herman Ambur, Oslo and Akershus University College of Applied Conservative sex in bacteria (20+10)
10:15-10:45	Dr Soren Overballe-Petersen, Natural History Museum of Denmark, University of Copenhagen, Denmark Why do we still have mitochondrial DNA? (20+10)
10:45-11:15	Coffee break (30 min)
11:15-11:45	Prof Rosanna del Gaudio, Università degli Studi di Napoli Federico II, Italy Triggering the emergence of life on Earth: a possible role of self-assembly M4 material for the origin of living-matter (20+10)
11:45-12:15	Dr Amr Aswad, University of Oxford, UK Unusual large dsDNA viruses discovered among genome data of 15 different fish (20+10)
12:15-13:15	Lunch break
	Chair: Dr Martin Dominik Theme: continuing with pre-RNA and RNA chemistry
13:15-14:00	*Keynote speaker:*Prof Ramanarayanan Krishnamurthy, the Scripps Research Institute, La Jolla, USA Heterogeneity to Homogeneity: Rethinking the RNA-world Hypothesis (30+15)
14:00-14:30	Mr Asif Iqubal, IIT Roorkee, India Thermal Condensation of Glycine and Alanine on Metal Ferrite Surface: Primitive Peptide Bond Formation Scenario (20+10)
14:30-15:00	Ms Laiken Shepherd, University of Arkansas, USA Potential Growth and Survival of Sulfate-Reducing Bacteria on the Martian Surface
15:00-15:30	Dr Claudio Maccone, IAA, Italy Evo-SETI : a mathematical tool for Cladistics, Evolution and SETI
15:30-16:00	Ms Ramandeep Kaur Horizontal Gene Transfer (15 + 5)
16:00-16:15	Summary and further instructions – Dr Sohan Jheeta
16:15-16:20	Closing of the meeting – Prof Nigel Mason

Day 1

Thursday, time: 09.00-09:45

The LUCA and Progenote Concepts – Lessons from the Study of Molecular Evolution and Phylogeny for the Early Evolution of Cellular Life

Keynote speaker: J. Peter Gogarten, University of Connecticut, Storrs, CT 06269-3125, USA
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Abstract

The concept of the Last Universal Common Ancestor (LUCA, also known as organismal cenancestor) pertains to the organism that was the most recent common ancestor of all now living cellular organisms, i.e., that organism at the deepest bifurcation of the Tree of Cells (ToC). Debate is ongoing, if one can reconstruct a detailed well resolved ToC from molecular phylogenies. (For discussion see [1]). One reason for the difficulty is Horizontal Gene Transfer (HGT), which has played an essential role in the spread of genetic and metabolic innovations between distantly related organisms. Because of HGT the most recent common ancestors of different molecules did not all coexist in the organismal LUCA. The molecular cenancestors existed in different lineages and at different times [2]. Nevertheless, molecular data for the translation machinery, combined with data from gene families that underwent ancient gene duplications and whose duplicates presumably were already present in LUCA's genome (ATPsynthases, elongation factors, amino acyl tRNA synthases) suggest that LUCA is located in the ToC between the bacterial domain on one side, and the archaeal domain and eukaryotic nucleocytoplasm on the other.

The progenote denotes a state in evolution, when the molecular machineries for replication, transcription and translation were "still in the process of evolving the relationship between genotype and phenotype"[3]. Woese [4] described a Darwinian threshold separating the progenote from cellular life whose phenotype is linked to its genotype. While different molecular system may have crossed this Darwinian threshold at different times, data from ATPsynthases and the translation machinery indicate that LUCA more resembled a modern prokaryotic cell than a progenote [5]. Molecular data suggest that the progenote stage and LUCA are connected by a very long evolutionary history [6–8].

Ancestral sequence reconstruction suggests that the ancestors of the bacterial and archaeal domains were extreme thermophiles, whereas the LUCA sequences reflect less thermophilic adaptations [9–11]. These observations are compatible with a bottleneck that occurred at the time of the domain ancestors. Only organism that had previously adopted to higher temperatures survived through this bottleneck. This inference is also supported through the tree shape of molecular phylogenies [2,12].
A candidate for the events causing this early bottleneck is the late heavy bombardment [13], or the tail of the early heavy bombardment. This explanation implies that life is older than 3.8*109 years BP, and had adapted to different ecological niches on early Earth already when the last nearly sterilizing impacts hit the Earth.

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Thursday, time: 09:45-10:15

Bioinformatics and comparative genome analysis unveil an evolutionary conserved phage NAD metabolism

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Abstract

Bacteriophages, in addition to genes essential for their own propagation, can harbor a second class of genes which are not directly implicated in the viral infection and replication. Although there is a general consensus that these genes confer selective advantage to viruses, there is a paucity of information on their possible function. Thus, more evidence is needed to support this paradigm. Enormous advances have been made in phage genomics in the last few years, offering novel opportunities to tackle this problem with bioinformatics approaches.

Using comparative genome analysis performed on nearly two thousand complete phage genomes currently available, we identified a group of nearly fifty phages encoding their own biosynthesis pathways to the essential NAD cofactor from the vitamin precursors nicotinamide (Nm) and nicotinamide riboside (NmR). This viral NAD synthesis is distinct from the bacterial host NAD biosynthesis which is supported by a different set of genes. A comprehensive genomic reconstruction of phage-encoded NAD metabolism, which included NAD-consuming activities, identified three distinct metabolic variants capable of i) synthesizing and consuming NAD, ii) consuming NAD, or iii) synthesizing nicotinamide mononucleotide, a rare NAD metabolic intermediate in bacteria. We propose that these variants reflect different strategies contributing to subvert the machinery of the host cell. Finally, a phylogenetic analysis of the phage NAD biosynthetic shunt revealed a complex evolutionary scenario dominated by cross-kingdom gene transfer events. Notably, these phages assembled their own NAD pathway by acquiring and possibly modifying functionally related genes from host cells, but also contributed to spread these functional roles across a diverse group of bacteria. This case may be a relevant, and yet undisclosed example of how viruses contributed to fine-tune metabolic processes in the early evolutionary history of life.

Thursday, time: 10:15-10:45

Deciphering modeling and engineering the regulatory codes encoded in the viral coding regions

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Abstract

A virus is a small infectious agent that replicates only inside the living cells of other organisms. While viruses possess similarities to known life forms (organisms/cells), they have often been described as 'organisms at the edge of life'. Furthermore, it is well known that viruses have important roles in horizontal gene transfer (HGT). Thus, studying the way viruses' genomes encode their replication efficiency should contribute towards better understanding the origin of life and HGT.

Some viruses encode several regulatory factors required for autonomously controlling different replication steps; however, all viruses require the usage of host factors for successfully completing their cell cycle. Hence, a natural research question is how are various codes related to gene expression and the viral life cycle encoded in the viral genetic material.

In the current study, we analyzed dozens of viral genomes and their hosts to understand the extent by which gene expression codes are encoded in the viral coding region. The analysis included dozens of viruses, most viral groups (e.g. dsRNA, ssRNA, dsDNA, ssDNA, etc), and numerous hosts (e.g. vertebrates, bacteria, fungi, etc). The analysis was performed with a novel statistical measure that enables capturing variable length regulatory signals.

We show that a large fraction of the viruses from all group types are enriched with such signals in the coding regions, and that these signals cannot be explained by simple features of the coding regions such as codon usage bias and di-nucleotide composition. Thus, the results shed light on the way regulatory signals are encoded in the viral genetic material and affect its evolution.

Thursday, time: 11:15-11:45

Evolution of energy converting enzymes: Vertical hereditary transmission versus horizontal gene transfer

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Abstract

Energy converting systems of modern organisms are sophisticated, fine-tuned networks of membrane-embedded protein complexes that use external energy sources such as light, nutrients or redox gradients to generate ion disequilibria across ion-tight membranes. The ion gradients formed can discharge through rotary membrane ATP synthases. In prokaryotes, bioenergetic cycles exist in two versions, with either protons or sodium ions being translocated though the ATP synthase. Earlier, by combining comparative structural and phylogenomic analyses, we have suggested the evolutionarily primacy of the sodium-dependent bioenergetics, which, in turn, could develop from an ancient system of cellular Na^+/K^+ homeostasis [1-7].

Indeed, the cell cytoplasm of archaea, bacteria and eukaryotes contains substantially more potassium than sodium, and the prevalence of potassium ions is specifically required for many key cellular processes. This distinct ionic composition and requirements have been attributed to the emergence of the first cells in K^+-rich habitats [4, 8]. Marine and freshwater environments generally show a $[K^+]/[Na^+] < 1.0$. Therefore, to invade such environments, while maintaining the cytoplasmic $[K^+]/[Na^+] > 1.0$, primordial cells needed means to extrude sodium ions. The foray of primordial cells into new, Na^+-rich habitats was the likely driving force behind the evolution of diverse sodium export pumps.

At high external sodium levels an ATP-driven rotary Na^+ export pump, still functioning in some prokaryotes [9-11], could change the direction of rotation and become a Na^+-driven ATP synthase. The resulting interplay between the ATP synthase and the sodium export pumps would have yielded the Na^+-dependent membrane bioenergetics [2, 3, 7].

Apparently, the emergence of modern energy-converting machinery could not be a one-time event. Rather, it should have been a evolutionary process gradually producing new energy-converting enzymes. Once emerged, the enzyme complexes would spread among bacterial and archaeal lineages either via vertical hereditary transmission or horizontal gene transfer.

Based on most recent findings [7, 12, 13], it would be discussed, which energy-transducing complexes could precede the Last Universal Cellular Ancestor (LUCA). The widespread energy converting complexes that came after the LUCA, would be related to their origin within Bacteria or Archaea, respectively.

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Thursday, time: 11:45-12:15

A proposal of the proteome before the last universal common ancestor

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Abstract

The search for understanding the biological nature of the last universal common ancestor (LUCA) has been a theoretical challenge and has sparked intense debate in the scientific community. We reconstructed the ancestral sequences of tRNAs in order to test the hypothesis that these molecules originated the first genes. The results showed that the proteome before LUCA may have been composed of basal energy metabolism, namely, compounds with three carbons in the glycolytic pathway, which operated as a distribution centre of substrates for the development of metabolic pathways of nucleotides, lipids and amino acids. Thus, we present a proposal for metabolism in organisms before LUCA that was the initial core for the assembly of further metabolic pathways.

Thursday, time: 12:15-12:45

Structural analysis of the proteome before LUCA

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Abstract

Carl Woose (1998) suggests that prognotes, primitive cells before the LUCA had limited metabolism and an imprecise translational system that would have probably been the first pathway to be developed. Following this, rudimental metabolic pathways with little or no necessity of enzymatic action evolved. Among the modern pathways, the Amino acids pathways, Glycolysis/ gluconeogenesis, Lipids pathways, Nucleotides pathways, Translation and Transcription or RNA replication are believed to have been present in or even before LUCA. This is based on the wide presence of these pathways distributed though the three domains. Also, their anaerobic characteristics that would have been necessary in a primitive Earth. Keller et al (2014) show evidence that Glycolysis/ Gluconeogenesis and the pentose phosphate pathways could have been constrained by the iron-rich oceanic environment of the early Archean ocean.

Storey et al (2004) suggests the first enzymes would have worked as binding domains that would simply increase the probability of the substrates to react to one another. Farias et al (2016) found similarities between transcripts of tRNAs and proteins from the pathways we assume to have been present in LUCA. This work is part of a series of others that will follow proposing the structural reconstruction of the metabolic network present in the prognotes, based on the proteome proposed by Farias et al (2016). That is, we are proposing how the ancestral form of the proteins present on these pathways reacted to the substrate and which parts of the docking system were preserved through time.

We obtained 400 protein sequences of the proteins found in the similarity analysis from NCBI (http://ncbi.nlm.nih.gov/). We calculated the best fit model of molecular evolution using ProtTest 3.2, which, for the proteins from the Glycolysis/Gluconeogenesis pathways pointed out to be LG (Le and Gascuel, 2008). A phylogenetic tree to establish ancestral sequences was constructed by Maximum Likelihood method (PhyML) through T-Rex (http://www.trex.uqam.ca), for each enzyme. Using the inferred trees and the sequences, with MEGA6 program we calculated the ancestral sequence. The structure of each ancestral sequence obtained was obtained by the Iterative Threading ASSEmbly Refinement (http://zhanglab.ccmb.med.umich.edu/I-TASSER/). The three dimensional models obtained were aligned with TM-align (http://zhanglab.ccmb.med.umich.edu/TM-align/). The obtained results indicate that during the process of origin and diversification of these proteins, on the early steps of the formation of the first biological systems, these pathways worked as binders of the substrates. This decreases the entropy of the system, increasing the efficiency of this proto-catalysis machinery. These data indicate the evolutionary routes of these main pathways of carbon usage. It suggests that these proto-enzymes worked as a binding center constituting what we call a “Bindomer” of the biological system previous to the Last Universal Common Ancestral. Keller et al. (2014) suggests that the first metabolic pathways related to carbon usage might have occurred in a prebiotic environment without the need of enzymes. Thus, with our results, we suggest that the development of the early translating machinery created the possibility of the evolution of the first proteins. Hence, the natural selection acted on these new entities, and according to what is suggested by Storey (2004), these systems that had proteins that increased the efficiency of preexisting pathways were positively selected. Moreover, we will discuss, based on this and on oncoming data, the chemical composition of the LUCA.

Thursday, time: 13:45-12:30

Better than Membranes at the Origin of Life

Keynote speaker: Helen Hansma, University of California at Santa Barbara, USA

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Abstract

Lipid bilayer membranes are fragile. Nonetheless they are a popular hypothetical environment for the origins of life. Most subcellular organelles are enclosed in lipid membranes. Some organelles, however, are membrane-less. The best known of these membraneless organelles is the nucleolus, which contains components of ribosomes. The nucleolus is, physically, a liquid-in-liquid phase separation within the nuclear matrix (1). Membraneless organelles such as the nucleolus are a logical organelle at the origins of life, because they do not need to be enclosed in fragile lipid membranes. Furthermore, the nucleolus is likely to be an organelle that formed near the origins of life, because ribosomes contain some of the most ancient protein and RNA molecules. This ancient origin for ribosomes further supports the idea that membraneless organelles such as the nucleolus were formed at the origins of life. The primordial nucleolus needs an enclosure during the origins of life. The spaces between Muscovite mica sheets provide an enclosure (2). The spaces between Muscovite mica sheets provide an environment high in potassium (K) ions, like the intracellular environment, and anionic crystal lattices with a spacing of 0.5 nm, which is also the distance between anionic phosphate groups in extended single-stranded RNA and DNA. Mica's anionic crystal lattices are above and below the K-rich layer, forming both a 'ceiling' and a 'floor.' An endless energy source for the origins of life is provided by 'open-and-shut' movements of mica sheets in response to temperature changes and fluid flow. This mechanical energy (work) is arguably the fundamental form of energy in enzymatic reactions, although the obvious form of energy for enzymatic reactions is now chemical energy, typically ATP. In the 'mica world' hypothesis, mechanical energy was used directly for forming chemical bonds, rearranging prebiotic polymers, and blebbing off protocells before a transition to chemical energy such as ATP.

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Thursday, time: 14:30-15:00

Why and how RNA refugeeism potentially outflees gene migrants from chloroplast to the nucleus

to eros effect underneath ellie

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Abstract

Keywords: cell evolution, endosymbiotic gene transfer, non-coding RNAs, bioenergetics, cytoplasmic inheritance

Gene loss from 'organellar' genomes (eg chloroplast, mitochondria) to the nucleus has occurred throughout the evolutionary history of eukaryotic cells. The transfer of these genes is mainly ruled out by DNA-directed mechanisms, while corresponding RNA phenomena remain to be an exception, especially when the movement of genetic material is coming from the chloroplast. Here, we try to understand to what extent the rarity of such RNA-mediated events is a real biological fact, by democratizing novel knowledge on the RNA modularity. Recently, evidence has emerged to indicate that small silencing RNAs can affect i) the (sub-)cellular redox poise as well as ii) they can trans-act in different sub-compartments, beyond the sites of their biogenesis. These mobile ribo-signals could shape the epigenetic memory of the organelle-nucleus dual since redox coupling synchronizes the genomes' functionality. To decipher the biochemical nature of the facilitator, lifetime methodologies on live-RNA tracking in combination with elegant biotechnological tools can overcome technical obstacles concerning detection of short biomolecules in contrast to previous attempts that failed to probe similar turnover. Therefore, experience on nucleic-acids topology & stability can explain the DNA chronicity in gene transfer processes as well as envisage under which micro-climatic circumstances, if any, RNA can rebel, as a gene integrating factor into the chromatin vicinity. Moreover, paradigms and biological analogies from the literature will be discussed, under this umbrella. Indeed, comparative data mining for editing commonalities in the genomes of photosynthetic extremophiles, via RNA species mediation can elucidate possibilities for ribo-traces trafficking in-between the genomic loci. Last but not least, the physiological significance of RNA intermediates in the major evolutionary transitions of eukaryotic genomes' architecture will be dismantled in relation to compartmentalization issues and the RNA world hypothesis.

Thursday, time: 15:00-15:30

Likely HGT in the Evolution of Signal Transduction in Bacteria and Archaea

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Abstract

The ability to sense the physico-chemical parameters in the environment, including the ambient temperature, pH, salinity, osmotic pressure, and presence of nutrients and poisons, is a key property of all live cells. This ability allows the cells to adjust their metabolism and the properties of the intracellular milieu to ensure cell growth and survival. The complexity of sensory and signal transduction systems even in classical model microorganisms has long hindered their systematic analysis. Now, the availability of complete genome sequences from key bacterial and archaeal lineages allows us to identify all (known) regulatory components in a given organism, compare their organization in various organisms, and try analyzing their evolution.

By studying the genomic distribution of signal transduction proteins, we were able to show that their total number grows approximately as a square of genome size, with different systems being able to cross-talk and compensate for each other. Comparative genomics revealed the presence of two-component signaling systems (sensor histidine kinases and response regulators), methyl-accepting chemotaxis receptors (MCPs), diadenylate cyclases, and Ser/Thr protein kinases and protein phosphatases, both in bacteria and archaea. Other signal transduction systems, such as adenylate and diguanylate cyclases and phosphodiesterases, ECF sigma factors, and PTS components have been seen so far only in bacteria. All these systems are widespread in various bacterial lineages, suggesting an early origin of the signal transduction machinery in the bacterial domain. In contrast, in archaea, phylogenetic distribution of signal transduction systems is extremely biased, indicating that archaeal MCPs and at least some sensor histidine kinases appeared in archaea through HGT from bacteria. Thus, only Ser/Thr protein kinases and protein phosphatases likely trace back to LUCA, which could be due to the higher stability of phosphoSer and phosphoThr as compared to phosphoHis and phosphoAsp residues. Whether sensor histidine kinases and diadenylate cyclases were already present at the level of LUCA remains an open question.

Thursday, time: 15.30-16:00

The Last Unique Community Ancestors: characterising a photosymbiotic interaction among pigmented organisms from the extreme Atacama Desert

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Abstract:

LIGHT harvesting systems should have played roles in ancient energy collecting mechanisms, feeding primitive chemical routes. Chlorophyllated micro-organisms appear to exist in early Earth. An epilithic community from a coastal arid Atacama Desert containing black fungi + chlorophyllated bacteria suggests melanoidins to switch UV into photosynthetic light by fluorescence emission, which we defined as a PHOTOSYMBIOTIC community, suitable to exist, or to set life, in high-UV planetary surfaces.

Thursday, time: 16:30-17:15

From Reductionism to Constructionism: Why copying Nature can help to understand

Keynote speaker: Giuseppe Battaglia, University College London, UK

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Abstract

From a physical point of view, living systems are the result of a very precise and balanced hierarchical organisation of molecules. This means that from atomic to macroscopic scale, biological processes evolve via the organisation (and disorganisation) of matter. Molecules are often joined together via controlled-sequence polymerisation forming macromolecules with specific chemical signatures that direct supramolecular interaction between themselves and/or with water. Such interactions are singularly low in energy (i.e. few kTs), and their combination allows the formation of dynamic mesoscopic architectures with exquisite spatial and temporal control. This process, known as self-assembly, is ubiquitous in Nature and is at the core of many biological transformations. Alongside positional self-assembly, Nature creates energy gradients by enclosing chemicals into aqueous volumes using gated compartments. Both compartmentalisation and positional self-assembly create structures whose surfaces express several chemistries performing their function holistically, according to specific topological interactions. As our knowledge of this natural phenomenon advances, so do the efforts in creating functional materials and devices that exploit the same principles. Among the different biomimetic efforts, we have focussed our attention in possibly one of the few that encompasses polymerisation, compartmentalisation and positional self-assembly in the same unit; Polymersomes. These are vesicles formed by the self-assembly of amphiphilic block copolymers in water. Copolymers can be fully synthetic and/or derived from biomolecules and their sequence can be engineered to control both interactions with water and among each other. In analogy to natural vesicles (typically formed by phospholipids), polymersomes can house controlled aqueous volumes to create chemical potentials across the membranes. However, the macromolecular nature of the polymersome building blocks allows the design of vesicle membranes with control over their thickness, brush density, mechanical properties, and permeability.

Thursday, time: 17:15-17:45

The Origin of Life on Primordial Volcanic Islands – From Prebiotic Chemistry to the First Organisms

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Abstract

On the early Earth four billion years ago, volcanic islands protruded from the primordial ocean. These islands provided many beneficial locations for prebiotic chemical processes which may have led to a protometabolism from which the first life originated. In this context, a very important property of volcanic coasts (dry land) is that in rock pools higher concentrations of organic molecules can be achieved. This is a result of both water evaporation and accumulation of the molecules. Therefore, it is more plausible that key prebiotic reactions took place in rock pools at volcanic coasts rather than in the open ocean. Low concentrations in the ocean, which were a result of a strong dilution effect, were unfavorable for virtually all chemical reactions and therefore adverse to chemical evolution. But even at higher concentrations, condensation reactions such as peptide, oligonucleotide and lipid formation are not straightforward in an aqueous “primordial soup.”

In addition to polymerization, amino acids could have reacted under the conditions of volcanic coasts to form products other than peptides. A series of experiments simulating the thermal alteration of amino acids and subsequent reactions have been performed in our laboratory. The experiments resulted in the formation to pyrroles and their polymerization to porphyrins (Fox and Strasdeit 2013). Furthermore, in the presence of suitable “Hadean” minerals, finally metalloporphyrins were formed.

Due to their exceptional stability and diverse properties, metalloporphyrins are an extremely interesting class of prebiotic molecules. Particularly remarkable properties of metalloporphyrins are the ability to transport electrons and to harness light. Exactly these functions are implemented by cytochromes and chlorophylls in modern organisms. Hence, it is obvious that porphyrin-type cofactors (PTC) could have played an important role in chemical evolution and thus in the origin of life. Once established in a protometabolism, PTCs could have enabled the formation of “unfavorable” products such as peptides and RNA/DNA. Biological evolution started at the latest when ribosomal protein synthesis emerged.

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Thursday, time: 17:45-18:15

Adaptation, diversification, and evolution of complexity of a simple artificial RNA self-replication system

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Abstract

One approach to understand the origin of life and the following evolution is to construct a simple self-replication system and investigate the evolution. As such a system, we have developed a translation-coupled RNA replication system by combining a reconstructed E. coli translation system and an artificial RNA genome encoding only a gene of Qβ replicase (RNA-dependent RNA-polymerase) which replicates the RNA genome once translated. This simple life-like system with only a small number of components and biological functions may resemble a molecular system in a preLUCA world. If encapsulated in a cell-like compartment, the system evolved according to Darwinian principles by introducing mutations into the genome through repetitive replications [1]. Recently, we have examined adaptive evolutionary ability of the system. Adaptive evolution is one of the most striking characteristics of living things, which allows them to survive in various environments and eventually diverge into distinct species. We repeated replication reactions in five different translation-impaired conditions, in which initiation, release, or entire translation process was partly inhibited by reducing different translation proteins. In all the conditions, the RNA genome adapted and exhibit higher replication activities by introducing mutations. For example, the RNA genome accumulated mutations around ribosome binding site and increased translation efficiency in a ribosome-reduced condition [2]. Furthermore, comparison of sequences between RNA genomes evolved in different conditions showed clear diversification depending on the conditions [3]. RNA genomes evolved in closer conditions converged into close sequences, and vice versa. These experiments demonstrated that a simple artificial self-replication system with only one gene has a certain ability of adaptive evolution. What is a next evolution? One crucial evolution in primitive life is undoubtedly evolution of complexity. Such evolution includes acquisition of components, genetic information, functions, and so on. However, we have not detected such an evolution in our system through continuous replication experiments, indicating that there may be hidden properties or conditions remaining to be provided. As a first step to reveal what is essential, we have expanded the RNA replication system to one in which two RNA genomes encoding different genes are linked in a hypercyclic network [4], and each of them cooperatively replicates depending on both the RNA genomes. By scrutinizing the stability and the evolutionary ability, some prerequisites for evolution of complexity in primitive life may be clarified. We would like to show and discuss our current situations.

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Thursday, time: 18:15-18:45

Hypothesis: Network of RNAs and their Influence on Life

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Abstract

RNAs are widespread and are involved in multilaterally adapted systems that control numerous cellular processes, the dimensions of which are still being explored. The RNA molecules are able to form primary (mRNA), secondary (hairpins), tertiary (RNA-induced silencing complex, RSIC) and quaternary (ribosomes) structures. Such structures are multifunctional and are broadly regulatory being involved in gene regulation as well as interfering with and processing of both small and large RNAs. Recent discoveries have also demonstrated that RNAs can act as riboswitches, whereby they regulate their own activity; and perform genetic control by a metabolite binding mRNA.

RNAs in addition act as triggers against invading mobile genetic elements thereby affording protection against such incoming attacks. Their actions are also well orchestrated, even to the point of efficient shedding of any unwanted RNAs - for example used mRNA within the cell is degraded by RISC centre.

During this oral presentation I will put a case for RNAs being involved in the overall cellular activities of cells and speculate that this 'cellular activity control' is passed on from one generation to the next, whereas the overall genetic information still resides with the DNA.

Day 2

Friday, time: 08:30-09:15

The Origin and Early Evolution of Information Transfer in Biological Systems

Keynote speaker: Andrew Pohorille, Mark Ditzler, Milena Popovic and Chenyu Wei, NASA Ames Research Center, USA

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Abstract

Was linear information transfer coded in nucleic acids present since the emergence of the simplest biological systems? Was there ever a biological world based on a single polymer? What was the imperative to develop precise mechanisms of information transfer? To what extent was early evolution of genomes predictable? What was the role of chance events during this evolution? The answers to these and a number of related, fundamental questions remain unknown, but we can obtain valuable clues through a combination of novel experimental and theoretical approaches. Some of these clues will be discussed in this talk with a focus on a possibility of obtaining a coherent picture of how information was transferred and evolved at the beginning of life.

Friday, time: 09:15-09:45

An Astronaut in Structure Space: Probing the structure, function and evolution of nucleic acids using synthetic organic chemistry

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Abstract

Modern terran life uses several essential biopolymers like nucleic acids, proteins and polysaccharides. The nucleic acids, DNA and RNA are arguably life's most important, acting as the stores and translators of genetic information contained in their base sequences, which ultimately manifest themselves in the amino acid sequences of proteins. But just exactly what is it about their structures; an aromatic heterocyclic base appended to a (five-atom ring) sugar-phosphate backbone that enables them to carry out these functions with such high fidelity? In the past three decades, leading chemists have created in their laboratories synthetic analogues of nucleic acids which differ from their natural counterparts in three key areas; (a) Replacement of the phosphate moiety with an uncharged analogue, (b) Replacement of the pentose sugars ribose and deoxyribose with alternative pentose and hexose derivatives, and finally (c) Replacement of the two heterocyclic base pairs adenine/thymine and guanine/cytosine with non-standard analogs that obey the Watson-Crick pairing rules. The talk will examine in detail the physical and chemical properties of these synthetic nucleic acid analogues, in particular on their abilities to serve as conveyors of genetic information. And if life exists elsewhere in the universe, will it also use DNA?

Friday, time: 09:45-10:15

Conservative sex in bacteria

Ole Herman Ambur, Oslo and Akershus University College of Applied Sciences, Norway

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Abstract

We learn that HGT is an important source of genetic innovation in living organisms today and a prerequisite for the early evolution of life itself. Notably, HGT in bacteria encompass three modes of DNA transfer: conjugation, transduction and transformation. I will argue that transformation differs in evolutionary rationale from the other two modes. Transformation is the process that is most similar to eukaryotic sex and may therefore share selective advantages. The study of small DNA Uptake Sequences in the Neisseriaceae family has revealed a conservative output from transformation, traceable in deep time. These and other observations will be discussed to generate an important nuance in the commonly held view that HGT generates novelty and innovation.

Friday, time: 10:15-11:45

Why do we still have mitochondrial DNA?

Soren Overballe-Petersen, University of Copenhagen, Denmark

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Abstract

The persistence of mitochondrial DNA (mtDNA) in the eukaryotic cell remains mysterious. Most mtDNA genes have re-located to the cell nucleus since mitochondria originated from bacterial endosymbiont hundreds of millions of years ago. Yet, across eukaryotes small mitochondrial genomes persist, which encode a highly conserved core of proteins that are subunits in transmembrane proton-pumps. Despite decades of investigation it remains debated why these core genes do not transfer and current hypotheses cannot explain their functional importance in mitochondria. The evolutionary history suggests that there is a strong negative selection against the presence of these mtDNA-encoded subunits in the nucleus. Empirical and theoretical considerations indicate that the long-term persistence across eukaryotes of the core of protein-coding mtDNA is linked to a strong physical-chemical function.

Based on protein structures and functional gene-transfers I propose that proton-channels that disrupt cellular integrity may be the reason why mtDNA genes are prevented from transferring to the nucleus and therefore persist in mitochondria.

Friday, time: 11:15-11:45

Triggering the emergence of life on Earth: a possible role of self-assembly M4 material for the origin of living-matter

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Abstract

The origin of life is one of the great unsolved enigmas of science. The steps in Earth's transition from a lifeless planet to a world harbouring Life being one of the main questions. It is very likely that the process or the processes of selecting, concentrating and organizing prebiotic organic molecules into the informational polymeric macromolecules typical of life have occurred, albeit the mystery of how life first emerged on Earth, remains unsolved.

Life as we know it is so complex that it needed many billions of years to evolve - the earliest life dates back to 3.8 billion years ago, emerging shortly after the cessation of the bombardment of the Earth by meteorites. Life could have originated elsewhere in the Universe and then taken refuge in the deep ocean environment during the bombardment.

In addition, many theories and experimental investigations have focused on the clue to the role that the mineral surfaces have played in the formation of proteins, lipid bilayers and polynucleotides, because the formation of peptide bonds requiring condensation is thermodynamically unfavourable in aqueous solution.

The possible roles of mineral surfaces in protecting, selecting, concentrating, templating and catalysing reactions of prebiotic organic molecules are recurrent themes in literature focused on life's origins.

The exact details of how, when and where life began remain an unsolved mystery and so I propose that the origin of life on Earth represents only one pathway among many, along which life can emerge.

In this research topic a new approach, aimed at revealing the ability of meteorites and some terrestrial rocks containing iron to perform catalytic reactions operative in present-day life was previously [1] and recently reported [2].

The aim of this work is to present and discuss the results of past [3], recent [4], [5], [6], and further ongoing (molecular and catalytic) studies supporting the multiple root genesis hypothesis (MuRoGe) already proposed [4] in order to approach the questions surrounding the origin of life.

In conclusion, the MuGeRo core hypothesis proposes that a non-enzymatic, photochemical or self-sustaining reaction might be a primitive form of reaction network, supporting abiogenic development of life on Earth or elsewhere in the Universe and probably responsible for the emergence of a large pre-biotic pool of molecules. These reactions appear sufficient to provide the variety and abundance of biologically favorable molecules from which Darwinian selection operating at molecular level may have seeded proto-metabolic reaction in pre-biotic contexts. This concept has to be considered in addition to the hypothesis that microbial or early forms of life were already present in our solar system at the time of Earth's formation [7,8].

To clarify I propose the hypothesis in which an Earth-centric origin of life is considered not necessarily alternative and biology is considered in a 'multiversal' perspective in which all living beings are descendant from a plurality of ancestral forms of life. Not only a single LUCA (Last Universal Common Ancestor) as proposed before (9) or IDA (Initial Darwinian Ancestor) (10) but a number of them. In conclusion,

my questions are that, “can we exclude that different organisms subject to similar environmental conditions gradually converge and can mask evidence of independent biogenic events? And, can we exclude that alien life forms have begun their activity on the Earth using a different set of amino acids evolving up using the same basic molecules appearing analogous to life forms of the current life tree?”

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Friday, time: 11:45-12:15

Unusual large dsDNA viruses discovered among genome data of 15 different fish

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Abstract

Metagenomics allows us to explore viral biodiversity at multiple taxonomic levels, while paleovirology, the study of ancient viruses, has developed out of a need to investigate evolutionary history at different phylogenetic depths. By combining these perspectives and methodologies, we demonstrate the value of mining public data of host genomes for the discovery of novel viruses (both ancient and extant). For example, we have previously described novel viral sequences related known primate herpesviruses in the genome records of their hosts. More recently, we have applied this technique to discover fifteen new viruses that belong to a new lineage of large DNA virus. This unusual clade of viruses is only distantly related to known families, and their genomes include many predicted ORFs that are not similar to known genes. Given that the generation of genomic data is outpacing our analytical capacity, we describe the transferability of this perspective to different research contexts, and discuss how we can use these findings to reconsider existing practices in genome sequences and viral discovery.

Friday, time: 13:15-14:00

Heterogeneity to Homogeneity: Rethinking the RNA-world Hypothesis

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Abstract

In the origins of life studies, the emergence of RNA is considered an important stage.[1] This has led to the RNA-world hypothesis which postulates that RNA appeared as the first self-replicating molecule that is capable of Darwinian evolution, and subsequently gave rise to all other important class of biomolecules.[1-3] While there are continuing efforts to have RNA available as early as possible through primordial prebiotic chemistry[4], it is paralleled by a continuing debate whether immaculate RNA can arise by prebiotic pathways.[1-3, 5,6] Arguments and considerations have been presented where RNA could have appeared at a later stage where both the chemical processes and the environment would have been more favorable for RNA's sustained formation and function.[5-7]

In our approach for understanding the emergence of RNA, we are investigating the base-pairing properties of potentially natural RNA-alternatives that would have been formed starting from the same building blocks, by the same potential prebiotic pathways that would have led to RNA.[8] This has, naturally, led us to investigate the properties of chimeric oligonucleotide systems, which have produced results that prompt us to question the current model of transition of one homogeneous-system to another ("genetic take over") in a primordial (prebiological and/or protobiological) world.[9] The presentation will focus on the recent work from our group which leads us to rethink the RNA world hypothesis as currently formulated and promulgated.

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Friday, time: 14:00-14.30

Thermal Condensation of Glycine and Alanine on Metal Ferrite Surface: Primitive Peptide Bond Formation Scenario

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Abstract

Amino acid condensation reaction on heterogeneous mineral surface has been regarded as one of the important pathway for the primitive peptide bond formation. Keeping in view of this, we have studied oligomerization of simple amino acids glycine and alanine on nickel ferrite ($NiFe_2O_4$), cobalt ferrite ($CoFe_2O_4$), copper ferrite ($CuFe_2O_4$), zinc ferrite ($ZnFe_2O_4$) and manganese ferrite ($MnFe_2O_4$) nanoparticles surface at the temperature range of 50-120°C for 1-35 days without applying any wetting /drying cycle. Among the metal ferrite tested for their catalytic activity, nickel ferrite produced highest yield of the products by oligomerizing glycine upto trimer level and alanine upto dimer level where as manganese ferrite behaved as least efficient catalyst by producing lowest yield of the products as well as shorter oligomer of amino acids under the same set of experimental condition. It produced primarily DKP (Ala) with a trace amount of alanine dimer in case of alanine condensation while glycine is oligomerized upto dimer level. The trend in the product formation is in accordance with surface area of the materials. The temperature as low as 50°C even favors the peptide bond formation in the present study which is important in the sense that the condensation process is highly feasible without any sort of localized heat that may originate from volcanoes or hydrothermal vents. However, at high temperature 120°C, anhydrides of glycine and alanine formation are favored while optimum temperature for the highest yield of product formation was found to be 90°C. Metal ferrites can be regarded as divalent metal ion doped iron oxide mineral and these structural characteristics of metal ferrite allow us to compare its catalytic activity with respect to pure iron oxide mineral. We found that divalent metal ion doping in iron oxide enhances the catalytic activity appreciably by giving higher yield of products as compared to pure iron oxide.

Friday, time: 14:30-15:00

Potential Growth and Survival of Sulfate-Reducing Bacteria on the Martian Surface

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Abstract

Though Martian surface conditions may appear too unforgiving to support the growth of any organism, life has been observed on Earth that thrive in comparable conditions. Extremophile sulfate-reducing bacteria can be regarded as an optimal model as they exhibit a high potential to flourish in these harsh conditions. The bacteria strains selected for this research demonstrate a survival tolerance for extreme conditions by using varying adaptive measures such has psychrophilic tolerance, chemolithoautotrophic metabolic systems, and sporulating capabilities. To be considered an appropriate candidate for theoretical survival on Mars, these bacteria will need to withstand temperatures of -50°C and pressures of 0.006 bar, among other stressors. Therefore, the purpose of this study is to determine the survival rates and biosignatures of sulfate-reducing bacteria (Desulfotalea psychrophila, Desulfotomaculum arcticum, and Desulfuromusa ferrireducens) in conditions that will replicate those existing on present-day Mars. Furthermore, identified biosignatures of the studied bacteria will aid NASA's Planetary Protection policy by assisting in the recognition and mitigation of potential contamination on extraterrestrial bodies. After the preliminary tests, growth was observed in each of the control experiments for all three organisms. DNA purification and isolation has led to successful PCR analyses for future DNA amplification. Further Mars simulation experiments will be conducted in the Pegasus Planetary Simulation Chamber at the Center for Space and Planetary Sciences at the University of Arkansas.

Friday, time: 15:00-15:30

Evo-SETI : a mathematical tool for Cladistics, Evolution and SETI

Claudio Maccone, *Director for Scientific Space Exploration, International Academy of Astronautics (IAA), Italy. Chair, IAA SETI Permanent Committee, Retired Director, Istituto Nazionale di Astrofisica (INAF, Italy)*

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ABSTRACT

The discovery of a larger and larger number of Exoplanets raises a question: where does a newly-discovered Exoplanet ***stand*** in its capability to develop of Life as we know it on Earth?

Our tentative answer to this question is our Evo-SETI Theory, a mathematical model aiming at casting Cladistics and the Evolution of Life on Earth over the last 3.5 billion years in terms of a few simple statistical equations based on lognormal probability distributions ***in the time***, rather than in the amounts of something else.

The first new notion is that of a b-lognormal, i.e. a lognormal probability density function (pdf) starting at time $b>0$ rather than at time zero. The lifetime of any living form may then be expressed as a b-lognormal starting at b, reaching puberty at the ascending inflexion point a ("adolescence (end)"), raising up to the peak time p, then starting to decline to the descending inflexion point s ("senility") and finally going down along a straight line up to the intercept with the time axis, that is the "death" of the individual. Based on all this, the author was able to derive several mathematical consequences like the Central Limit Theorem of Statistics re-cast in the language of Evo-SETI theory: from the lifetime of each individual to the lifetime of the "big b-lognormal" of the whole population itself to which the individual belongs ("E-Pluribus-Unum Theorem").

In addition, this author discovered the ***"Peak-Locus Theorem" translating Cladistics*** in term of Evo-SETI: each SPECIES created by Evolution over 3.5 billion years is a b-lognormal whose peak lies on the ***exponential*** in the number of alive Species. More correctly still, this exponential is not the exact curve telling us exactly how many Species there were on Earth at a given time in the past: on the contrary the exponential is the ***mean value of a stochastic process*** called "Geometric Brownian Motion" (GBM) in the mathematics of Finances, so that also the Mass Extinctions of the past are incorporated in Evo-SETI Theory as all-lows of the GBM.

But then: what is the Shannon ENTROPY of each b-lognormal representing a Species? Answer: the Shannon ENTROPY (with a reversed sign) is the MEASURE OF HOW EVOLVED THAT SPECIES WAS, or is now, compared to other Species of the past and of the future. That means ***MEASURING EVOLUTION, at long last: a number in bits, typical of Shannon's Information Theory, rather than a mountain of words!***

One more key point: what is the equivalent of the MOLECULAR CLOCK in Evo-SETI Theory? Answer: it is the STRAIGHT LINE behavior in time of the Shannon Entropy if (and only if) the exponential is the enveloping curve of all the b-lognormals representing the various Species (called "Evo-Entropy" in our papers).

Concluding top remark: this author was able to GENERALIZE his Peak-Locus Theorem from the simple exponential case to the GENERAL CASE when the mean-value-envelope is not just an exponential, but rather an ARBITRARY CURVE that you may chose at will: for instance, it as a polynomial of the third degree in the time in the Korotayev-Markov (2007) model of evolution, leading then to a non-linear entropy. What a neat mathematical tool for future biologists willing to understand our statistically simple Evo-SETI Theory!

Friday, time: 15:30-16:00

Types of Horizontal Gene Transfers

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Abstract

A broad definition of HGT can be construed as a mechanism whereby there is a transfer of genetic material between donor and recipient cells or the active take-up of heterologous DNA from the environment by recipient competent cells, followed by recombination or replication (Sohan Jheeta, NoR HGT & LUCA Chairman, 2013). I will give a short introduction on the modes of HGT in nature.

Additional abstract received

The Ski-Lift Thermodynamic Pathway and its Possible Bearings of Horizontal Gene Transfer

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Abstract

In all living systems, complexity is a hallmark of their structure and evolutionary progress, and information is a basic currency, alongside with matter and energy, which they exchange with the environment and process within them. The quantitative measures of complexity and information are famously based on the thermodynamic measure of entropy. How, then, do living systems create and maintain these currencies? Surprisingly, the most efficient pathway is to create a too-ordered state first, eventually letting it "deteriorate" into a complex or informational one. The same holds for transitions from one complex/informational state to another. I present several biological examples for this dynamics, which I argue to be ubiquitous. I conclude with some possible support of this dynamics to the likelihood and importance of Horizontal Gene Transfer.

Lithium's Role in the Emergence of Life

Gary Giulian, NIST Gaithersburg, USA

Abstract

Lithium as a hydrated monovalent cation is used to treat Bipolar Depression, plays an important role in preventing suicide and ameliorating Alzheimer's Disease. Its biological Mechanism of Action (MOA) remains unknown. As an element Lithium has ancient biological roots and appears to be relevant to the transition from pre- to early biotic life and HGT. Lithium is found in biologically relevant concentrations (~ 1 mM) only at undersea thermal vents and on land at thermal springs. Under a thermal spring model for pre- to early life transitions Lithium had a unique opportunity to impact pre-biotic chemistry, early enzymatic activity and HGT. Once evolving life moved from thermal springs to the greater ocean and landscapes Lithium's biological impact would diminish as its free concentration diminishes from mM to uM levels. New solution NMR evidence supports a ternary complex of Li-Mg-ATP with a Li+ Kd≈1 mM. The co-binding effect for the cation (< 1 mM Kd) is also observed for PPi, PPPi, 2,3-DPG, F1,6BP, and IPx. The highest concentration of Lithium in treated patients is found in the hydrated outer bone layer rich in magnesium and free phosphates adjoining the mature HAP bone. This evidence supports a general concept of Lithium co-binding to Mg/phosphate rich sites such as those commonly found in a number of essential/ancient co-factors: NTP (ATP), NDP (ADP), Pxi Acetyl-CoA, NADP, andhexose/pentose/inositol di-x-phosphates. Prior to an RNA World (polynucleotides) the chemical components of nucleic acids, amino acids, and enzymes must be present. These co-factors building blocks such as ATP (NTP/NDP/NMP) pre-date more complex structures and require soluble metal ions such as Mg, Mn, Zn, Fe and I. Lithium is simply another metal ion with inducing biological effects, although restricted to specific locations (thermal fields) and time sequence (ancient). Using the Brenda and Manet databases >175 enzymes were identified with published Lithium effects and crystal data for protein fold assignment. For more than 80% of these enzymes the earliest fold type is ancient >3 Gya. All of the enzymes require LMW co-factors/substrates/metals linked to Lithium co-binding. We postulate that Lithium's biological effect evolved in a pre-biotic/early biotic era along with the chemical formation of essential co-factors (e.g. ATP). Lithium "tagged along" with key cofactors at vent sites and then its role diminished during later evolution. The most common bio effects for Lithium are correlated to ancient information transfer, sugar metabolism and signal transduction pathways. The ancient enzymatic pathways appear essential to understanding Lithium's MOA. Thermal vent sites are known for significant HGT events in prokaryotes/Archea. Lithium and calcium are used in laboratory-based HGT methods. The combination of thermal site chemistries and their dynamic physical environment (e.g. recently identified micro-electrical fields) support thermal field HGT events during early evolution. In sum a co-factor model is presented that impacts on Lithium's MOA and its role in the emergence of life.

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