THEME 1: Emergence and Evolution of Microbial Life

Wednesday, September 7th 2023

The Gaian Bottleneck Solution to Fermi's Paradox

Charley Lineweaver
Australian National University, Canberra, Australia

Abstract

There are billions of Earth-like planets in our galaxy. On average they are 2 billion years older than our Earth. If life has emerged on them, they will have had 2 billion years longer than life on Earth has had to evolve. Two billion years is plenty of time for star-faring life forms to colonize the entire galaxy. Where is everybody? This is Fermi’s paradox. I will present a solution to Fermi’s paradox that depends on the uncommon early microbial Gaian regulation of a rocky planet’s atmosphere.

Between Chemistry and Microbiology: Features of the Transition to Life

Vladimir Kompanichenko
Institute for Complex Analysis of Regional Problems RAS, Birobidzhan, Russia

Abstract

The presentation will consider the evolution of metabolic processes during the origin of life on Earth. The basis is the developed concept of thermodynamic inversion, in which the transition from chemical to living systems is considered through a change in the balance "total entropy contribution (Sc) / total free energy contribution (Fc)" from positive to negative [1]. According to the inversion approach, this transition occurred through an intermediate state that was maintained in an oscillatory regime. In microbiology, a resting bacterial cell occupies a similar intermediate position between non-living and living: it is unable to resist the growth of entropy, but retains structural memory of the previous living state (for example, stored RNA transcripts). From this follows the idea of the possibility of correlation of these processes - prebiological and microbiological, the starting point of which is an intermediate state.

In both cases, the further development of metabolism proceeded against the background of an increase in the reserves of free energy in the system, contradictory trends towards heterogeneity and cooperation, and the prevalence of synthesis over destruction. Using the experimentally established sequence of metabolic changes during the release of a resting cell from anabiosis as a basis, the following stages of the origin of metabolism under oscillatory conditions of hydrothermal systems on the early Earth are distinguished: 1 - self-assembly of organic microsystems; 2 - their transition to an intermediate state, weak respiration (protocells); 3 - formation of the protein-synthesizing apparatus (living subcells); 4 - formation of the genetic apparatus and growth cycle (living cells). Thus, the stages of the origin of life are conserved in the stages of the exit of a resting bacterial cell from anabiosis and are repeated each time during the anabiotic process.

References: [1] Kompanichenko V.N. Thermodynamic Inversion: Origin of Living Systems. Springer, Cham (Switzerland), 2017, 275p

Castor and Pollux: the Twin Sons of LUCA and the Two Origins of Cells

Francisco Prosdocimi
Universidade Federal do Rio de Janeiro, Brazil

Abstract

Castor and Pollux: the twin sons of LUCA and the two origins of cells (a presentation based on this article https://doi.org/10.1016/j.biosystems.2021.104371, together with new ideas we developed since then. Our model predicts two origins for cells, one for Bacteria and another for Archaea, and I can present some arguments in favor of this model.)

The Non-equilibrium Thermodynamics of the Origin and Evolution of Life

Karo Michaelian
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Abstract

The most general scientific framework incorporating the laws of Nature, applicable to most known processes to good approximation, is that of thermodynamics and its extensions to treat out-of-equilibrium phenomena. In this talk I employ the non-equilibrium thermodynamic framework to describe the origin of life as a set of microscopic dissipative structuring events leading to a “Pigment World” once the initial conditions and the external force over the system are specified. Inherent non-linearity in the chemical and photochemical reactions gives rise to numerous stationary states permitting the system to evolve, on amplification of a fluctuation, towards concentration profiles of pigment molecules and their complexes providing generally greater photon dissipation through thermodynamic selection on dissipative efficacy. The example of the dissipative structuring of a UVC pigment, and one of the fundamental molecules of life (found in all three domains), adenine, from HCN in water solution under UVC light is presented.

THEME 2: Microbial Life in Extremes and Astrobiology

Thursday, September 7th 2023

Astrobiology of Venus

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Khanty-Mansyisk, Russia

Abstract

In recent years, the interest of astrobiologists to Venus drastically increased due to an active discussion of the habitability of its cloud layer where the existence of the so-called aerochemo(photo)lithotrophic microbial community, using sulfur and iron compounds as the main elements for energy production is hypothesized.

To date, there are various concepts of the geological past of Venus, in which the availability of water on its ancient surface is discussed. The absence or presence of water reservoirs on the ancient surface of Venus can directly support one or another hypothesis of the possible origin of life on Venus.

These hypotheses include the surface or subsurface scenario, in which life emerges in the process of increasing complexity of molecular systems. In addition, the clouds themselves can also be considered as a system that meets the requirements for the emergence and further evolution of living organisms. An alternative concept is panspermia, which transforms the problem of the origin of life into that of its delivery to Venus from the outer space and further adaptation of alien organisms to conditions in the Venusian clouds with their subsequent evolution.

In general, Venus is a unique cosmic body, on the example of which it is possible to model various concepts of the origin of life and scenarios for its further evolution.

Elusive Microbiota in the Subglacial Antarctic Lake Vostok – a Challenge to Justify (by DNA Fingerprints)

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Abstract

The subglacial Lake Vostok is the largest, deepest, and most studied lake among more than 675 subglacial lakes (water features) inventoried through airborne radio-echo sounding and satellite altimetry surveys. It is located beneath the Russian Vostok Antarctic research station and has already been unsealed in triple. The naturally refrozen lake water, or accretion, ice collected by deep drilling and used as a proxy for the lake water has proved exceptionally clean, though much diluted, leading to

controversial biological and chemical analyses. Nevertheless, the likely indigenous DNA fingerprint of thermophiles and some other bacteria seem to fit with the lake's extreme environment.

Although the Russians were the first to enter a subglacial Antarctic Lake at a significant depth (3769 m) and were able to perform the lake entry triple, the drilling technology used (electromechanical drill along with kerosene drilling fluid with the use of foranes as densifier) proved to be inappropriate to collect the liquid water in general and clean samples in particular. More technological developments are needed to face the challenge and justify the microbial findings.

Finally, since the subglacial Lake Vostok may be viewed as the only extremely clean (microbe-free) giant aquatic system on the Earth, it provides a unique test area for searching for life on icy worlds such as Jupiter's moon Europa or Saturn's moon Enceladus. Confirmation of life living in Lake Vostok would strengthen the prospect of the possible presence of life on icy moons and planets.

Microbial Life in Highly Chaotropic Environments

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Abstract

Recent observations of Martian surface have revealed the eventual presence of acidic, hypersaline, magnesium- and/or calcium-rich paleolakes that were intermittently available on ancient Mars. Because of their potential for habitability and preservation of biosignatures in sediments deposited in a quiescent environment, paleolakes are considered high priority targets for astrobiology research. The problem of life at high concentration of divalent cations has provoked a resurgence of interest in the study of similar geological formations, which can also be found on Earth in the form of Mg2+-saturated (5.0M) Mediterranean deep-sea anoxic lakes Discovery, Hephaestus and Kryos and Ca2+-saturated (6.0M) surficial pool Don Juan Pond (DJP) (Dry Valleys, Antarctica). Tremendous salinity, low water activity and extreme chaotropicity attributes these hydrological formations to the harshest and polyextreme environment on Earth, where presence of liquid water is insufficient to support life. Indeed, there are no conclusive evidences of microbes able to dwell in Kryos, Hephaestus and DJP brines and sediments. This is because Mg2+ and Ca2+-rich brines denotes substantial thermodynamic distance across the water-activity scale between the point where life is known to cease (0.585 water activity, aw) and the aw value of Discovery, Kryos, Hephaestus and DJP brines (0.382-0.411). However, biological activity has been occasionally documented on the DJP waterside and in the seawater-brine interfaces of Discovery, Kryos and Hephaestus, where both salinity and chaotropicity is reduced. Goal of our study was to decipher the microbial communities that thrive on the edge of life and to understand to what extent life can withstand the multiple stresses occurring in these intriguing environments.

Astrophysical Source of Radiation and Life in the Universe

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Abstract

Astrobiology explores the possibility to find life outside the Earth in other planetary bodies, but which are the fundamental factors that can be beneficial or detrimental to the existence of life on other planets? Radiation plays a fundamental role in it, therefore is essential to study its impact at different scales in the universe to unravel which regions of the universe, and ultimately which planets, could host life. Additionally, it is essential to note that, based on "life as we know it", microorganisms are considered par excellence models of "life" in astrobiological-related research, given that this biological search is mainly oriented towards the finding of simple life forms. In this talk, I will make a brief review of the current knowledge we have on the topic of the influence of the astrophysical sources of radiation on life (e.g.: stellar radiation), and I am going to focus on some particular cases of microbiological experiments under laboratory conditions used to simulate radiation environments to obtain some answers in reference of the effects of stellar radiation at planetary scales.

Atacama Desert (AD) Natural Lab. Why the Different Stakeholders of the AD are Interested in the Territory's Microbiology?

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Abstract

The Atacama Desert (AD) is considered a natural laboratory because it hosts unique environments relevant for research on different disciplines for getting relevant knowledge. Indeed, it possesses fundamental exceptional features: exposed geological consequences of subduction tectonics; hyperaridity; life inhabiting extreme conditions; geochemical anomalies of valuable resources (Cu, Li, Au, Ag, B, Mo); v) resilient peoples; a manifested Anthropocene. Coupled to the clearest skies in the world, those features have shaped and still currently shaping several exceptional places and conditions such as i) water stress and saline domain hazards and risks like

earthquakes, ii) volcanism and high level of arsenic and borate, iii) presence of paleoclimatic records, fossils, biosignatures, and archaeological records, iv) concentrations of Mars analogues, v) unusual impact on “One Health” and vi) the occurrence of an unique flora, fauna and microbial diversity. In addition, human activities of exceptional production and impact (transhumant agriculture and livestock, mining exploration and production, tourism, sustainable biotechnological applications, exploitation of non-conventional energy resources, astronomical observation, research on Mars analogs) also take advantage on those unique features.

Our work with the different stakeholders has allowed us to decipher their interest in the territory's microbiology. It points out that mining and energy enterprises, as well as the public sector and the community are interested in the mining impact of saline/metal deposits exploitation as well as the “green” energy plant operations on the microbial diversity. Mining enterprises are also interested in the microbiology of their industrial bioleaching operations, the biggest in the world. Farmers, ranchers, and the community are interested in microorganisms which play a role in the contamination events of the only river crossing the AD. The community is interested in the potential of that unique microbial diversity on the development of biotechnological processes/industries for economic diversification. The scientific community is interested in research on the limits of microbial occurrence and metabolisms, and on Mars analogues. Moreover, based on their cosmovision which fundaments their identity, the aboriginal communities consider microbial communities inhabiting the salt flats, with their colours and structures, as the hot spot where life started. We´ll present research results highlighting the current knowledge of the microbial diversity in the ecosystems that take the attention of the stakeholders.

DNA: a Single Molecule with Multiple Origins

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Deputy CEO of NoRCEL and Head of NoRCEL’s Sessions group

Abstract

One of the major evolutionary transitions that led to DNA replacing RNA as the primary informational molecule in biological systems is still the subject of an intense debate in the scientific community. DNA polymerases are currently split into various families. Families A, B, and C are the most significant. In bacteria and some types of viruses, enzymes from families A and C predominate, whereas family B enzymes are more common in Archaea, Eukarya, and some types of viruses. A phylogenetic analysis of these three families of DNA polymerase was carried out. We assumed that reverse transcriptase was the ancestor of DNA polymerases. Our findings suggest that families A and C emerged and organized themselves when the earliest bacterial lineages had diverged, and that these earliest lineages had RNA genomes that were in transition-that is, the information was temporally stored in DNA molecules that were continuously being produced by reverse transcription. The origin of DNA and the apparatus for its replication in the mitochondrial ancestors may have occurred independently of DNA and the replication machinery of other bacterial lineages, according to these two alternate modes of genetic material replication. The family C enzymes emerged in a particular bacterial lineage before being passed to viral lineages, which must have functioned by disseminating this machinery to the other

lineages of bacteria. Bacterial DNA viruses must have evolved at least twice independently, in addition to the requirement that DNA have arisen twice in bacterial lineages. We offer two possible scenarios based on what we know about bacterial DNA polymerases. One hypothesis contends that family A was initially produced and spread to the other lineages through viral lineages before being supplanted by the emergence of family C and acquisition at that position of the principal replicative polymerase. The evidence points to the independence of these events and suggests that the viral lineage's acquisition of cellular replicative machinery was crucial for the establishment of a DNA genome in the other bacterial lineages, since these viral lineages may have served as a conduit for the machinery's delivery to other bacterial lineages that diverged with the RNA genome. Our data suggest that family B initially established itself in viral lineages and was transferred to ancestral Archaea lineages before the group diversified; thus, the DNA genome must have emerged first in this cellular lineage. Our data point to multiple evolutionary steps in the origins of DNA polymerase, having started off at least twice in the bacterial lineage and once in the archaeal lineage. Given that viral lineages are implicated in a significant portion of the distribution of DNA replication equipment in both bacterial (families A and C) and Archaeal lineages (family A), our data point to a complex scenario.