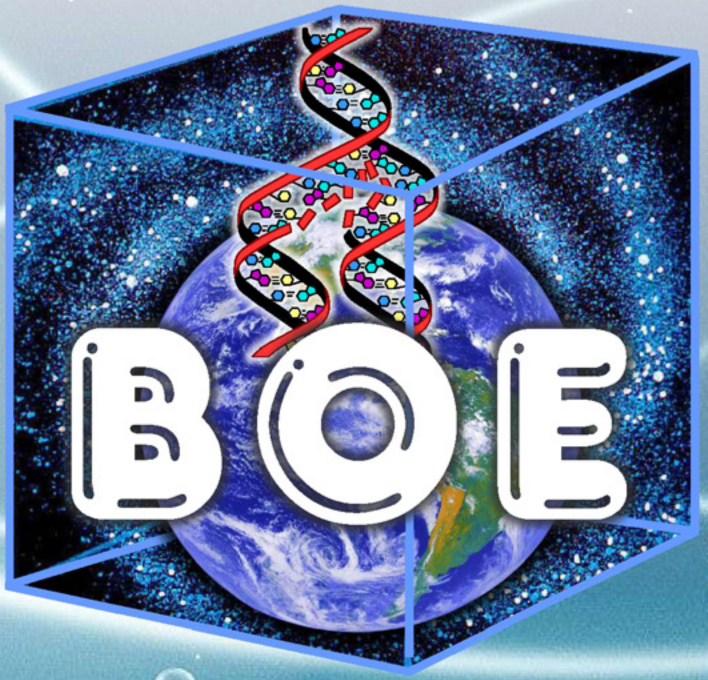
III International Conference

BIOSPHERE ORIGIN AND EVOLUTION

OCTOBER 16 - 20, 2011

RETHYMNO, CRETE, GREECE



ABSTRACTS

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III International Conference "Biosphere Origin and Evolution"

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ABSTRACTS

Novosibirsk, 2011

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PLENARY LECTURES

PL-1

EARTH AND PLANETS ORIGIN: HOW DO WE VIEW AND MODEL IT?

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Solar system origin is regarded as a cornerstone of the planets formation and eventually Earth evolution towards biosphere set up. While planets birth from gas-dust discs is quite routine process in our and other galaxies, solar system configuration, and specifically Earth, seems to be unique. Obviously, multiple physical and chemical processes underlied this event and ensured specific scenario to distinguish solar system from other planetary systems. Understanding and reconstruction of these processes is the main goal and the great challenge of the planetary cosmogony. The contemporary views and further progress in the field are supported by astronomical observations of the numerous gas-dust discs around young solar type stars, escalating discoveries of extrasolar planets, and computer modeling of the planetary systems formation and early evolution based on the advanced theoretical approach and enormous advancement in computing capacity.

Complex problems are addressed in the models development, data of observation placing important constraints on the models validity. Our approach is based on heterogenic mechanics of turbulent media involving in-depth study of disc thermodynamics on the accretion stage from which the key cosmochemical consequences emerge. In particular we argue that because in the region of Earth-Venus orbit temperature was not lower than 300–500 К, the reduced water-lacking matter different from CI carbonaceous chondrites by absence of hydrosilicates and volatiles would originated. This means that Earth and its neighbors has born as water-poor bodies and an other source of volatiles, probably of exogenic nature, would require to compensate such a lack and to make possible their hydrosphere/atmosphere appearance. Comets and asteroids impacted inner planets at the very early stage of the solar system formation are invoked as such a plausible source.

Disc dynamics is thoroughly evaluated with the involvement of dust subdisk formation in the near-equatorial plane and its fragmentation into dust clusters due to gravitational instability accompanied by the angular momentum transfer. Numerous solid bodies of asteroid size appeared from subdisk at this early stage within the first million years after solar system formation – evidence that is supported by radio isotopes dating of iron and stony meteorites available as collisional fragments of these bodies which are regarded as the first planetesimals (embryos of planet-size bodies). The follow up evolutionary dynamics of the protoplanetary disc appears to involve the continuing processes of remaining dust clusters and planetesimals of different size collisions. Basically our dynamical models are focused on the molecular dynamics approach and weighted Monte Carlo algorithms for numerical evaluation of dust clusters formation including coagulation processes and solid bodies interaction under various physical-chemical parameters and geometry. Peculiarities of gas-dust clumps interaction with different mass ratio and collision velocities, as well as physical mechanisms occurred in the contact zone of interacting solid bodies involving energy redistribution and some other non-linear effects were investigated.

The models developed allow us to distinguish between the more or less realistic mechanisms of planets grow from planetesimals incorporating chronology emerging from radio nuclides isotopy. Some important questions remain open, however, in particular those about stability maintenance of dust clusters and solid bodies within ring compression, time scale of the processes of interaction and phase transitions including, first of all, condensation and coagulation. These questions and prospects of further study are discussed in terms of their impact on the intriguing problem of life and biosphere origin.

PL-2

ANALYSIS OF ISOTOPE SYSTEM DATA (Hf-W, Rb-Sr, J, Pu-Xe, U-Pb) AS APPLIED TO THE PROBLEM OF PLANET FORMATION. CASE STUDY: EARTH-MOON SYSTEM

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Isotope data provide important geochemical constraints for models of accumulation of planets, including the Earth-Moon system.

Short living isotope ^{182}Hf decays into ^{184}W with $T_{1/2}$ ~ 9 million years, so that Hf-W system enlightens the very early stage of accumulation of planets. In particular, analysis of the ^{182}Hf/^{184}W system shows that the Moon could not have come into existence earlier than 50 million years after formation of the Solar system. Since, on the other hand, there are certain rocks on the Moon whose age has been estimated as approximately 70 million years after formation of the Solar system, the Hf-W system indicates that the likely interval of formation of the Moon would be 50-70 million years.

In contrast to ^{182}Hf ^{87}Rb is a very long living isotope, yielding ^{87}Sr. The lunar initial ^{87}Sr/^{86}Sr suggests some higher Rb content in the Moon than it is observed. Rubidium may have been lost as a volatile element. But because of its high atomic weight, it cannot run away from the lunar surface. Rb may escape only from the heated surfaces of small bodies or particles. It makes likely that the pre-lunar material existed in a dispersed form at the time preceded to emerging of the Moon as a condensed body (i.e. during about 50-70 Mln years).

Indications on the preliminary dispersed stay may also have been inferred as regard to the Earth accumulation. There is so called the xenon isotope paradox, the gist of which is that the atmospheric xenon contains considerably less ^{129}Xe and ^{134}Xe isotopes generating from ^{129}J and ^{244}Pu than it could be expected. It appears to be as though the radiogenic Xe that had been generating during the initial 120 million years of existence of the Earth was lost. Xe is an atmophilic element that concentrates in the atmosphere of the planet. But due to its high atomic weight, it cannot run away from the surface of a planet. It may have been lost either owing to catastrophic loss of the atmosphere happened 120 millions years, or in case the primary Earth substance spent the initial 120 million years in dispersed condition, as particles or small bodies.

A similar situation is observed with regard to the U-Pb system. There is a certain lack of radiogenic lead isotopes ^{206}Pb and ^{207}Pb, as though the primary Earth's lead had been lost. Some authors believe that it is due to early sink of the lead into the Earth core. However Pb way escape as a volatile element. Due to its high atomic weight, it could not have been lost from the surface of the planet. But it may have been easy lost from a hot surface of small bodies and particles.

Combined solution of equations for the ^{238}U-^{206}Pb and ^{231}U-^{207}Pb systems yields 120 mln years for consolidation of the Earth from the dispersed stay, right the same, that follows from ^{129}J-^{129}Xe, ^{244}Pu-^{136}Xe systems.

Thus, the isotope systems data are in concordant agreement with an idea that a planet may form through condensation of a particle cloud rather than by consequential growth of a massive planetary body. As regards the Earth-Moon system, one may suggest that by the time about 50-70 million years had passed, the primary particle cloud undergone fragmentation, which result in separation and formation of the Moon, while full condensation completed in about 120 million years, when the Earth took shape as a consolidated body.

PL-3

EUKARYOTES AND THE HISTORY OF THEIR APPEARANCE IN THE BIOSPHERE

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1. It is obvious that organization level of organisms is correlated with environmental parameters.
2. The appearance of Cyanobacteria in the geological record and latter appearance of unicellular eukaryotes, multicellular eukaryotes, then Metaphyta and Metazoa determine the amount of atmospheric oxygen, temperature and other parameters.
3. To define the organization level of fossil organisms from the ancient rocks, often metamorphized, is one of the most difficult problems.
4. A simple morphology (sphere, dumbbell, thread, etc.) hampers the fossil identification.
5. The size of fossils, complicated wall structure, presence of pores and apophyses give some chance for recognition of eukaryotic organisms.
6. Important data come from the analyze of the material forming fossils. For instance, the contraction folds of large spherical forms quite confidently prove the pectic nature of envelopes.
7. The major importance of eukaryotic origin is explained by the fact that eukaryotes are undoubted aerobic organisms.
8. At present the following order of organisms origin seems the most plausible; to different extent this is supported by actual material. Recently, some dating have become older and older:

   3.5 Ga – possible cyanobacteria (Australia);

   3.0 Ga – reliable and numerous finds of cyanobacteria (Karelia) [B.V. Timofeev's finds of probable eukaryotes (trichomes and large spheres) and forms with apophyses or contractions folds have the same age];

   2.4 Ga – multicellular algae (Metaphyta) in weathering crusts;

   2.0 Ga – protists and fungi, and possible Metazoa

   1.6 Ga – Coelomata.
9. The data on biomarkers completely correspond to the above mentioned sequence of organism appearance.

10. If the high-carbon rocks are found, we can suspect that during the time of its formation some destructors have worked, and, first of all, fungi can play such a role.
11. The finds of forms similar to eukaryotes in the carbon chondrites principally change the problem. In such a case we need to search the moment for their appearance on the Earth.

PL-4

EVOLUTION OF LIPID BIOCHEMISTRY OF LIVING MATTER IN PROTEROZOIC AND PHANEROZOIC

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ON THE COMPLEXITY OF PRIMORDIAL BIOLOGICAL OBJECTS

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The pioneering paper of Kolmogorov (1965) had opened the way to compare the complexity of two objects (or of their states) represented as finite strings (sequences). After significant contributions of Chaitin, Solomonoff, Gacs, Li, Vitanyi, and some others, a very close connection between complexity and information content of objects was revealed. We suppose here that the notion of complexity in biological world is differentiated, and that the developmental and evolutionary dynamics of types of complexity can be effectively used to characterize the period of transition from chemical evolution to biological one.

To use this idea at the reconstruction of the properties of the systems operating during the transition period, we need to define two classes of primordial biological objects. In the first class we include the objects on the earliest stage of their individual development like spores, zygotes and so on. In the second class we combine the objects of the "simplest" organization like viruses, mycoplasmas, small bacteria. Comparative analysis of complexity of these objects and their more advanced counterparts can give the new knowledge about evolution of complexity in the course of making of biological world.

Following the definition of biological object [1], there are two main representations of biological object – internal and external ones. Accordingly, the complexity of any conditionally singled-out biological object can be roughly understood as a sum of two types of complexities. First type is a part of classic Kolmogorov-Chaitin-Solomonoff (KCS) complexity which, in general case, is an objective measure for the information in a single object [2]. Here we investigate a part of KCS complexity (KCS'), which reflects the information transformation in the course of becoming of the object (complexity of internal maps from a germ cell up to the daughter germ cell). This complexity we associate here with the states of chromatin.

The context-dependent complexity reflects the relations of object with surroundings; it is a complexity of external maps. This complexity we associate with the states of phenotype in the classic representation of phenotype via observables. The complexity of this plane is a complexity of multiple of finite binary strings, whereas the multiple can be interpreted as a set or as a list of strings (with different calculus implied [2,3]). In spite of striking difference between these two types of complexity considered here, the general idea that the information about *x* contained in *y* is defined as $I(y:x) = K(x) - K(x|y)$ can be used in comparison of primordial and advanced objects of both classes. However, the content of *x* and *y* must satisfy the requirements of scope selected.

In this report, the biological objects of different hierarchical and evolutionary status will be shown to be characterized by variable contribution of complexity of different types. In the course of the individual development, the KCS' complexity remains nearly equal for different states of chromatin and especially for chromatins of the parent and daughter germ cells. At the same time the context-dependent complexity is variable because the different stages of development of biological object are represented by the different sets of observables; accordingly, the meaning content of term "context" varies too. The context-dependent complexity has a tendency to grow in the course of the individual development of object.

The evolutionary primordial objects possess the lowest KCS' complexity in comparison with more advanced ones. However, their context-dependent complexity (complexity of external relations) can be of relatively high value because the list and length of external strings increase to support the reproduction of primordial objects of this class. In the case of viruses, e.g., even the operational moiety of chromatin (host structures) acquires the status of external in relation to that of primordial object.

These observations can be generalized in the implication that objects of biological world demonstrate a tendency to compensate the deficit of KCS' complexity by means of increase of context-dependent complexity. Approximating this tendency in the scope of pre-biology, one can suggest that at least some of problems of transition to objects with biological level of complexity were settled through the substitution of one type complexity with another. Nevertheless, a question remains: if the highest values of context-dependent complexity in pre-biological systems can be sufficient to ensure the total complexity comparable with that of primordial biological object or of intermediate objects at period of transition from chemical evolution to biological one.

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MICROFOSSILS, BIOMOLECULES AND BIOMARKERS IN CARBONACEOUS METEORITES: IMPLICATIONS TO THE ORIGIN AND EVOLUTION OF THE BIOSPHERE

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Work carried out since the early 1960's has conclusively established that pristine CI1 and CM2 carbonaceous meteorites contain indigenous and extraterrestrial biomolecules (e.g., chiral protein amino acids, carboxylic acids, nucleobases, etc.) and biomarkers (e.g., geologically stable diagenetic breakdown products of biomolecules such as nitrogen and sulphur heterocycles, porphyrins, pristane, phytane, cycloalkanes, polymers of isoprenes, etc.). Scanning Electron Microscopy studies in the United States and Russia have detected large numbers of permineralized and carbonized filamentous microstructures embedded *in-situ* in freshly fractured interior surfaces of the meteorites. The size, size range and distinctive morphological characteristics such as differentiated sheaths, trichomes and specialized cells and structures for nitrogen fixation (heterocysts); survival and reproduction (hormogonia, baeocytes and akinetes) and attachment (fimbriae) demonstrate that many of these filaments are convergent with morphotypes of known genera of trichomic cyanobacteria and other filamentous trichomic prokaryotes. Energy Dispersive X-Ray Spectroscopy (EDS) studies have shown many of the filaments have O/C ratios consistent with bitumen or kerogen and nitrogen content typically < 0.5%, which is far below the range (2-18% atomic) measured under identical conditions for living cyanobacteria or dead (Holocene – Pleistocene) biological remains (hair and tissues of mummies and mammoths). These measurements exclude the interpretation of the filaments as recent terrestrial bio-contaminants. Furthermore, many independent studies have shown that these carbonaceous meteorites do not contain unstable biomolecules that are essential to life and found in living and recently dead organisms (e.g., 12 protein amino acids; the nucleobases thymine and cytosine; RNA and DNA sugars - ribose and deoxyribose; metabolites, enzymes and pigments - NADH, ATP, chlorophyll and chlorins). This has led to the interpretation of the recognizable biogenic filaments found in the meteorites as indigenous microfossils that were present in the meteorites when they entered Earth's atmosphere. It is suggested that the detection of indigenous biological remains in carbonaceous meteorites may have significant implications to the origin and evolution of the terrestrial biosphere. Understanding the nature and characteristics of the mineralogy and thermal and aqueous alteration of the meteorite parent body may provide useful insights to guide theoretical and experimental investigations concerning the fundamental problem of the origin of life.

PL-7

CONVEYING RNA-BASED MOLECULAR MACHINES AS A PREREQUISITE TO THE ORIGIN AND EVOLUTION OF THE ANCIENT RNA WORD

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The appearance of catalytic RNA molecules (ribozymes) capable of synthesizing oligoribonucleotides and polyribonucleotides is supposed to be a key event in the origin of the ancient RNA world. By now the synthetic ribozymes with template-directed RNA-polymerizing activity have been created under laboratory conditions. However, as the products of these ribozymes are complementary to their templates, they inevitably collapse into the form of very stable RNA double helices incapable of acquiring catalytic activities (conformational paradox [1]). The emergence of *ribozyme-based molecular machines* of the conveying type capable of unwinding secondary structures of polynucleotides is postulated here as a revolutionary occasion that allowed the RNA world to evolve towards the living world.

The main principle of molecular nanomachines is the use of the Brownian motion as a driving force for the movement of the machine, instead of the use of mechanical power strokes in macromachines. The unidirectionality of the movement is provided by energy-dependent “pawls” (back stops) that allow molecular machines to move ahead and impede backward moves (rectification of random motions). In the present-day biological world, RNA and DNA polymerases, translating ribosomes and the systems of intracellular transport (such as actin/myosin and kinesin/tubulin systems) are the best studied examples of such molecular machines of the conveying type. All of them, except ribosomes, are built of proteins, whereas the ribosome is an RNA-based nanomachine [2]. Being a processive ribozyme, the ribosome is capable of energy-dependent unidirectional moving along a polyribonucleotide chain as a template (conveying machine function) and simultaneously synthesizing polypeptide chain from amino acids (peptide polymerase function). It is important that during its movement along the template polyribonucleotide, the ribosome unwinds the secondary structure of the template chain (RNA helicase function).

We hypothesize that the first RNA-based conveying machine of the ancient RNA world was an RNA-polymerizing ribozyme with coupled helicase (“unwindase”) activity. It could be the immediate evolutionary precursor of a more complex ribozyme-based conveying machine, namely the template-dependent peptide polymerase called ribosome. Factually, these two types of nanomachines are similar in their capacities to directionally move along a polynucleotide template at the expense of the free energy of polymerization reaction itself, and to use the incoming substrates of the reaction as the "pawls" preventing backward movements of the machine, without additional energy sources and special pawl devices.

At the same time, in order to prevent the formation of stable double-helical complexes between the template and the product, a ribozyme-based RNA polymerase nanomachine should couple its RNA-helicase activity with a mechanism for producing single-stranded RNAs. Two different mechanisms are known from the contemporary living world. One is the so-called *semi-conservative replication* of a double-stranded polynucleotide typical of the process of DNA duplication [3]. In this case the newly synthesized polynucleotide displaces the old one, step by step during polymerization reaction; as the replaced polynucleotide has no complementary partner, it remains single-stranded and thus allowed to self-fold into a potentially functional globular form. Thus, the production of stable double-stranded RNAs as intermediates followed by displacement of single-stranded RNAs from the double helices, could be a solution to the problem of the conformational paradox in the ancient RNA world.

Another way to solve the same problem could be a non-covalent *circularization of an RNA template* during template-directed polymerization of a complementary RNA product. In such a case the complementary interaction of the template and the product would be precluded by sterical constraints for the formation of extended double-stranded RNA helices during replication. The mechanism of this type has been recently suggested to explain the replication of the single-stranded RNA of bacteriophage Qβ [4]. In this case the circle is formed due to simultaneously binding and keeping together both the 5' and the 3' ends of a template polyribonucleotide by the phage RNA replicase.

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PL-8

MOLECULAR COLONIES AS A PRE-CELLULAR FORM OF COMPARTMENTALIZATION

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The need for compartmentalization

The main feature of a cell which distinguishes it from a mere aliquot of a biochemical solution is that the cell must be capable of evolution. However, evolution cannot occur without compartmentalization, some kind of segregation of the cell from its environment [1-3]. It looks tempting to consider liposomes as a pre-cellular form of compartmentalization of biochemical reactions. Liposomes are capable of spontaneous proliferation by incorporating new lipid micelles or molecules followed by breaking down into smaller vesicles. Moreover, it was shown that if a liposome was loaded with RNA, NTPs, and a replicase, the liposome division was coupled with RNA replication [4], which is reminiscent of cell division. However, in using liposomes as cell analogs there are a lot of yet unresolved problems, of which the most serious is that lipid membrane is hardly permeable to hydrophilic low molecular weight compounds, such as nucleotides or their precursors needed for the synthesis of biopolymers, which had to enter the cell from the environment. Even passive diffusion of such compounds is very slow, with the half time required for transmembrane equilibration exceeding 10 h [5]. This makes the rate of intra-liposome synthesis of nucleic acids unacceptably low even at the extra-liposome concentration of nucleotide substrates as high as 5 mM, which can hardly be expected of the ‘primordial soup’.

Molecular colonies as an alternative to liposomes

Another form of compartmentalization of biochemical reactions could be molecular colonies that formed when RNA or DNA are amplified in a porous solid medium [6]. The synthesized copies remain nearby the parental template, and make up a spherical cluster of molecules which resemble a cell. The principal difference from the cell is that it is not enveloped with a lipid membrane. Nevertheless, compartmentalization is achieved here, as the colony is separated from the surrounding medium. It was shown that all basic biochemical reactions needed for reproduction and functioning of a living cell, such as RNA or DNA replication, transcription, and even translation, can occur in molecular colonies. Moreover, molecular colonies were shown to be able of linking the phenotype to genotype which is needed for the natural selection and of evolution.

Clay as a suitable matrix for the origin of life

Clay is a porous mineral and therefore it might serve as a matrix in which pre-biotic molecular colonies could originate and grow. It seems that the most suitable for this purpose was montmorillonite, a layered aluminosilicate whose pores upon hydratation of the clay become comparable in size to biopolymers. Montmorillonite was abundant on the early Earth, and also was found in meteorites and on Mars [7]. Due to its high ion-exchange capacity, it is capable of >10,000-fold concentrating nucleotides from the surrounding solution [8]. It also has a high affinity to polynucleotides, especially to their single stranded form [9], and hence might serve as an early substitute for SSB (single strand binding) proteins that stabilize the single stranded state of nucleic acids necessary for replication. It is capable of catalyzing the polymerization of nucleotides [10], and the formation of their precursors from simple organic compounds such as methanol [11]. Moreover, its particles increase by 100-fold the rate of liposome formation from a lipid emulsion and becomes internalized by the liposomes, together with the adsorbed poly- and mononucleotides [12]. Therefore, at some stage of evolution the molecular colonies growing in the montmorillonite matrix might become enveloped with a membrane, thereby giving rise to the first protocells.

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PL-9

GENE NETWORKS AND THE EVOLUTION OF BIOLOGICAL SYSTEMS

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Gene network represent the functional group of coordinately expressed genes and provide a basis underlying any morphological trait. For example, formation of each organ requires complex coordinated expression of genes hierarchically organized into the gene network. In this report we will discuss how molecular evolution of genes through their hierarchically organized networks affects the evolution at the level of organism.

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PL-10

THE METAL CLUES OF LIFE

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Hydrogen metabolism seems to be a historical thread that connects recent biota with the very origin of life. Hydrogen is the most abundant chemical element in the Universe. High availability of H_2 on early Earth, extraordinary diffusion mobility, low activation energy of H_2, and formation of protons and electrons at the contact of molecular hydrogen with metals, – all these qualities gave H_2 a major role in the rise of energy metabolism.

The reasons for this hypothesis are as follows. The H^+ gradient that is being used by the cell in the synthesis of ATP is a universal mechanism for all living organisms. Molecular hydrogen as a key intermediate of the reactions of anaerobic metabolism plays a universal trophic role between micro-organisms that live on different substrates – the most important ecosystem factor from the very start of life and further on. Many groups of modern prokaryotes are using H_2 as electron donor and energy source. Their enzymes carry out the H^+ cation transfer. Anion hydrogen H^- (the equivalent of two electrons) is known as the "energy currency" of the cell. The soft hydrogen bonds provide stability and versatility of the macromolecules in the living organisms.

Molecular hydrogen was a reducing factor in the primary environment of life, it formed the proton gradients as a mechanism of electron transfer that is the key universal feature of energy metabolism. The main sources of abiogenic hydrogen on early Earth were degassing upper mantle magmatic systems, the hydrolysis of iron minerals of mafic volcanic rocks, photolysis and radiolysis of water.

Biochemical reactions involving Hydrogen are catalyzed by hydrogenase, which are dominated by Fe-Fe- and Ni-Fe-proteins. The leading role of nickel and iron in the catalysis of reactions of hydrogen metabolism seems to be an ancient biochemical relic of those epochs when these metals were mobile and abundant in oxygen-free and hydrogen-rich reducing environments of early Earth.

The physical and chemical parameters of the biosphere irreversibly departed from the initial conditions due to a decrease in the concentration of hydrogen in the early biosphere, an increase in the concentration of oxygen in the ocean, the changes in the bioavailability of metals known as activators of enzymes – decreasing role of Fe, Ni, Co, V, W, and the growing importance of Cu, Mo, Zn.

The decreasing sources of molecular hydrogen gradually stimulated the involvement of its simple volatile compounds (CH_4, NH_3, H_2S, and, finally, H_2O in oxygenic photosynthesis) as the substrate of life. The by-products of metabolic reactions that involved those simple hydrogen compounds, ultimately determined the chemical composition of Earth's atmosphere with a sharp dominant nitrogen and oxygen.

There is some correlation between the shift from the molecular hydrogen to its simple compounds as a substrate of life and a switch from the “archaic” metal activators of enzymes to the “modern” ones. In part this correlation may be related to the energy required to split the molecules of the simple hydrogen compounds mentioned above in order to get access to hydrogen as a “primary fuel”.

The early evolution of metabolic systems, including the formation of a complex functional structure of eukaryotic cells, could be considered as a process that compensated the irreversible changes in the geochemical characteristics of the biosphere. A major role in this process belonged to multiple symbiogenesis which began with the formation of stable symbiotic relationship of prokaryotic organisms that are dependent on each other metabolic products (see "hydrogen" hypotheses of symbiogenesis leading to the origin of the eukaryotic cell). Compartmentalization of biochemical reactions inside the cell, the complexity of metabolic chains, symbiogenesis of prokaryotes, various forms of symbiosis in higher organisms is fundamentally similar (coenosic or syntrophic) way to cope with environmental stress.

Evolutionary response to the depletion of the geochemical basis of life was the formation of the mechanisms of extraction, accumulation and retention of ancient metal-activators in the cell and in the ecosystem, as well as the involvement of new metals. Biota of the ocean has become the main sink and transport mechanism of metals in the biosphere. The sequence of metabolic reactions of living cells to some extent reflects the main events of co-evolution of geochemical and biotic processes in the ancient biosphere.

The emergence of eukaryotic cells, the growing role of heterotrophy, the emergence of multicellular and tissue organization, increasing biodiversity and complexity of trophic relations, accelerating cycling of biophilic elements and other features of the eukaryotization of biosphere are largely a response to the narrowing of the geochemical basis of life. Turning point in the long process of the biosphere eukaryotization was a series of ice ages in the Late Proterozoic (750-540 million years ago) and active oxygenation of the ocean that opened opportunities for global expansion of eukaryotic organisms.

The ideas presented above are important for studying such issues as:

a) the primacy of inorganic catalysts (transition metals and their simple mineral compounds) in the origin of life;
b) hydrogen metabolism as the oldest living line of evolution, which is fundamental in anaerobic environments, including hydrothermal vents and the "deep biosphere";
c) the major role of biota in the mobilization and concentration of chemical elements in ancient ecosystems that is represented by the largest ore deposits of Fe, Mn, U, Au, Ni, Cr, Cu, and others confined to the Archean and Proterozoic basins);
d) design the metalloenzymes for biotechnologies taking into account the data on the evolution of metabolic systems;
e) the crucial (and still underestimated) importance of microelements, especially metals, in a global ecological paradigm.

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EMERGENT LIFE DRINKS ORDERLINESS FROM THE ENVIRONMENT

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Microbes both at the bottom of the evolutionary tree and the base of the food chain hydrogenate carbon dioxide. Four billion years ago our water-world could do the same (as it does still)—abiotically generating methane like an inorganic methanogen, though not nearly so quickly. More rapid reduction appears to be life's raison d'être. So how did life begin? We can think of life's emergence as being, in part, enabled by a series of self-organizing "negative" entropy traps with serpentinization the first "demon", transferring energy from the mafic crust to open-system convecting ocean water in the form of heat, hydrogen, methane, ammonia as well as hydroxyl and sulfide ions (Martin et al., 2008, *Nature Rev Microbiol,* 6, 806). The initial trap would be set across the inorganic membrane, formed spontaneously at the site of exhalation of the reduced alkaline fluid now differentiated and separated from its mother liquor—the acidulous, phosphate- and ferrous iron-bearing carbonic ocean (Nitschke and Russell, 2010, *J. Cosmol*, 10, 3200; Simoncini et al. *J. Cosmol*, 10, 3325). Inorganic transition metal sulfides could act as precursor catalysts to hydrogenase, nitric oxide reductase, carbon monoxide dehydrogenase and acetyl coenzyme-A synthase, while phosphate could be polymerized to pyrophosphate by protons streaming through the spontaneously precipitated inorganic membrane, in turn condensing and polymerizing the first organic products of hydrogenation and amination. Resulting highly flexible uncoded and heterochiral peptides could locally also lower entropy by sequestering inorganic sulfide and phosphate clusters, thereby improving and tuning their catalytic and energy-storage propensities. Thus, such a system would already be capable of evolution through the survival of those peptides that nested or otherwise interacted with the inorganic entities within the compartments (Milner-White and Russell, 2010, *J. Cosmol*, 10, 3217; Kurland, 2010, *Bioessays* 32, 866). Products not taking part in further interactions would tend to be entrained in the slowly diffusing effluent and be lost to the system. In further conceptual steps Dieter Braun and collaborators (e.g., Baaske et al., 2007 *PNAS*, 104, 9346) have demonstrated how convectively-driven polymerase chain reactions whereby

DNA molecules that are replicated, albeit with the involvement of *taq* polymerase, are concentrated against entropy in “cold traps” within inorganic compartments through thermal diffusion driven by thermal gradients acting across the margins of a hydrothermal mound. We know entropy traps are also required for the onset of the RNA world. For example, Sievers et al. (2004, *PNAS*, 101, 7897) show that the peptide bonding rapidly effected in the ribosome is mainly a result of juxtaposing the substrates—perhaps aided by an unfolded peptide—to the partial exclusion water (and see Hsiao et al., 2009, *Nucl Acids Res*, 37, 3134; Wallin and Åqvist, 2010, *PNAS*, 107, 1888).

PROTOBIOLOGICAL STRUCTURES, PREBIOLOGICAL AND BIOMINERAL COEVOLUTION

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Abiogenic highly structured solid carboniferous substances and hydrocarbon molecular crystals, rather widely developed in terrestrial and extraterrestrial objects, possess structural and functional elements of protocell, protogene, contain building components of protoprotein and represent the most appropriate prebiological systems for creation of information genetic apparatus and for development to the simplest living organisms. They can be considered as models of protobiological systems. We have conducted detailed researches of composition, molecular and supramolecular structure of various natural carboniferous substances and hydrocarbons, their comparative analysis with biological materials and biomineral aggregates.

Abiogenic hydrocarbon structures, the most homological to bioorganisms, are crystallized to relatively high thermal and high baric conditions in hydro-gaseous mineralized environment with carbonate-chloride-sulphate magnesium-potassium-sodium composition in the presence of ammonia, sulphur gas, methane, carbon dioxide and other components, in reducing conditions. Biological life could be originated under similar conditions.

The formation of biomolecules and other components of life began yet at astrophysical stage. The first acts of biogeniesis apparently developed not on the Earth surface, but in hydrothermal systems, pegmatites, volcanos, possibly even in gaseous cavities of hardening melts. These events occurred in the beginning of crustal stage (4.5-4 Ga) characterized by melting of basalts and their granulite metamorphism.

Not casual events, but certain geoecological and physical-chemical conditions resulted in the life origin. Life formed from prebiological material as single integrated whole, not as separate parts, casually united, or successive events.

The simplest biological systems were hemoautotrophic. Prebiosphere was characterized by subsurface localization. The life was matured after protoorganisms were brought out to surface reservoirs, having changed to photoheterotrophic way, in warm water puddles and in ocean. The primary biosphere had local insular character, then archipelago, and complete biosphere cover was acquired by the Earth at about 3.8-3.7 Ga.

Thus, the biosphere history includes: a) period of subsurface prebiosphere characterized by nearly exploding origin and enaction of the simplest life, b) period of formation of surface and near-surface biosphere, c) stagnation procaryota-eucaryota period, about 1.7 Ga, d) period of exponential biosphere expansion from 2.3 Ga to present.

On the basis of quantitative, structural and event-driven analysis of development of mineral and biological systems the mechanisms and regularities of biomineral coevolution were studied.

During prebiological history of the planet the number of minerals increased from a dozen of nanosize phases in prestellar molecular matter to fifty in the primary preplanetary chondrite matter and to 250 – in primary planetary (crustal) one. This mineral substrate resulted in the sources of life origin and development. Mineral formation processes of non-biological nature supported mineral diversity in about 1500 mineral species, about 100 of them were generated by granitoid magmatism, granitization of granulites and related hydrothermal processes.

A powerful biogenic factor was included into the evolution of mineral world together with life appearance on the Earth, which considerably renewed and complicated the evolution process. This factor became one of the leading in the formation of mineral pattern of near-surface lithosphere, and as a consequence the number of mineral species increased at 3 times to 4500 known today. Oxidation processes are playing a great role in it.

The biomineral evolution is characterized by precisely directed “loosening” of mineral matter expressed via decreasing total density of atomic array in minerals (PA) from 0.50 in preplanetary chondrite material to 0.44 – in basalt minerals, 0.40 – crustal, 0.38 – in modern mineral world. The total symmetry index decreased the same way: 33.58 29.00 21.95.

Thus, biomineral interactions and their coevolution resulted in cardinal changes of mineral world of lithosphere expressed in sharply increasing mineral diversity, complicating structure, decreasing structural density and total symmetry, accelerating rate of biomineral genetic events. They promoted formation of modern appearance of lithosphere and biosphere, creation of modern biological and mineral diversity.

ORAL PRESENTATIONS

ROLE OF COMETS IN THE ORIGIN OF LIFE AND ITS EVOLUTION

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I. A current standard scenario of the origin of the Solar System is presented [1, 2]. The results of research of the earliest evolution stages of circumsolar protoplanetary disk with the Sun before its exit on the main sequence Hertzsprung–Russell diagram is considered. We examined the evolution of ensembles of gas-dust clusters and planetesimals both in astrodynamical aspect and in terms of interiors thermal history of surviving in the collisions of bodies. The calculations take into account new data on the injection of ^{60}Fe into the young Solar system and the new value of a half life (2.62 million years instead of 1.5) of this nuclide. Calculations (ours and other authors) have shown that radionuclides ^{26}Al and ^{60}Fe have provided heating and differentiation of the interiors of planetesimals early in the first 3-4 million years after formation of CAI.

In the terrestrial planet zone early melting bodies with sizes ranging from tens to a few thousand kilometers makes it possible to explain the formation of differentiated bodies in the first 3-4 million years of the Solar system existence and data on early differentiation of the planet's interior. In the zone of outer planets long before the formation of the planets themselves into planetesimals with sizes ranging from tens to hundreds of kilometres, formed from the gas-dust clusters, the ice melting, the differentiation into the shells and cores descended from dust and its aggregates with organic matter occured.

For astrobiologists, this result points to the need of searching for traces of anaerobic forms of life in the ice bodies of the Solar system or their fragments – comet nuclei. For geophysicists, our results on the heating of bodies of lunar size by short-lived isotopes remove the old problem of early heating of the central regions of the growing planets.

II. The role of comets is important not only in the formation of Earth, but also throughout its evolution. In a recent survey [3] it was noted, that neither hypothesis is not suitable to explain the mass extinctions of biota and the Glacials (duration about 30-100 million years) on the Earth. Since 1960, several well-known geologists (W. Brian Harland, Joseph Kirshvink – author of the term "Snowball Earth", Paul F. Hoffman and others) have developed a theory of the great glaciations. But the very causes of the fall in average temperatures by at least 2-5 °C were not clear.

Many authors attribute some of globally recurring events with the motion of the Solar system in the Galaxy. During this movement, the Solar system have repeatedly met with the giant molecular clouds, periodically crossed the galactic plane, passed through the branches of the spiral structure, i.e. passed through the area of increased density of matter in the galaxy. During such periods, frequency of close encounters of stars with Solar system increased. This caused disturbance of comet orbits of the outer and inner parts of the Oort cloud, which, in turn, could lead to comet showers. Hundreds of comets were transferred to higher eccentric orbits and penetrated into the central regions of the Solar system, some of them collided with the Earth. But the comet's collision with Earth couldn`t lead to global catastrophe, it`s a local scale event.

Vityazev A.V. [4] proposed a new mechanism of the Galaxy action on events on the Earth. During periods of comet showers stream of comets, moving in the direction of the Sun, crosses the asteroid belt. Cross section of collision of comets with numerous asteroids is on orders greater than their cross section of collision with the Earth. Calculations showed that the collision of a comet with an asteroid even much smaller in size but with higher density at an average velocity of comets in the asteroid belt about 30-40 km/sec leads to complete destruction of comet and ejection of dust into interplanetary space. Estimations have shown that during the periods of cometary showers of a dust can be formed enough that reduction of an insolation of the Earth has led to approach of the next glacial age.

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GRAVITATIONAL INSTABILITY IN THE PROTO-PLANET DISK

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In spite of numerous studies, the main question of how the planetary system of the Sun has been formed remains still open.

Large-scale gravitational instability of the proto-planet solar disk might be a physical process that leads to the formation of planets. However in the scientific society there is no common opinion concerning this question. Some researches consider the proto-planet disk in the gas phase to be stable [1, 2]. Other researchers keep the opposite point of view [3, 4]. Thus, Pavlyuchenko and Friedman have found [4] existence of the gravitational ring-shaped instabilities in the proto-planet solar disk, which can lead under specific conditions to the formation of the solar planetary system. In calculations, they used a flat disk model with sufficiently small thickness.

The purpose of the present paper is to study large-scale gravitational instabilities at the initial stage of the proto-planet solar disk evolution. The problem of the proto-planet disk evolution in the general formulation is extremely difficult. In order to simplify this problem and make the treatment of the results obtained possibly unambiguous, several assumptions are employed. The medium of the disk is considered to be single-phase and ideal. Of all physical processes, which occur in the proto-planet disk, we leave only basic ones that influence the gravitational stability of the disk: gas-dynamic processes, the Sun gravitational field, and the disk own gravitational field. The initial state of the proto-planet solar disk is set up in accordance with the analytical solution by Roche [5, 6].

In this formulation, the proto-planet disk has the form of a slim torus, whose internal part becomes narrow, if we go towards to the center. Strong gravitational field of the Sun draws the gaseous medium of the proto-planet disk to the center, and due to this effect the density of the gaseous medium reaches maximum values near the internal edge of the disk. This creates significant density gradients.

The problem of the proto-planet solar disk evolution is solved numerically. A numerical two-dimensional axisymmetric gasdynamic model, which accounts both the gravitational field of the Sun and the field of the disk has been developed. This model describes the basic processes at the initial stage of the evolution.

The description of gasdynamic processes is carried out in the Eulerian coordinates. The governing equations represent the basic conservation laws. These equations are discretized with the numerical method proposed by S. K. Godunov and A. V. Zabrodin [7] for solving gasdynamic equations in complex geometries on arbitrary moving grids.

The whole computational domain is divided into a set of subdomains separated by moving boundaries. This approach allows us to sufficiently resolve different scales of the proto-planet disk dynamics. The computational grid consists of 124800 cells in total.

The developed numerical model simulates the initial stage of the disk evolution in the Roche's approximation, when the disc inner field is neglected, and also with taking it into account. The comparison of these two calculations provides data on how the disk inner gravitational field influences on the process of the proto-planet disk evolution.

The analysis of the computational results shows that switching on the disk inner field changes the flow structure. Ring-shaped domains begin to form, in which the flow so develops that it results in the mass concentration in certain radial cross-sections of the disc. This can be clear seen from snapshots of instantaneous streamlines. When the inner gravitational field is switched on one can see the formation of several subdomains. The gas in each of these subdomains tends to move to a radial cross-section, with the density being increased near this section. In comparison with the flow without the inner field, the flow in subdomains above the cross-section lines oppositely changes the direction of motion.

The contour lines of density in the proto-planet disk are changed in accordance with the change in behavior of the streamlines. In Figs. 1 and 2 density contours are shown at two different time moments. As can be seen, the inner gravitational field causes the flow instability that develops in the form of the rings of density (Fig. 2). Local maximums and typical cross-clamping of contour lines are well-defined in the density distribution of the proto-planet disk at the moment t=0.685 (non-dimensional). The structure of rings is physically intelligible: appearance of the Jeans instability (i.e., local increase in gas density) leads to local mass concentrations that begin to gravitationally attract surrounding masses of gas, in consequence of which local maximum and cross-clamping in contour lines come out. This corresponds to local decrease in the thickness of the proto-planet disk.

Typical sizes of gravitational instabilities are equal in order of magnitude to the distances between the planets. The masses of the rings of the local maximums of density comprise fractions of the masses of the corresponding planets.

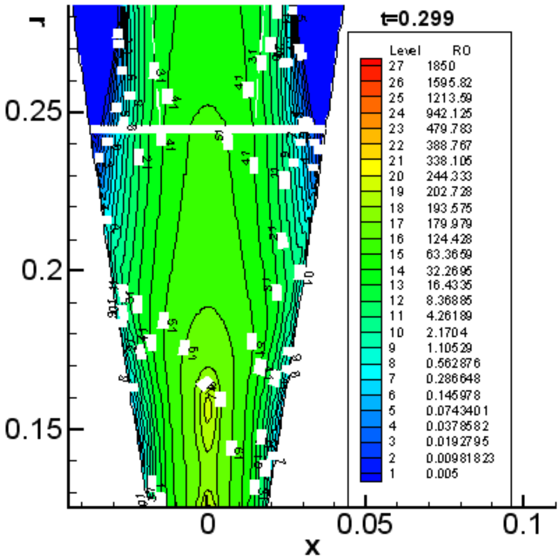

Fig. 1. Density iso-contours at time=0.299.

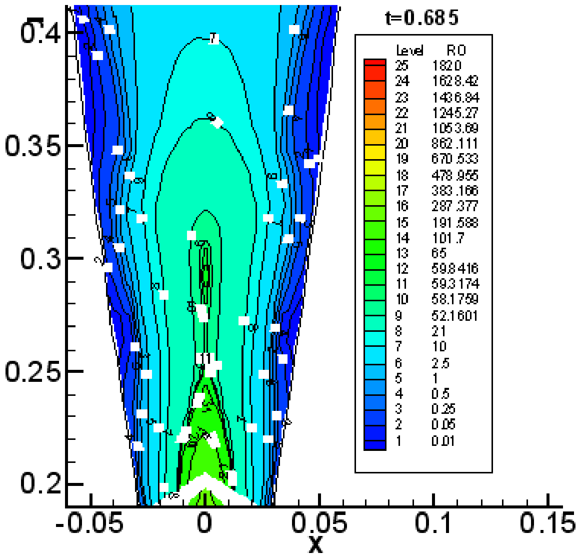

Fig. 2. Density iso-contours at time=0.685.

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OP-3

HOT ABIOGENESIS AND EARLY BIOSPHERIC EVOLUTION

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We argue that hyperthermophilic abiogenesis leading to a hyperthermophilic Last Universal Common Ancestor (LUCA) of life is supported by a wide range of recent research. If the ambient ocean during abiogenesis was cold, then primitive mesophiles should have emerged. The absence of deeply-rooted mesophiles in molecular phylogenetic trees suggests that either primitive mesophiles did not survive a near sterilizing event in the Hadean or a hot Archean climate, or alternatively did not emerge because of a hot Hadean climate. Drawing on a plausible scenario of hydrothermal abiogenesis near the seafloor ((Russell and Hall 1997; Koonin and Martin 2005; Russell 2007), we propose that a spectrum of Bacterial and Archaeal protocells, including ancestors of extant prokaryotes, emerged simultaneously in the redox potentials of a thermal gradient between a hydrothermal source on the seafloor and the ambient climatic oceanic temperature in Hadean time. The transition from RNA to DNA and the efficient repair of single and double strand breaks in DNA, rather than being the result of a mesophile to hyperthermophile transition could be a consequence of the protocell emergence in a high temperature and high radiation environment due to intracellular K^{40} and C^{14}. Therefore the early accumulation of neutral ''clock-like'' substitutions could plausibly be driven by this radiation dose as a function of time, with the surviving record having the potential of providing the time of emergence of the earliest metabolisms. The strong anti-correlation of maximum growth temperatures (Tmax) of thermophiles with their rRNA and tRNA phylogenetic distances from the LCA supports their Tmax being close to the environmental temperature of each organism at emergence. A climatic temperature close to 70- 80 deg C in the late Hadean/Archean is consistent with paleotemperatures derived from oxygen isotopes in marine cherts ((Knauth, 2005), and the measurement of melting temperatures of proteins resurrected from sequences inferred from robust molecular phylogenies (Gaucher et al., 2008).

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VUV PHOTOPHYSICS OF PREBIOTIC MOLECULES IN THE CONTEXT OF THE SEARCH FOR LIFE ON EXOPLANETS

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One of the important aims of the study of extrasolar planets is to identify markers that could be associated with the presence or possible future existence of life on these far-off objects. Thus the identification of prebiotic molecules and elementary biotic building blocks is a valid objective [1]. Since the atmospheres of extrasolar planets is increasingly studied by spectroscopic means, permitting the prevailing physical environment, in particular the molecular and particulate content, and the local radiation field, to be determined, it is imperative to understand the viability of prebiotic and biotic molecules under these conditions. Furthermore, these extrasolar planets will most probably also be subject to inflow of material from local comets and asteroids and these could give rise to observable effects. These objects could also be sources for the molecular building blocks of life and they could penetrate whatever atmosphere exists on an exoplanet and thus deliver these key molecules to the atmosphere, the surface or any liquid haven. One must also include the possibility that material can be transferred from one planet to another, as illustrated by the existence of Martian and Lunar meteorites on Earth. In addition, cosmochemistry in the interstellar medium (ISM) can be a source of prebiotic molecules that eventually are deposited on planetary sites.

I will present the results of extensive studies of the VUV spectroscopy and photophysics of a number of molecules carried out in collaboration with the group of Helmut Baumgärtel, Free University, Berlin, at synchrotron radiation sources BESSY I and BESSY II, Berlin, and LURE, Orsay. Our studies have involved both optical spectroscopy (absorption, fluorescence) and photophysical studies such as photoion mass spectrometry (PIMS), including the measurement of photoionization yields. Spectroscopic studies are essential for predicting observational possibilities in astronomy and for the interpretation of laboratory photophysical results as well as astrophysical observational measurements. The species studied fall into two groups: 1) small molecules, such as ammonia [2], formic acid [3,4], acetic acid [5,6], acetonitrile [7,8], formamide [9] and its methyl derivatives [10], that are considered to be the reactants in a prebiotic chemistry which culminates in complex molecules such as amino acids and nucleobases; 2) the monomeric building blocks of biopolymers, e.g. the aminoacids glycine, alanine, valine etc [11], which are the building blocks of proteins, and a number of purines and pyrimidines [12], including the nucleic acid bases adenine, thymine and uracil [13], which are part of the nucleotide building blocks of the informational molecules DNA and RNA. These results will be presented and discussed in the context of the survivability of these species under various conditions of irradiation and in settings corresponding to (exo)-planetary atmospheres and cometary and asteroidal environments.

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STAGES OF CHEMICAL EVOLUTION IN CIRCUMSOLAR DISK

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The pre-planetary circumstellar disk as most probable time and place of the primary abiogenic synthesis of prebiotic organic substances from simple molecules along with the "RNA world" and the life origin. The sequence of self-organization stages that gave rise to the Earth biosphere is determined. Results of computational experiments using supercomputers are used to determine conditions of abiogenic organic compounds in the Earth biosphere.

The stage of the astrocatalysis for the primary abiogenic synthesis of the major mass of organic compounds corresponds to the stage of the formation of large bodies in the solar system. At the stage of the astrocatalysis the abiogenic synthesis of primary organic compounds occurred directly by the formation of the primary bodies and protoplanets during the development of collective gravitational instability with the simultaneous assembly of numerous small bodies.

OP-6

ASTROCHEMISTRY OF THE COMPLEX MOLECULE FORMATION IN THE INTERSTELLAR MEDIUM

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A new field of space research, astrochemistry, investigating the chemical evolution and chemical diversity of interstellar matter (Shematovich, 2006) has been rapidly developing in recent years. The interstellar medium (ISM) is a unique laboratory, where chemical processes are often run under conditions strongly different from terrestrial. The chemical composition of the ISM is quite diverse and rich. Astronomical observations of interstellar and circumstellar space reveal the chemical diversity of space on different scales: cometary comae, gaseous envelopes of solar system planets and exoplanets, circumstellar envelopes, diffuse and dense molecular clouds (the list of cosmic molecules detected during observations шы given, for example, at the site http://astrochemistry.net). Of the over 150 different molecular species detected in the ISM, approximately 50 contain 6 or more atoms. These molecules are labelled as complex molecules in the astrochemistry. Such complex molecules contain the element carbon and so can be called organic. Some of the recently detected interstellar molecules have a prebiotic nature such as a first interstellar sugar – lycolaldehyde (CH_2OHCHO), a direct precursor of the simplest amino acide glycine – amino acetonitrile (NH_2CH_2CN), and etc. The nature of the gaseous complex species depends on the source where they are found: in cold, dense regions they tend to be unsaturated (hydrogen-poor) and exotic, whereas in young stellar objects, they tend to be quite saturated (hydrogen-rich) and terrestrial in nature. Because they are detected in young stellar objects, complex molecules are expected to be common ingredients for new planetary systems.

One of the ways to describe the chemical diversity of the interstellar matter is the application of astrochemical systems, which include physical models of the studied astrophysical objects and networks of chemical reactions, connecting a variety of chemical compounds via the largest possible set of chemical reactions. Astrochemical models of different astrophysical objects usually include the following groups of chemical processes: (a) gas-phase chemistry, (b) diffusive chemical reactions on the surface of the dust fraction, and (c) chemical exchange between gas and dust fractions via adsorption and desorption processes. Mentioned above astrophysical objects are usually rich in both gas-phase molecules and icy mantles of molecules atop dust particles. Both the dust particles and their icy mantles are major reservoirs for heavy elements and their surfaces are believed to support catalytically the formation of complex molecules. To investigate numerically the astrochemical systems of the complex molecule formation it is necessary to use both the macroscopic methods of chemical kinetics and consideration of chemical reactions on the molecular level of description. In the latter case one of the most efficient methods is a stochastic approach to the description of physical and chemical processes in the rarefied media (Marov et al., 1996). In the frames of this approach the kinetic Monte Carlo method was developed to investigate the gas-phase chemistry, catalytic diffusive chemical reactions on the surfaces of the interstellar dust grains and chemical exchange between solid and gas fractions of the interstellar medium (Stantcheva et al., 2002; Herbst and Shematovich, 2003; Shematovich et al., 2005; Shematovich, 2008). The investigation of the chemical pathways of water, formaldehyde, and methanol formation on the icy surfaces of interstellar dust grains in the starless and protostellar cores of the dense and cold molecular clouds was an important application of the developed approach (Stantcheva et al., 2002; Herbst and Shematovich, 2003). Another interesting application of the stochastic approach is the investigation of the chemical exchange between icy surface of the Jovian satellite Europa and its rarefied atmosphere formed due to the sputtering of the icy surface by the high-energy magnetospheric ions (Shematovich et al., 2005; Shematovich, 2008). Theoretical prediction of the composition and chemical evolution of the atmosphere-icy surface interface is important for the estimates of the biological potential of this Jovian satellite.

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OP-7

ABIOGENIC SYNTHESIS OF OLIGOPEPTIDES IN OPEN SPACE CONDITONS

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The complex chemical processes could take place on surface of small bodies inside any planetary systems at different stages of their evolution. There are a huge chemical reactor in the course of all star system's history and the transport of prebiotic and biotic molecules from outer space to planets is considered as an important source of organics.

All young star system objects are subjected to energetic processing by photons and ions. As a result, the chemical and physical properties of the materials composing these objects will change significantly over time. Energetic processing of organic compounds into more complex species can be driven by a significantly enhanced UV–field in star forming regions, high-energy particle bombardment, and UV–radiation from the T–Tauri phase in stellar birth; at the early stage of evolution and at the present, UV–radiation of different wavelengths, protons of the Solar wind, and flares can drive this process. Among several energy sources available for abiogenic synthesis of biomolecules in space, UV–light with different wavelengths and cosmic rays are two of the most abundant.

The reactions of the amino acids in solid mixtures were the primary objective of our investigation — primarily, the abiogenic synthesis of oligopeptides from mixtures of simple amino acids. Four mixtures of aromatic (tyrosine or tryptophan) and aliphatic (glycine or alanine) amino acids were investigated usually. Amino acids were irradiated in solid state with different sources of energy: (1) VUV–light of 145 nm; (2) UV-light of 265 nm; (3) high energy protons (2-6 MeV); (4) γ–radiation, and (5) were installed on the surface of biosputnik in outstanding container when they were exposed to the action of all spectra of the open space energy sources during the entire time of flight — 327 hours.

We have shown experimentally that the solid mixtures of amino acids produce more complex compounds when they are exposed to either UV photons or ionizing radiation. Both irradiation and photolysis may destroy molecules as well as allow the synthesis of new and more complex ones. The chemical reaction of solid-state amino acids induced by different energy sources has been of increasing interest in several fields such as chemical evolution, polymerization of simple molecules, origin of homochirality in biomolecules and so on. The aim of our work was also to study the influence of mineral substrates on the reaction of oligomerization of amino acids under the action of vacuum ultraviolet (VUV) radiation with wavelengths less than 200 nm, one of the main energy sources of the Sun.

Simple oligopeptides can be formed on solid material not only by VUV–light but also by proton radiation, heat, and γ–radiation. Thus, it can be assumed that the chemical evolution would have taken place during the early stage of the Solar system origin and reached the stage of polymerization before the end of planet accretion. Polymerization is an essential step in prebiological evolution and we have shown that this process probably could take place even at early stage of the Solar system formation, on the surface of small bodies and inside them.

The aim of our work is to study the influence of mineral substrates on the reaction of oligomerization of amino acids under the action of different energy sources also. The presence of mineral components (montmorillonite, kaolinite, volcanic ash, olivine, piroxene, SiO_2) have different influence on the yields and products of the oligomerization reaction.

The delivery of organic compounds by carbonaceous chondrites to the early Earth and other planetary bodies could have been an important source of prebiotic compounds including simple biopolymers required for the emergence of life.

OP-8

FLAVIN AS A POSSIBLE COMPETITOR OF CHLOROPHYLL IN THE EVOLUTION OF SOLAR ENERGY CONVERTERS

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Photosynthesis, *i.e.* the conversion of photon energy into the energy of chemical bonds of molecules is the main source of energy for the Earth's biosphere. The key event of the process is a transfer of electron from the excited chlorophyll molecule situated in the reaction center (RC) which results in a conservation of energy of absorbed photon in phosphoanhydride bonds of ATP or reduced molecules of NAD(P)H. Further, these compounds provide the energy and reducing power for dark reactions of CO_2 assimilation. Excitation of the RC chlorophyll molecule occurs not only by direct photon absorption, but also through the resonance energy transfer from the excited antenna pigments – chlorophylls, carotenoids and bilins. The participants of excitation process as well as energy and electron transfer reactions are hydrophobic pigments localized in the lipid membrane.

Here we consider the possibility of the evolution of an alternative energy conversion system. Like in photosynthesis, excited pigment in this hypothetical model is involved in electron transfer, and the antenna may participate in its excitation. Functioning of the system depends, however, on the excitation of other pigments than in photosynthesis, its antenna is organized quite differently, and the proposed phosphorylation mechanism has no analogues in the organisms.

The model is based on the activity of excited flavins, i.e. derivatives of izoalloxazine (2,4-dioxo-benzo-*[g]*-pteridine). Flavin mononucleotide (FMN) and flavin adenine dinucleotide (FAD) are famous cofactors of "dark" enzymatic reactions. Excitation strongly increases activity of the flavin molecule in electron transfer and when excited, flavins sensitize the photoreactions leading to accumulation of free energy in products. In a templated organic system simulating the processes in prebiotic environment, they efficiently sensitize phosphorylation of ADP by orthophosphate to form ADP [1].

Electron transfer reactions with the participation of excited flavin molecules operate in photobiological processes. FMN and FAD play a key role in the functioning of photoenzymes (DNA photolyases) and photoreceptors of developmental and adaptational processes such as cryptochromes and the LOV- and BLUF- domain-containing proteins [2]. Excitation of flavin in the reaction center of DNA photolyases and cryptochromes occurs with a participation of the antenna, which role is played by the other flavin molecule, deazaflavin or pterin. The evolution of these proteins resulted in the formation of the complex of antenna and reaction center which organization is fundamentally different from the photosynthetic apparatus. The difference refers to the structure of pigments, their stoichiometry and relative ability of the antenna and RC pigments to absorb light. The study of the properties of the excited flavin and pterin molecules has revealed some structural features that were important in the process of selection of the chromophores for photoreceptor proteins.

Since the flavoprotein photoreceptors from different families are structurally very distant from each other, we can conclude that the "invasion" of flavins into the mechanisms of reception of light occurred repeatedly in the history of biosphere. We believe that in biological evolution, there were prerequisites for the formation of the photon energy converting mechanism based on the chemical activity of excited flavins and able to conserve the photon energy in macroergic phosphoanhydride bonds of ATP. The photoreceptor could be complemented with a light harvesting antenna using pteridine or benzopteridine derivatives.

The proposed model utilizes the shortwave visible and UV-A radiation with a main maximum in visible areas at 450-470 nm. Its spectral sensitivity almost ideally corresponds to the spectrum of solar radiation, not distorted by the atmospheric ozone shield, *i.e.* it is consistent with the conditions of early Earth. The presence of ozone in actualistic atmosphere shifts the irradiance maximum reaching the planet's surface to longer wavelengths what makes the situation less favorable for flavin-based photoenergetics. An important disadvantage of the flavin model as compared to chlorophyll photosynthesis, is a low photon absorptive capacity. The ε_{max} value for the long-wavelength absorption maxima are as λ_{450} = 1,2 10^4 M^{-1} cm^{-1} for FMN and λ_{680} = 5 10^4 M^{-1} cm^{-1} for chlorophyll. Another drawback of flavins as compared with chlorophyll is that the flavin molecule’s absorption is restricted by the shortwave visible (blue) and ultraviolet areas and even when assisted by the antenna pigments, flavins cannot utilize photons of the whole range of visible spectrum.

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OP-9

SYNTHESIS OF BIOLOGICALLY IMPORTANT METABOLITES FROM FORMALDEHYDE VIA PHOTOINDUCED AND CATALYTIC PROCESSES UNDER "PREBIOTIC" CONDITIONS

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The majority of the proposed chemical evolution hypotheses recognize the importance of the first step of the 'origin of life' process, i.e. organic synthesis of the biologically important molecules (amino acids, sugars, nucleobases, etc.) from the simplest inorganic substrates. Our own and previously reported data on catalytic and photochemical processes yielding biologically important molecules will be analyzed in the presentation.

It have been shown UV-irradiation of formaldehyde aqueous solution yields acetaldehyde, glyoxal, glycolaldehyde and glyceraldehyde [1], which can serve as precursors of more complex biochemically relevant compounds. In turn, photolysis of aqueous solution of acetaldehyde and ammonium nitrate results in formation of alanine and pyruvic acid [2]. Dehydration of glyceraldehyde catalyzed by zeolite yields pyruvaldehyde. Monosaccharides are formed in the course of the phosphate-catalyzed aldol condensation reactions of glycolaldehyde, glyceraldehyde and formaldehyde [3]. The possibility of the direct synthesis of tetroses, keto- and aldo- pentoses from pure formaldehyde due to the combination of the photochemical production of glycolahyde and phosphate-catalyzed carbohydrate chain growth is also demonstrated. Erythrulose and 3-pentulose are the main products of such combined synthesis with selectivity up to 10%. Biologically relevant aldotetroses, aldo- and ketopentoses (particularly ribose) are formed as products of izomerisation of erythrulose and 3-pentulose and are more resistant to the photochemical destruction owing to the stabilization in hemiacetal cyclic forms.

The conjugation of the concerned reactions results in a plausible route to the formation of sugars, amino and organic acids and pyruvaldehyde from the simplest C_1 (formaldehyde) and N_1 (ammonia) substrates under presumed 'prebiotic' conditions which could have been realized on the early Earth.

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OP-10

CLOSING THE CIRCLE: SMALL MOLECULE CHEMISTRY AND THE RNA WORLD

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Our current understanding of biology suggests that modern life was preceded by a ‘RNA world’. At the heart of this hypothesis is the requirement for RNA machinery able to manipulate and recognize small molecule substrates so as to make a self-replicating RNA system. From the perspective of an RNA based metabolism we will discuss a range of ribozymes able to either synthesize or manipulate nucleotide substrates. From the perspective of RNA dependent replication we will discuss recent progress with an RNA polymerase ribozyme called B6.61. This polymerase consists of two RNA domains, both of which are required for RNA polymerization to occur. We will discuss how these domains interact so as to make an interesting RNA polymerase machine.

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OP-11

NATURAL SELECTION IN PREBIOLOGY: GENERAL CONSTRAINTS, BASIC PROBLEMS, AND PHYSICAL VIEW ON THE SOLUTIONS

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Originally, the idea of natural selection had to do with the organisms as carriers of biological reproductive function. Now, it spreads up to the molecular level. New concepts of prebiotic evolution put forward, which argue that the selection of specific macromolecules under autocatalytic (or cyclic) fabrication transforms "absolutely impossible events (probability 10^{-100}) into absolutely reliable ones (probability 1)" (see, for example, [1]). In fact, such ideas are completely incorrect because the selection critically depends on the precision of reproductive function. This fact was first realized in [2] by analyzing the kinetic model of the following form

$$\frac{dS_i}{dt} = \left[\left(k_i^+ w_i - k_i^- \right) - k^{pop} \sum_{j=1}^{n} S_j \right] S_i + \sum_{\substack{j=1, \\ j \neq i}}^{n} k_j^+ w_{ij} S_j \ , \qquad (1)$$

where $S_i, i = 1,2,\ldots,n$, is the number of objects of *i*-th type, k_i^+ and k_i^- are the rate constants for reproduction and destruction respectively, w_i is the conditional probability for appearing an exact copy, and k^{pop} is the rate parameter of nonselective population pressure that keeps constant the total number of objects. The last sum in the right hand side of the equations (1) describes production of the objects of *i*-type due to erroneous reproduction of the objects of other types: w_{ij} is the conditional probability for such event in an act of reproduction.

Model (1) shows nontrivial characters of the selection. Under absolutely precise reproduction ($w_i = 1, w_{ij} = 0$), the selection of so-called a "wild species" with the highest value of "fitness" $\left(k_i^+ - k_i^- \right)$ is carried out. The assertion that the selection transforms "absolutely impossible events into completely reliable ones" is based just on this abstract situation. In fact, the distribution of "species" is localized around the "wild species" if and only if the precision of reproductive functions exceeds some critical value (error threshold). It is crucial that the error threshold strongly depends on *complexity* of the objects. (About the meaning of the term "complexity" in the context of natural selection see [3]). The more complex objects are, the more precise reproduction must be. If not, then as far as the error threshold is reached the selection regime sharply goes into *the random mode generation*. It is important that the critical behavior holds at the level of oligomeric complexity, therefore, the operational precision is required on prebiology, too. For this reason, abiogenic emergence of functional carriers like the "molecular machines", i.e. molecular structures capable of carrying out precise operations at the molecular level, seems to be an important target of the prebiotic evolution. It should be emphasized that we are talking about the operational accuracy, but not catalytic activity. From the physical viewpoint, it is fully meaningless to consider something like the Fox's proteinoids or Oparin's coacervates as the functional carriers. On the other hand, native proteins and RNA can hardly be regarded as prebiotic molecular machines, because sophisticated operational systems are needed to fabricate such macromolecules. To find a way, we need the deep insight into the physics of molecular machines, the principles of their organizations, the ways of their emergence under statistical, not operational, control, as well as the self-assembly of such functional carriers into autonomous operational systems. These are just the issues of modern physical trends in the origin of life field (see, for example, [4]), which still are weakly presented in the BOE Program (see, for example, [5]).

Two important results relevant for the modern trends will be presented in the talk. One is the self-similarity of fluctuation-induced protein mobility on anomalously wide range of time scales up to a dozen of orders [6]. It allows to look at the molecular machine as hierarchically organized scale-free dynamical system and opens up new ways for designing molecular machines beyond the proteins and RNAs. Another result relates to a new class of artificial networks, the random hierarchical networks, with topological properties very close to the operational systems like the networks of neurons [7]. Again, this finding opens new approaches to the prebiotic operational networks, as well as to the architecture of early metabolism.

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OP-12

ABIOGENIC MODEL OF PHOTOPHOSPHORYLATION OF ADP TO ATP. CHARACTERISTICS OF PIGMENTS-SENSITIZERS AND THE ROLE OF ORGANO-MINERAL MATRIX

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The light radiation of the Sun is the main source of energy for the functioning of the biosphere and, presumably, was the dominant source of energy for the processes that gave rise to living matter. In the organisms there exist mechanisms converting light energy into chemical bonds, particularly to energy of macroergic bonds of adenosine triphosphate (ATP). In the photophosphorylation process the light energy is converted into electronic excitation energy of the photoreceptor, and then, to the electrochemical energy and, further, mechanochemical energy that provides the operation of ATP synthase and formation of ATP.

We have developed a model in which the conversion of photon energy into the energy of macroergic bonds of ATP is performed by abiogenic products of thermal amino acids condensation. These products are the pigments conjugated with proteinoid polymers. Two-dimensional scanning of excitation and emission fluorescence spectra of pigment material revealed the presence of only two groups of compounds - flavins, and in addition, pteridines.

Functional properties of the photochemical system were dependent on the original composition of chemical substrates. Changing the amino acid precursor entailed changes in the structure of the synthesized pigment, and as a consequence, the change in the action spectrum of the process. Thus, replacing in a starting mixture of glycine to alanine resulted in preferential formation not flavin, but pteridine and, consequently, to a hypsochromic shift of the main maximum of the photophosphorylation action spectrum from 450 nm to 350 nm, i.e. from the visible area to ultraviolet.

Flavin pigments sensitized efficient phosphorylation of ADP to ATP only when staying in complexes with the colloidal silicate particles. These complexes begin to function as active matrixes. The presence of the matrix enhances the yield of ATP in flavin-dependent photophosphorylation by two orders of magnitude as compared with the aqueous solution.

A question arose concerning the role of the given mineral component polysilicic acid (H_4SiO_4) in the functioning of the photochemical process. Therefore, we investigated the phosphorylation of ADP with orthophosphate to form ATP in the presence of colloidal nanoparticles of polysilicic acid (diameter $\leq$ 200 nm). In addition to proteinoid, containing abiogenic flavin and pteridine pigments we investigated as photosensitizers the preparations of protoporphyrin-IX, riboflavin, 6,7-dicarboxypterin as well as melanoidins formed by heating of an equimolar mixture of glycine with ribose. Electron donor used in experiments was Na_2-EDTA and the electron acceptor was atmospheric oxygen.

The emerged supramolecular organo-mineral matrix sensitized photophosphorylation of ADP to ATP under the action of UVA light (Hg-lamp, λ_{max} 365 nm, active zone from 290 to 380 nm was cut by glass filters). All the samples were equalized by the absorption at 365 nm. The analysis of photophosphorylation in the presence of the above mentioned pigments as a part of organo-silicate matrix showed that the most effective were flavin-conjugated proteinoids as well as melanoidins (20% and 18%, respectively). Protoporphyrin-IX, riboflavin and 6,7-dicarboxypterin were in this reaction were less efficient. In the control samples containing a suspension of silicon oxide nanoparticles without pigments, or solutions of pigments in the absence of nanoparticles of silicon oxide, no phosphorylation was observed. Considering the possible physico-chemical mechanism of the process, it is necessary to take into account the interaction of the adsorbed pigments-sensitizers with silicate colloidal particles and, consequently, change of their electrochemical characteristics.

The presence on the primitive Earth of photoactivated supramolecular matrices, apparently, was an important prerequisite for the occurrence of various processes of prebiological evolution, including the process of phosphorylation with the formation of ATP.

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OP-13

STATISTICS OF GENOME SIZE AND NUCLEOTIDE CONTENT USING DATA OF COMPLETE PROKARYOTIC GENOMES

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Research on evolution of early unicellular organisms relies on complete genome sequencing data abundant last years due to new sequencing technologies. Rapid growth of data banks allows us reexamine sequence features necessary for minimal genome size and minimal gene set as unit of evolution. Several theoretical and experimental studies have estimated the minimal set of genes that are necessary and sufficient to sustain a functioning cell under some ideal conditions. The *M. genitalium* genome has the smallest genome size, comprising 580 Kbp, with a capacity to encode only 482 genes. The minimal nature of the *M.genitalium* genome triggered particular interest to the conception of a minimal cell (Mushegian&Koonin, 1996). A comparison of the first two completed bacterial genomes, those of the parasites *H.influenzae* and *M.genitalium*, produced a version of the minimal gene set consisting of approximately 250 genes (Koonin, 2000), with later re-estimations. More recent studies have attempted to reconstruct its genome by chemical synthesis (Gibson et al, 2008), even to engineer a new living organism, referred to as *Mycoplasma laboratorium* (Endy, 2008).

Several thousand complete and assembled of bacterial and achaeal whole genome sequences were downloaded from NCBI ftp site (ftp://ftp.ncbi.nlm.nih.gov/genomes/Bacteria/, latest release, May 2011). We compared genome size with gene number and GC content for groups of the organisms (Figure 1). For 2065 whole genome assemblies we found high linear correlation between genome size and gene number (0.81), that been expected, and, more interestingly, between genome size and GC content (0.46). Thus, larger genome size is strongly related to higher fraction of G and C nucleotides. Correlation between GC content and genome size is 0,35 (for 104 archaeal) and 0,59 (for 1478 bacterial) species. Correlation of GC content to genome size follows the same trend in archaeal and bacterial groups. We also have compared Kolmogorov complexity of genomic sequences (Lempel-Ziv estimation) using software developed earlier (Orlov&Potapov, 2004) and computer resources of Shared Facility Center “Bioinformatics”.

We aimed to relate entropy measures of DNA sequences, number of protein-coding genes and sequence features (GC content) in genome scale for different environment niches of the organisms under study (Table 1).

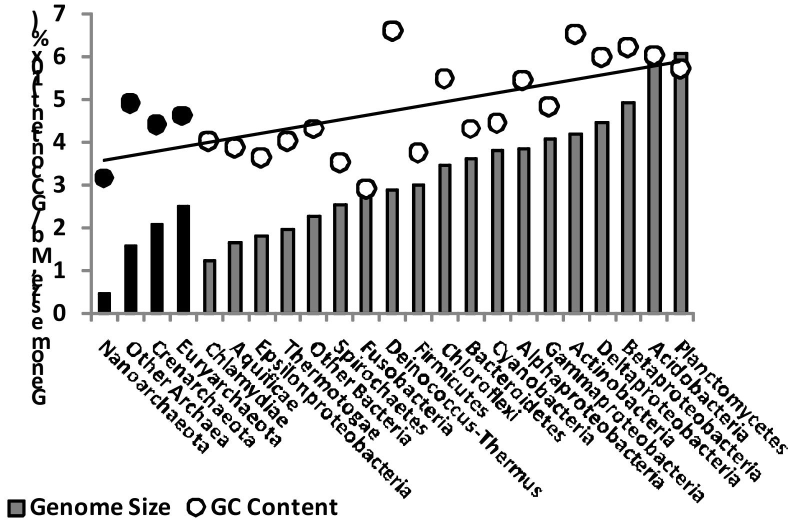

Figure 1. Genome size and GC content for 1586 prokaryotic genomes sorted by groups. Axis Y: Average genome size, Mb (bars), and GC – content, % in 10x scale, (cycles). Trend shows correlation between genome size and GC content.

Table 1. Habitat, temperature range, genome size and GC content.

Habitat	Genome	GC
Specialized	2,767	47,3
Host-associated	3,019	44,9
Aquatic	3,893	49,5
Multiple	4,561	46,3
Terrestrial	6,674	61,1
N/A	3,689	45,3

Temperature range	Genome	GC Content
Hyperthermophilic	2,084	43,9
Thermophilic	2,736	47,9
Mesophilic	3,909	47,2
Psychrophilic	4,448	43,9
Cryophilic	5,223	41
N/A	3,761	47,6

It is interesting to note, that smaller genome size is associated with specialized habitat, hyperthermophilic temperature and microaerophilic oxygen requirement. In all cases it is related to lower GC content.

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OP-14

WOLBACHIA – A NASCENT NEW ORGANELLE OF THE EUKARYOTIC CELL

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The eukaryotic cell has been associated at its very origin with with symbiosis. Evolutionary progress post biochemical evolution of eubacteria and archaea lead to association of some bacteria into an united cytoplasmic system. Division of the cytoplasmic space into compartments made it possible for the new cell to protect genetic information from mutagenic factors, to restraint horizontal transmission among cells, to intensify energetic processes as well as to alter sizes and forms of the cells. However, the moment of the eukaryotic cell appearance in evolution of the Earth biosphere has been shrouded in mystery, with the principal absent of palaeontolological evidence. Can new compartments alike mitochondria, plastids or nucleus appear in the modern eukaryotic cell?

At present a lot of examples of symbiotic associations are known and they can actually demonstrate, with certain reservations made, examples of evolutionary process of organellogenesis. Most of these facts relate to intracellular bacteria-invertebrata host associations, an in the majority of cases these bacteria provide the host with nutrition (1). The γ-proteobacteria *Buchera* – aphid system exemplifies one of the first and most ancient symbioses (~200 Mya) that were investigated. There is *Buchera* population in specialized cells of the host, bacteriocytes; a functional role of *Buchera* consist in biosynthesis of essential amino acids to the host. *Buchera* has lost autonomy due to of the loss of many genes and biochemical pathways. The bacteria are transmitted via eggs and thus Buchera is passed on to following generations of the aphid. The host genome is responsible for the control of expression of certain bacterial genes and cellular processes, i.e. the size of the bacterial population. In other words, the host has a *biofactory* and runs it.

There are a lot of other examples of bacteria-animal intercellular symbiotic assosiations where we can observe the whole gradual transition from parasitic to obligate mutualistic interactions of the organisms (1). Distribution of the most bacteria within the host taxon is restricted by the family or genus rank.

An α-proteobacteria Wolbachia is an unique phenomenon amonf intracellular bacteria as it forms persistent symbiotic interrelations at least within two phyla: Nematoda and Arthropoda. The origin time of these genus bacteria has been estimated basing on 16SrRNA gene sequence as about 100 Mya. The analysis of the Wolbachia strain distribution pattern and the genus age makes it evident that there is horizontal transmission of Wolbachia among distant taxa and it is frequent. According to the recent estimations (2), only among insects the number of infected species can be more than 60%. *Wolbachia* transmission to the host next generations takes place strictly via eggs. The effects of *Wolbachia* upon the host are rather diverse. First of all Wolbachia is a reproductive parasite that may causes cytoplasmic incompatibility, parthenogenesis, male-killing and feminization. Also *Wolbachia* positive influence on the host fitness is well known. Therefore bacteria can be considered a mutualistic symbiont.

Our present study of infected insects and strait genotyping by MLST as well as be comparing them with the data available in the DB (http://pubmlst.org/wolbachia/) made it possible to clime existence of “groups in fashion” of *Wolbachia* strains that are found among various insect taxonomic groups. It is important to notice that it does not depend on location of a population or ecological features of a species. It is interesting that strains classified as identical by MLST can bring about different reproductive alterations in different hosts. Hymenopterous insect parasites are likely to be transmitting agents of these bacteria. It is known that *Wolbachia* as well as mitochondria can migrate from one cell of the host to another. An endoparasitic wasp egg in the body of the victim can be destroyed by means of the immune system of the host. If the wasp was infected then some portion of the bacteria can migrate into the cell of the victim and if Wolbachia reaches the host’s gonad it can be inherited. A reverse situation may take place, a growing larva of the wasp may be infected by the bacteria of the victim and henceforth it inherits the acquired strain. Since biological diversity of wasps and their victims is enormous the exchange of different *Wolbachia* strains among insects turns out noticeable. The “strains in fashion” may have an ability to exist in cells of larger-scale range of hosts or to have efficient means to protect themselves from the aggressive habitat of their new host’s cells in comparison with other strains.

Thus Wolbachia spreads among some invertebrata as a facultative component of the genome and the formation of a new organelle can take place in a long evolutionary perspective independently in various Nematoda and Arthopoda taxa.

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OP-15

SPACE FLIGHT EXPERIMENTS WITH NON-TERRESTRIAL MINERALS AND BIOORGANIC MOLECULES

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Life has probably existed on Earth for about 3.5 billion years. It is supposed that organisms as complex as bacteria had emerged within 0.5-1 billion years. But, this seems a rather short timescale for such an important step and suggests that some basic building blocks of life may have reached Earth from space. The main point of the reported experiments was to identify an abiotic process that results in complex organic compounds, the monomeric units of nucleic acids and amino acids, on the surface of comets, asteroids, meteorites, and cosmic dust particles. At the same time, the task was to reveal catalytic or/and protective properties of meteorites and similar terrestrial minerals. The synthesis of 5'-monophosphates and dipeptides, the predominant reaction products, along with other chemical derivatives, has been carried out under interplanetary conditions and in presence of minerals simulating the surface of small space body. The reaction must proceed under solvent-free conditions and incident ultraviolet radiation in a vacuum. Short UV radiation (145 nm and 154 nm) was used as a trigger for photochemical processes. Two types of substances (amino acids and nucleosides) were examined in respect with their chemical reactivity in presence of lunar soil, Allende meteorite, Murchison meteorite and terrestrial minerals of similar composition (pyroxene and olivine). Our task was to distinguish principal differences, if any, of minerals participating in chemical processes and to figure out the most efficient mineral matrix. The main application of these laboratory experiments is selection of the most “chemically active” mineral to be employed at next flight experiment onboard “Bion-10M” Russian space satellite. Since the space and weight on the experimental platform is very limited, it seems incredibly important to make the right choice. Hardware of Bion experiment has been designed exactly for that kind of scientific tasks, software and general strategy of the whole experiment will be reported as well. It should be outlined that fulfilling such a task became possible after several series of flight and laboratory experiments and as a result of continuous efforts of different professionals, both researchers and engineers. Previous data and strategy, selection of materials and methods were taken into serious consideration, and the basic presumption was to demonstrate yet another evidence of photochemical transformation in cosmic media related to early evolution stage. The chemical evolution of life may have started in space as well. We are not neglecting the endogenous origin of life but suggest extraterrestrial delivery of organics could accelerate all the processes on Earth and thus reduce the early evolution period. It is presumed that these space-made organic molecules could be safely transported to Earth's vicinity by being associated with mineral grains which would not only protect them from UV degradation, but trigger chemical processes as well.

OP-16

EVOLUTIONARY TRENDS OF GENOME AMPLIFICATION AND REDUCTION

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The comparative modeling of populations' adaptivity and biodiversity dynamics is carried out. Populations consist of symbiotic unicellular haploid asexual organisms inhabiting in a biotope of limited volume in which the nonspecific substrate (NS) inflows externally. Organisms consume NS and it is necessary for every of them. Symbiosis is provided by intra-populational exchange of specific substrates (SS). Using the original software package "Evolutionary Constructor" [1] allowing varying both genetic and trophic structure of a model, we have studied the evolution of a community initially represented as the trophic ring-like web consisted of three populations. Each population utilized only one SS and produced another one (SS): first population "fed" second one, the second fed the third, and the latter fed the first one. During calculations the processes of horizontal genes transfer (between cells of different populations) and loss of genes were modeled stochastically with probability 10^{-7} per generation per cell. It led to the origin of novel populations, which cells combined various sets of utilized and synthesized substrates. Cells reproduction rate was also regulated by genome size. A large genome assumed to be associated with more complex metabolism, larger time of replication, and consequently less cells reproduction rate.

It has been shown that in the case of average values of genome-length penalty and in pessimal environmental conditions (low concentration of NS in the inflow and low SS synthesis efficiency in cells) the majority of biomass is formed by populations which possess metabolically complete or almost complete genomes. Metabolically poor populations in the long term were either displaced from trophic system or became commensals being survived at rich populations' expense.

In another model, there was only one metabolically rich population. At the same time the genome-length penalty was higher than one in the previous model. At first, only deletions occurred, and after origin of metabolically incomplete populations, both deletions and horizontal gene transfer could occur. Both actions occurred repeatedly and partially compensated each other. Subcomfortable/comfortable environmental conditions were modeled by the varying of inflow concentrations of NS. Stable trend of genome reduction was shown to be major in both subcomfortable and comfortable conditions. The most primitive populations had only two genes for utilization: one for NS, another for SS. They displaced all other populations. In subcomfortable conditions this led to the death of the primitive one by reason of SS depletion. In comfortable conditions SS concentration supported by inflow and the primitive stayed alive.

After that we have studied the influence of a phage infection on possible evolutionary trends in communities of unicellulars. Addition of temperate phages into community led to infection of all populations. A fraction of infected cells depended on both phages and cells concentrations in environment. The development of infected population was determined by conditions the “parent” population was in the moment of its infection. If it steadily grew, all infected cells lysed with the formation of novel portion of phages. Contrariwise, if parent population was in pessimal conditions and steadily depopulated, infected cells (all or a part of) switched to lysogenic cycle and became phage carriers, immune to infection by that particular phages. As a result, infection significantly changed evolutionary dynamics of community. It suppressed or even destroyed well-growing populations and consequently maintained less competitive ones. On a series of computational experiments it has been shown that in pessimal environmental conditions the populations which are far from metabolic richness can survive and become leaders. It contrasts with the trend of genome amplification mentioned above. Possible change of evolutionary trends caused by phage infection was also found in cases of communities living in optimal environmental conditions.

Computational modeling results have a stochastical character. In some experiments infection killed community. In other cases community perished before infection due to rapid growth of primitive populations. However the change of evolutionary trend occurred not always.

Therefore, our results show that the infection process of unicellulars’ community by temperate phages has a capability to change evolutionary trend of community.

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OP-17

HABITALS AND ENERGETICS OF FIRST CELLS

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Life can exist only when supported by energy flow(s). Here, it is argued that the evolutionarily relevant, continuous fluxes of reducing equivalents, which were needed for the syntheses of first biomolecules, may have been provided by the inorganic photosynthesis and by the redox reactions within hot, iron-containing rocks. The only primordial environments where these fluxes could meet were the continental geothermal systems. The ejections from the hot, continental springs could contain, on the one hand, hydrogen and carbonaceous compounds and, on other hand, transition metals, such as Zn and Mn, which precipitated around the springs as photosynthetically active ZnS and MnS particles capable of reducing carbon dioxide to diverse organic compounds. At high pressure of the primordial CO_2 atmosphere, both the inorganic photosynthesis and the abiotic reduction of carbon dioxide within hot rocks should have proceeded with high yield. Among a plethora of abiotically produced carbonaceous molecules, the natural nucleotides could accumulate as the most photostable structures; their polymerization and folding into double-stranded segments should have been favored by the further increase in the photostability. It is hypothesized that after some aggregates of photoselected RNA-like polymers could attain the ability for self-replication, the consortia of such replicating entities may have dwelled within porous, ZnS-contaminated silicate minerals, which provided shelter and nourishment. The energetics of the first cells could be driven by their ability to cleave the abiogenically formed organic molecules and by reactions of the phosphate group transfer. The next stage of evolution may be envisaged as a selection for increasingly tighter envelopes of the first organisms; this selection may have eventually yielded ion-tight lipid membranes able to support the sodium-dependent membrane bioenergetics. Lastly, the proton-tight, elaborate membranes independently emerged in *Bacteria* and *Archaea* and enabled the transition to the modern-type proton-dependent bioenergetics.

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OP-18

EVOLUTION OF REPLICATORS ON MINERAL SURFACES: A SOURCE OF PREBIOTIC RIBOZYMES?

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One of the most important problems that prebiotic evolution has to face is the explanation of the appearance of a genetic self-replicating system able to evolve in critical conditions like those present in the primeval terrestrial habitats, characterized by an intense UV and cosmic radiation, and the lack of an efficient enzymatic system of repair.

As pointed out by Eigen, if the copy fidelity of a replicating system is not sufficiently high it falls into the "error catastrophe" losing the capability to transfer its information to the next generation and to evolve towards an increasing complex organization (1).

Different theories have been proposed to overcome this problem. In particular, it has been suggested that the presence of a "mineral surface", i.e. a system with a well defined spatial structure, could preserve and enhance the information potential of a self-replicating system (2).

In this communication we present the results of our investigations on the evolutionary potential of simple RNA molecules, such as hairpin and hammerhead ribozymes, using both a theoretical approach with computer simulation, and an experimental approach based on the adsorption of nucleotide bases, nucleotides, oligonucleotides, and ribozymes on mineral substrates represented by solid particles of extraterrestrial origin (i.e. carbonaceous chondrites) and other inorganic matrices.

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LIFE ORIGINATION HYDRATE HYPOTHESIS (LOH-HYPOTHESIS): QUESTIONS AND ANSWERS

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I. Introduction: the principles

We develop the OK-hypothesis (Ostrovskii–Kadyshevich hypothesis). It covers the period from the Presolar Star up to origination of the cellular life at the Earth. The OK-hypothesis consists of several sub-hypotheses, one of which is the Life Origination Hydrate hypothesis (LOH-hypothesis), which was repeatedly published in Russian and in English. When developing it, we adhere to the following principles. (1) The gross-scale processes in nature proceed progressively in the direction of decrease in the free energy in the Universe subsystems that can be approximated as the isolated ones. (2) All natural phenomena proceed as a result of regular and inevitable transformations regulated by the universal physical and chemical laws. (3) The Newton principle of simplicity ("…for Nature is pleased with simplicity, and affects not the pomp of superfluous causes"). (4) The principle of repetition of supposed events and of the presence of individual features in the reproduced events. (Nature created many similar but somewhat differing events and no unique event without close analogues.) (5) The principle of the unity of the event point. Separation of an event into several sub-events proceeding in different points with the subsequent interaction between the sub-events decreases the probability of the resulted event, because it multiply decreases the degree of repetition of the event as a whole. (6) Nature makes no jumps (Nature non facit saltus (Lat.)).

An analysis of the phenomenon of living matter led us to the conclusion that the hypothesis of its origination should take into account the following statements. (1) The DNA occurrence and reproduction is the principal feature of living matter; the proteins are side products. (2) The Earth's living matter had originated on our planet from inorganic and simplest organic substances as an inevitable product of the atomistic world. (3) Stable undisturbed conditions favoured living matter origination. (4) The reacting system transformed so slowly that it passed all possible states step by step in the direction of gradual decrease in the Gibbs free energy. (5) The diversity of the available forms of living matter is caused mainly by some variations in parameters of the native medium. (6) The nature of the physical and chemical processes of origination and subsequent development and replication of living matter should be of the same nature.

II. The LOH-hypothesis

Just as a result of the directedness of natural phenomena, researchers are principally capable of mental doubling back the way the nature went and, thus, of revealing the main milestones in Nature’s movement. A naturalist must search for a “hook” in the environment in order to catch on it and, having the thermodynamic laws as the guiding thread, to guess the logics used by Nature in its development. It is very likely that we found such a hook.

According to the LOH-hypothesis, the living matter simplest elements (LMSEs), i.e., N-bases, riboses, nucleotides, nucleosides, DNA, and RNA, originated and, possibly, originate in our days from CH_4 (or other CH_4-hydrocarbons), niters, and phosphates under the Earth's surface or seabed within honeycomb structures of hydrocarbon hydrates. The underground deposits of CH_4 and other hydrocarbons are produced by the reaction between H_2 and CO_2, and CO_2 is produced from carbonates as a result of their thermal decomposition induced by the gravitational compression of the young-Earth crust. Thus, the living-matter sources are H_2, carbonates, and phosphates resulted from transformation of the nebula that arose as a result of the presolar-star explosion.

The following questions will be answered in the presentation. (1) In what phase did the LMSEs form? (2) From what substances did the LMSEs form? (3) By what mechanism did the LMSEs form? (4) Is Nature capable of synthesizing LMSEs with no external energy? (5) How had CH_4 hydrate originated? (6) How did CH_4 and NO_3^- meet? (7) Why nothing but NO_3^- reacted with CH_4-hydrate? (8) How did DNA- and RNA-like molecules form from nucleosides? (9) Is there a relation between DNA and RNA formation, on the one hand, and the atmosphere composition, on the other hand? (10) Why do only five chemical elements usually enter the DNA and RNA? (11) Why are N-bases entering DNA and RNA similar in their composition and structure? (12) Why are N-bases and riboses limited in size? (13) Why are N-bases not identical? (14) Why do only five N-bases usually enter DNA and RNA, and why do other N-bases, such as xanthine, sometimes enter them? (15) Could D-ribose (DR), desoxy-D-ribose (DDR), Thymine and Uracil exist simultaneously in a mixture containing CH_4 and niter? (16) How had it happened that the sequences of N-bases in DNAs and RNAs are not random? (17) Why did Nature choose DR and DDR, but not their L-enantiomers or mixtures of enantiomers for DNA and RNA syntheses? (18) How did proto-cells originate?

The LOH-hypothesis is supported with numerous thermodynamic calculations.

OP-20

PREBIOLOGICAL EVOLUTION OF MACROMOLECULES

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The foundation of life phenomena are (1) significant decrease of the diversity of macromolecular structures comparing to the possible repertoire; (2) functionalization of macromolecules. In this study the approach describing these observations utilizing the idea of thermocycle as a driving force of evolution, principles of combinatorial and supramolecular chemistry is considered. Kinetic models of the process are analyzed and their parameters are compared with the true time of prebiological evolution.

All natural polymers are products of trifunctional monomers polycondensation generating polyamids (aminoacids polycondensation) and polyethers (nucleotide polymerization).

The nature of thermocycle is considered. Thermocycle provides thermodynamical possibility of polypeptides and polynucleotides formation, including polymization and partial depolymerization stages. The key question at the stage of macromolecules evolution is a supramolecular interactions of monomers with synthesized polymers. Combinatorial effects appear as a result of partial disassembling of polymer to monomers due to hydrolytic processes under conditions close to liquid-gas transition.

Kinetic processes both in open and closed (the model of evolution in a drop) systems are analyzed in detail. The general principle of evolution is nonrandom distribution of monomer in polymer chain due to supramolecular interactions; primary synthesized polymers serve as matrixes for sorbtion and partial selectionof monomers with subsequent polymerization. Due to supramolecular interactions of monomer with polymer, polymer influences the products composition.

Selection principle and competitive advantage are (1) better thermodynamical stability; (2) better resistance to hydrolytical destruction; (3) uprise of catalytical properties in reactions of peptides, polypeptides, monomers formation aminoacids polymerization, polycondensation of nucleotides. These processes provide transition from pure statistical to evolutionally directed synthesis.

An interdependent coexistence of three biopolymers’ ‘universes’ (proteins, RNA and DNA) are considered. In hydrolytical degradation mode in a system peptides and nucleic acids accumulate, they are affine to each other, i.e. form stable supramolecular complexes. In such systems supramolecular complexes is a main selection principle. Processes of information recording and transfer from protein to DNA (hieroglyphic script) are considered.

The main principle of the presented study is quantitate calculation of different kinetic models.

OP-21

EVOLUTION OF GEOLOGICAL PROCESSES ON THE EARLY EARTH AND THEIR IMPACT ON THE EARLY BIOSPHERE

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It is known that the Earth's ecological systems in the Middle Paleoproterozoic were subjected to essential changes, which promoted to acceleration of the biosphere expansion and development, and finally led to the appearance of multicellular organisms. Though life has been already existed in the Paleoarchean [9], the multicellular organisms appeared only in the middle Paleoproterozoic (~ 2.0 Ga ago) [9]. The first cardinal change in evolution of the Earth occurred at 2.5-2.35 Ga, when the Earth entered to Cratonic stage, which was marked by vast eruptions of lavas of siliceous high-Mg series accompanying by great glacial epoch. However, this stage did not lead to significant changes in bioorganic world represented at that time by abundant and diverse microfossils existing since Archean, which was possibly related to the geochemical signatures of this magmatism, in particular, low contents of many biophile elements. Then, within period from 2.35 to 2.0 Ga, a cardinal change in the type of magmatism occurred: the early Paleoproterozoic high-Mg magmas derived from depleted mantle gave place to the geochemical-enriched Fe-Ti picrites and basalts, similar to the Phanerozoic within-plate magmas. New type of magmas was characterized by elevated and high contents of Fe, Ti, Cu, P, Mn, alkalis, LREE, and other incompatible elements (Zr, Ba, Sr, U, Th, F, etc.) [10]. At the boundary of 2 Ga, the plume tectonics was replaced by plate tectonics, which led to gradual replacement of ancient sialic continental crust by secondary oceanic (mafic) crust.

That time was marked by the appearance of first fungi [2]. All microorganisms of that period caused the decomposition of organic matter and served as active agents of biological weathering, playing an important role in biogeochemical cycle of biophile elements, including aforementioned metals and other elements (primarily, Fe, Cu, Zn, Co, Ni, and P), and correspondingly their supply in the World Ocean. A large-scale influx of alkalis in the World Ocean presumably neutralized its water, making it more suitable for the life, while input of Fe-group metals, P, and other trace elements, which are required for metabolism and fermentation, rapidly expanded the possibility for the development of biosphere. Judging on appearance of oxidative atmosphere ca. 2.3 Ga (Great Oxidation Event) [3], it promoted especially to explosion of photosynthesizing organisms.

The manifestation of this geochemically enriched magmatism was correlated with the first finds of eucaryotic heterotrophic organisms at ~ 2 Ga, for example in the black shales and phosphorites of the Paleoproterozoic Pechenga complex, Kola Peninsula [7]. For instance, a significant increase in amount of spheromorphides and remains of filamentous algae is observed in the Upper Jatulian deposits (~ 2.0 Ga) of Karelia [1]. The vital activity of the organisms significantly increased the oxygen content in atmosphere, which was marked by the formation of cupriferous red beds at all Precambrian shields, generation of the first hydrocarbon deposits (shungites, Karelian craton), rock-salt in Karelia [6], and phosphorites with age of 2.06 Ga on the Indian and Kola cratons [4].

Thus, a fundamental change in character of tectonomagmatic activity acted as the trigger for environmental changes and acceleration of biospheric evolution, supplying a qualitatively new material on the Earth's surface. This event gave impetus to wide expansion of biosphere, which fixed by appearance of oxidative atmosphere, and enhanced biosphere mass as demonstrated by appearance of hydrocarbon deposits. However, rapid enhanced of the bulk of biosphere did not accompanied by the same increasing of the biodiversity; new forms (especially multicellular organism) appeared in small quantity and long time did not essential evolved.

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OP-22

GLOBAL REORGANIZATION IN THE BIOSPHERE TROPHIC STRUCTURE AND ITS RELATION TO THE EXPLOSIVE GROWTH OF BIODIVERSITY THROUGH THE ORDOVICIAN EVOLUTION OF THE EARTH (495 TO 439 MA)

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Evolution of the biosphere can be presented as the following processes: (1) emergence of new ecologically specialized groups (guilds), providing a more efficient use, transfer, and transformation of matter and energy in ecosystems; (2) spatial expansion of life throughout the Earth (gradual transition from a discrete to continual biosphere on exploration of new bionomic zones and biotopes; (3) complication of the trophic structure of ecosystems (from simple Archean autotrophic-heterotrophic prokaryotic systems to modern global ecosystems); (4) variations in the spatial and power parameters of biogeochemical cycles. In this context, the Ordovician can be regarded as one of the greatest critical stages in the biosphere evolution. In the Ordovician, the emergence of new taxa (ecologic guilds) with better trophic adaptability in benthic associations and settling of pelagic zones in euphotic sea areas resulted in dramatic changes in sea ecosystems, which predetermined further evolution of marine biotas. The chief evolutionary strategy of Precambrian marine organisms was to improve adaptation to physicochemical environmental settings by complication of biological organization and separation of metabolic and reproductive functions within a body. In the Early Cambrian, main phyla of marine invertebrates emerged, and multistage trophic relationships between autotrophs and heterotrophs, with division of ecologic functions, began to form. Adaptation to the biotic environment became as evolutionarily important as adaptation to abiotic conditions. Starting in the Ordovician, the ecologic mechanisms of organism interaction became the key factor of the evolutionary strategy in biota associations owing to the gradual stabilization of abiotic parameters in sea basins. New edificator groups first appeared in abundance in the Ordovician and reached their acme in the Middle Ordovician: articulate brachiopods and sessile colonial (tabulates, tetracorals, heliolitoids, and stromatoporoids), aggregated (crinoids), and colonial-aggregated (bryozoans) niter-feeding organisms with carcass skeletons. This resulted in the breakdown of biotopes and complication and heterogeneity of food webs. The lowest trophic level was dominated by ostracodes, first small aquatic universal eaters simultaneously belonging to several trophic levels and capable of a deeper transformation of organic matter. In the Ordovician, the pelagic zone became a constant rather than facultative, as before, habitat for zooplanktonic and nektonic organisms: graptolites, radiolarians, conodonts, nautiloids, meroplankton (mainly larvae of colonial organisms and brachiopods), pelagic trilobites, ostracodes, and early primitive fishes. Some spatial rearrangement of the lowest trophic level, major producers, took place in the same period. This had a dramatic effect on the stage and lateral structure of trophic chains. Until the early Middle Ordovician, the main photosynthesizing producers were bottom cyanobacterial associations, or meadows (mats), which were widespread in Late Precambrian and Early Paleozoic epicontinental seas. At the Early-Middle Ordovician boundary, the areas of these meadows decreased, and phytoplankton became the main producer. The global ecologic event was accompanied by the greatest (in the Phanerozoic) burst of the diversity of Ordovician marine biotas followed by rapid stabilization. Later, the stability was maintained by a phylogenetic succession of ecologically equivalent taxa, with some ecologic guilds replaced at critical borderlines. Thus, in the Ordovician, sea ecosystems became multistage, their trophic structure became more complex, and a global closed biogeochemical cycle formed for the first time throughout the sea area. The Ordovician global biotic events matched large-scale geologic events (abrupt climatic changes, maximum range of transgressions and regressions of epicontinental seas, changes in Mg and Ca balance in marine sediments, increase in the content of oxygen in the Earth's atmosphere and hydrosphere, and formation of the ozone screen). It is supposed that the appearance of the ozone screen and increase in the content of oxygen in sea water had a crucial impact on the settling of heterotrophs in the pelagic zone and formation of coherent (ecologically complete) benthic ecosystems. At the initial metastable stage of the development of the ozone screen, eustatic fluctuations of the World ocean level caused dramatic biodiversity fluctuations in bottom and pelagic associations determined by profound changes in spatial parameters of sea shelves, the main habitat of biota. The Late Ordovician extinction of marine biotas resulted from an abrupt shrinkage of the shelf habitat caused by a lowering of the World ocean, which, in turn, resulted from the fixation of huge volumes of water in continental glaciers after the Ordovician transgression maximum.

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THE EFFECT OF IMPACT-INDUCED ACCRETIONARY PROCESSING OF THE EARTH

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Emergence of terrestrial life occurred very early in the Earth's history. Investigations indicate the presence of life forms in the found most ancient sedimentary samples with ages ~3.8 G.a. (Schidlowski, 1993). The origin of life thus dates to the period between the planetary accretion ~4.5 G.a. to the age of the most ancient terrestrial samples. The early emergence of life enforces to consider conditions on the early Earth in more detail since this may give a key to the answer on the most fundamental question about the mechanism of life origin.

The accretion period of the Earth group planets (at least its latest stages) was characterized by massive impacts of planetesimals. Impacts of planetesimals provided an output of enormous energy that resulted in the early deep processing of planetary material. There are three major result of such processing: 1) the release of impact-generated atmosphere; 2) the release of water to form primordial ocean; and 3) development of primordial crust due to impact-generated differentiation of planetary siliceous material.

Low-velocity impacts decompose volatile-bearing minerals to release H_2O, CO_2 and SO_2. Hypervelocity impacts, which provide vaporization of colliding material, are characterized by complex vapor plume chemistry and result in formation of specific gases from volatile elements in the plume. Experimental study of impact plume chemistry (Mukhin et al.,1989, Gerasimov, 2002) showed that the released gas mixture was characterized by the presence of both reduced and oxidized volatile elements components what provided an input of highly nonequilibrium species into ecosystem. Thermal decomposition of petrogenic oxides provides the release of sufficient quantities of molecular oxygen into primordial atmosphere though its presence could be temporal due to rather high sink (Gerasimov, 2002). Gas mixtures formed by impacts are in disequilibrium at normal conditions. Significant quantities of oxidized and reduced components could be present simultaneously in the evolved gas mixtures (e.g. H_2 and O_2, SO_2 and H_2S, CO_2 and CH_4). The most abundant reduced gases in quenched mixtures could be H_2, H_2S, CH_4, and light hydrocarbons up to C_6H_6. The instability of the ecosystem was also provided by the redox behavior of siliceous materials. Iron was present as Fe^0, Fe^{+2}, and Fe^{+3} reflecting complex redox processes in the vapor. The main rock-forming element, silicon, also had complex redox behavior forming Si^0, Si^{+2}, and Si^{+4} states (Yakovlev et al., 1993). Many chemically active gasses had low life time and rapidly dissipated due to reactions from the atmosphere after their release providing primordial atmosphere composed of stable gases (N_2, CO_2, etc.). A noticeable amount of organic molecules is synthesized in impact-generated plume including aliphatic hydrocarbons, polycyclic aromatic hydrocarbons (PAH), carbonyl compounds and unsaturated fatty acids, kerogens (Gerasimov and Safonova, 2008).

The amount of released water exceeded the volume of modern terrestrial ocean (Gerasimov et al., 1985). Different models give various fate of the primordial ocean from runaway greenhouse huge steam atmosphere to moderate temperature water ocean.

An important output of the impact-induced processing of siliceous material of the planet was formation of the protocrust. The mechanism of its formation was based on the separation of elements between melt and vapor phases. Volatile elements are converted into the vapor plume by secondary impacts more easily and from larger target volume than refractory portion of the mixture. Plume condensates could be concentrated in the upper planetary layer to form protocrust. Concentration of volatile components in the upper planetary layer resulted in decrease of sink of atmospheric gases and water into the regolith what provided stabilization of atmosphere and ocean at the earliest stages of planetary evolution.

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OP-24

CUATRO CIENEGAS: A PRECAMBRIAN ASTROBIOLOGY PARK

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The Cuatro Cienegas Bolson, an oasis in the Chihuahuan desert in the state of Coahuila, Mexico is a rare place. It has a biological endemism equal to the Galapagos, it presents anomalous elemental stoichiometry with regards to phosphorus, and its hydrologic system is dominated by living stromatolitic features. As such it has proven a distinctive opportunity for the field of Astrobiology. CCB is a reasonable proxy for an earlier time in earth's history, the late Precambrian, the biological frontier when microbial life was giving way to the dominance of more complex eukaryotic organisms. It is an extant ecological time machine that provides investigative collaborative opportunity for geochemists, geologists, biologists, and population biologists to study the evolutionary process of earth based life, especially microbial ones. It can and is being prospected for the designing of biosignatures of past and present life that can be used in our search for life extra-terrestrially.

We summarize research efforts that began with microbial population biology based projects and expanded into correlative efforts in biogeochemistry, comparative genomics. We outline the future of CCB as a Precambrian Park for Astrobiology.

PROCARYOTIC ASSEMBLAGES OF EARLY PRECAMBRIAN (AR-PR$_1$)

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Recently our ideas about the most ancient stages (AR-PR$_1$) of life evolution on Earth were greatly expanded as a result of bacterial-paleontological investigations. Wide distribution of fossil bacterial remains in ancient sedimentary and volcanogenic sequences testifies that their assemblages were the most important factor of biosphere evolution and sedimentogenesis on the Earth surface beginning with Archaean.

Almost all sedimentary rocks, except for rudaceous rocks, are deposited and transformed during diagenesis with some participation of bacterial (microbial) constituent or other. At present it is known, that biogenic factor plays significant role in formation of such mineral groups as native minerals, diverse sulphuric compounds, oxides, silicates, carbonates, phosphates, sulfates, tungstates and organic acids salts. Fossil microorganisms, biofilms and microbial mats are similar in morphology with modern bacteria, biofilms and mats.

As exemplified by process of genesis of phosphorites and the ancient weathering crusts formation it is possible to infer that mechanism of rock and mineral formation remained practically unchanged through the whole Earth history from Archaean to Holocene.

It is important to emphasize that almost all known mineral compounds of phosphorus in the Earth crust are the salts of orthophosphoric acid H_3PO_4 and that atmospheric oxygen is necessary to form of this acid. Thus phosphorites, including Early Proterozoic ones, were formed under conditions of rather warm shallow-water basin with oxygenated waters.

The most ancient (AR-PR$_1$) microbial assemblages were confined to volcanogenic sediments of the past and to hydrothermal systems. As well as nowadays ancient bacterial life thrived just after an eruption as the surface, covered with lava, became colder. Bacteria, including cyanobacteria, developed on the “lava – water” interface. Cyanobacterial assemblages formed and even some unicellular eucaryots probably existed. Moreover quality and quantity of microbial assemblages of volcanogenic areas differed according to ancient conditions.

OP-25

In shallow-water marine assemblages, connected with pillow-lavas, all consistuents of cyanobacterial mats, including cyanobacteria, are discovered. In the areas of trappean volcanism and connected with them continental basins conditions for cyanobacterial mat formation were probably somewhat less favourable. So practically all volcanogenic rocks, especially, volcano-sedimentary, are rather perspective for finding fossil bacterial structures.

As early as in the Early Precambrian microorganisms (bacteria, perhaps cyanobacteria and even possible unicellular eucaryots) accompanied and promoted formation of weathering crusts, i.e. weathering crusts initially were formed with the participation of bacteria. Probably, there is continuous sequence from weathering crusts to primitive soils and to true soils. Fossil microorganisms which were found in ancient weathering crusts are crucially important because they allows us to conclude that land has been already colonized by microbes in so ancient times.

All carried out bacterial-paleontological investigations have demonstrated enormous possibilities of research of microorganisms in all types of sedimentary and volcano-sedimentary rocks of different degree of metamorphism and of almost every age.

The study of the most ancient (Archaean – Early Proterozoic) microfossils revealed: apparently very early appearance of cyanobacteria in geological annals; much more earlier than it was assumed to be; intensive atmosphere oxygenation as early as in Archaean; rather low Earth surface middle temperatures (30-40^{o}); obvious land colonization by microorganisms in Archaean.

Bacteria and biofilms are nicely preserved under fossil condition, they present in all sedimentary and volcano-sedimentary rocks. Probably bacteria presented everywhere, in all environments, on every surface; neither weathering, nor transportation of material, nor sedimentation, nor diagenesis could occur without microbes.

The study was executed within the framework of the complex program of basic research of the Presidium of the Russian Academy of Sciences “Origin of Biosphere and Evolution of Geo-biological Systems” (subprogram II) and was supported by the Russian Foundation for Basic Research, projects 08-04-00484 and SS-65493.2010.4.

OPTIMIZATION OF STRESS RESPONSE AS A MECHANISM OF RAPID ADAPTATION

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Full-genome projects have revealed the amount of genetic variability: within- and between-species comparisons claim from 3 million to 10 million SNPs per genome depending on the species. Any genome contains a large number of degenerate regulatory sites, which a few substitutions can turn active [1]. On the other hand, Haldane's Dilemma prevents an adaptive evolution of too many genes simultaneously (in eukaryotes, this number is ~10-15 genes). Consequently, the evolution of a small population (especially if it lives peripherally close to tolerance limits, which requires rapid adaptability) by way of flashes of increased mutability[1] [2] appears extremely demanding, and so does the gene-copying of modifications [3], which is the selection of mutations that raise the probability of adaptive modifications (whether they are adaptive or not will be tested by selection) during ontogenesis.

If the realized niche is not larger than the fundamental niche [5], the econiche cannot be escaped but only divided according to Gause’s rule. Invasion beyond the econiche absolutely requires preadaptation. Noteworthy, if the preadaptation is something that is not an aromorphosis, the invader at once or in a long term[2] will be in a less advantageous situation than any aborigine polished by evolution[3]. Aromorphoses are rare and take a long time to emerge [3, 5], while invasion from original niches is a common (but not mass) occurrence, which takes place even if there is no strong competition in the original econiches [6, 7]).

Abundance of polymorphisms in the genomes requires that the organisms address on a non-trivial evolutionary problem: reduce the cost of natural selection by letting only those mutations go that hold most promise for fitness. As a non-specific adaptation-related syndrome (after H. Selye [8]), stress provides resistance to adverse factors (cross-resistance - CR) in a short term; however, it depletes and kills in a long term. Thus, it appears as though a

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[1] Admittedly, this genesis of rapid adaptation will work in larger populations [2] or if an increase in mutability is due to a single gene [4].

[2] Because invaders are few (unless “waves of life” are concerned), they will eventually become vulnerable, because the genetic diversity in their population is lower than that in the aboriginal population.

[3] Zherikhin [5] explained a particular case: invasion is successful if the comers-in disrupt early stages of succession by gradually ousting the aborigines from their niche but not competing with them directly.

small population will be better off if it adjusts organism's *internal* environment so that they, faced with having to produce a prolonged stress response (by rapid entry into the CR phase or by dampening down the deleterious effects of stress (distress) in the anxiety and depletion phases) can function as normal as possible by selection among the mutations in a limited number of stress-genes rather than try to adapt to each of the many adverse effects of the *external* environment separately by trying all available mutations. The identity of stress responses and the phylogenetic antiquity of many stress systems provide parallelism in such adaptation in different populations and/or taxa. The parallelism is maintained at least at three levels: the occurrence of the same ancient genes in many different organisms, the identity of functions (even though the set of genes performing the same function may vary) and a limited selection of working 3D protein structures. It is not before selection arranges stress response elements into a new homeostasis system that divergent adaptations to the *external* environment begins: selection consistently tries all available mutations and/or recruits paralogs of stress-genes into gene networks of ontogenesis. Cases of this evolutionary scenario at the molecular and organismal levels have been found and its applicability limits have been defined. Selection for CR prolongation automatically leads to stabilization (in the sense of Shmalgauzen) of associated modifications. Unlike gene-copying in the sense of Shmalgauzen [3], this scenario does not require that they be tested for adaptiveness, because their adaptation is warranted by CR. In the CR phase, individuals can for not too long, but consistently leave their econiche[4], and this ability can be fixed by selection.

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[4] In fact, this implies that the realized niche should be extended with a stress-periphery, which will reach beyond the fundamental niche and will be accessible by the subpopulation of stress-resistant individuals.

OP-27

LICHENS COULD BE RESPONSIBLE FOR THE DEVELOPMENT OF FIRST ORGANIC-MINERAL SOILS

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Soil formation is a major process in transformation of land surface into habitable biosphere. Soil is differentiated from the weathering profile by presence of organic matter which mostly occurs as coatings on mineral grains. When in the history hypergenic weathering was complemented by accumulation of soil organic matter represents geochemical problem of the large scale. Ultimate precondition for soil formation is development of terrestrial biota which serves as a source of precursor material for soil humus. About 90% of humus is composed of humic substances (HS) - recalcitrant and macromolecular N-containing products of dead organic matter hydrolysis and oxidative transformation (humification). In modern soils the main structural precursors of HS are various polyphenols of plant origin. These undergo oxidative coupling with nitrogenous and other compounds to form polymeric substances. Fungal oxidases (laccases, peroxidases) are considered to be the major catalysts of the process. Thus, formation of soil organic profiles, analogues to those occurring in modern biosphere, requires presence of biota which serves as a source of phenolic compounds. The earliest steps in colonization of terrestrial environment might be linked to the microbial and algal biofilms on the weathered crust. This event occurs in Early Proterozoic (Retallack 2003). However, bacteria and algae lack phenolic compounds in sufficient amounts. The upper known limit for soil formation is Devonian (about 0.4 Ga) when colonization of land by vascular plants took place. Before this time no fossilized record of organic soils was found and it is not known when and how first organic soils were formed.

In the present work we are going to consider lichens as possible candidates responsible for early humification processes. Lichens are symbiotic organisms, comprising of a fungus (commonly Ascomycete) and the photobiont - an alga (usually *Trebouxia*) and/or a cyanobacterium (commonly *Nostoc*). In modern Earth they form the dominant plant cover in extreme environments. A variety of physiological and chemical adaptations enable lichenized fungi to tolerate severe abiotic stresses such as dessication, rapid rehydration, temperature extremes and high UV light intensities (Nash, 2008). Lichens are often pioneers on rocky surfaces and are well known for accelerating mineral weathering. Besides, lichens colonizing fine-earth or disturbed soil often act as stabilizers of their substrate preventing surface erosion. Lichens can contribute to primary accumulation of soil organic matter via products of thalli decomposition or leached-off phenolic and nitrogenous compounds. They also produce laccases and tyrosinases which are well known catalysts of polyphenols polymerization into humic substances (Laufer et al 2006 ab, Zavarzina and Zavarzin, 2006). According to the first fossil records lichens colonized soil in Ordovician-Silurian (480-400 Ma). This time might be considered as the beginning of the formation of organic-mineral soil.

ROLE OF CYANOBACTERIA FROM DIFFERENT ENVIRONMENTS IN FORMATION OF SEDIMENTORY ROCKS

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Cyanobacteria have been recognized as key players in the precipitation, formation and transformation of some minerals (phosphates, carbonates, siliceous and clay minerals). These bacteria produce extracellular polysaccharides (EPS), which act as binding sites for anions and cations. Also they are able to increase pH of environment as a result of photosynthetic activity. Both processes contribute to precipitation of sedimentary rocks and influence on morphology and mineralogy of sediments (Dittrich, Sibler, 2011).

To study processes of phosphatization, carbonatization and siliciphication in laboratory were used a variety of cyanobacteria, such as halophilic strain of *Microcoleus chthonoplastes*, alkaliphilic *Phormidium* sp. and '*Euhalothece natronophila*', thermophilic *Oscillatoria terebriformis* and *Mastigocladus laminosus*. These species of cyanobacteria are usual enough and spread worldwide in their ecological niches, so we can judge about universal mechanisms. The results of our laboratory experiments were related to field observations.

To study process of phosphatization we conducted comparative analysis of field observations of Khubsugul phosphorites (Mongolia) with results of laboratory experiments using halophilic cyanobacterium *Microcoleus chthonoplastes*. It was demonstrated that formation of phosphorite was connected with replacing of cyanobacterial trichomes by calcium phosphate. This process elapsed with rapid speed (first hours, days) and may be associated with the change of seasons or with a significant shallowing of the basin (Gerasimenko et al., 1998). Laboratory fossils were similar to fossils from Khubsugul phosphorites.

A role of alkaliphilic cyanobacterium *Phormidium* sp. in carbonate mineralization was studied in model experiments in laboratory. Carbonate precipitation can occur when sea water enriched with Ca^{+2} and Mg^{+2} mixes with continental water enriched with sodium carbonate. In particular, the relationship between chemical composition of the environment and precipitation of carbonates was studied. Our observations show that formation of mineral layers is restricted to conditions when mineral components are supersaturated. Higher concentration of magnesium caused magnesite precipitation at first, then formation of various Ca-Mg carbonates. Its mineralogy changes in time and depends on the cultivation conditions. Dolomite could be formed in the mat during transformation of magnesian calcites in presence of alkaliphilic cyanobacterial mat under both photosynthesis and anaerobic destruction (Zavarzin et al., 2003; Zaitzeva et al., 2007).

The process of fossilization with calcium carbonates of unicellular alkaliphilic cyanobacterium '*Euhalothece natronophila'* isolated from soda lake Magadi was studied in experiments (Gerasimenko, Samylina, 2009).

It was shown that cyanobacteria play active role in silicon accumulation in laboratory and in nature (caldera of volcano Uzon, Kamchatka). Only mucous sheaths and EPS between trichomes of cyanobacteria *Mastigocladus* and *Oscillatoria* are mineralized in live cultures, but in dead ones trichomes are also mineralized (Gerasimenko, Orleansky, 2004).

So, cyanobacteria isolated from different environments are involved in deposition and formation of sedimentary rocks. There are differences in mineral formation dependent on the specific composition of cyanobacterial cells, pH fluctuations, amount of organic matter, and changes in ion concentrations in the water of environment.

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COMPUTER TOOL FOR MODELING THE EUKARYOTES ORIGIN AND EVOLUTION OF EARLY EUKARYOTIC ECOSYSTEMS

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The formation of eukaryotes in the interior of prokaryotic ecosystems was the evolutionary process involved all levels of organization of living matter from genetic and metabolic to ecocenotic level. A huge amount of mathematical models of various detailness had been developed over the past century. At the present moment the development of more complex and composite models using past experience becomes the key problem. The topicality of such models is caused by rapid growth of production of experimental and field data related to all levels of biological organization on one hand, and growth of computational power on another. The first requires more and more powerful tools for data analysis and experiment design, while the second affords ground for that.

The software platform "Diploid evolutionary constructor" (DEC) has been developed by us for constructing the models of population genetic and evolutionary processes for polyploid eukaryotic organisms. The multilayer modeling approach previously applied by us for implementation of haploid evolutionary constructor [1] was served as the methodological basis for DEC. Each layer of a model is represented by its own submodel describing a certain hierarchical level of biological organization. Every particular implementation of a submodel satisfies a set of specifications (requirements) defined by corresponding layer.

We consider the following base layers in DEC: genotype, phenotype, and fitness which are the parts of individual's macro-layer; there are also population and ecosystem layers.

An individual's genotype is modeled as a vector of chromosomes each of which is represented as an ordered list of genes. Several various implementations (classes) are used for describing genes: there are implementations in the shape of sequence of letters (e.g. nucleotide), numbers, enumerated type element etc. Various values of genes correspond to various alleles. Chromosomal genome organization makes possible to model polyploidy, crossover, rearrangements and translocations, duplication and sexual process. Traits which are coded by genes may be either monogenic or polygenic. Compensable traits are also considered to describe the realization of hidden reserve, variation, and resistance to mutations and/or inbreeding. Thereby the modeling of both polymery and pleiotropy is possible.

An individual's phenotype is modeled as a list of traits, which are also described with several various implementations. Traits can be either quantitative or qualitative. An individual is described, in addition, by parameters like age and state (presence of substrates and regulators). Those parameters in combination with phenotype affect the fitness of an individual. While describing fitness, we distinguish the fitness with respect to population (number of offsprings) and survival of an individual. The first is defined as a result of an interaction individual-population, while the second – individual-environment.

Environment has fixed dimensions and spatial location. It contains individuals of a population (or several populations), substrates and non-substrate regulators. In this case substrates are exhaustible; their presence in environment depends upon organisms' living. At the same time non-substrate regulators are exhaustless in the sense that their presence does not affected by individuals, instead of this they depend on another external factors.

In order to describe the mutual influence of various levels of organization we use special submodels – "strategies" which describe the laws of layers changing. From a software engineering point of view, the layers contain data while strategies manipulate those data. In the present DEC version we consider the following strategies types: mutation and recombination (refer to genotype layer); "genotype to phenotype" (binds corresponding layers); "phenotype to fitness" (determines fitness and survival of an individual with regard to its phenotype, population and environmental conditions); reproduction strategy (determines the law of population size change taking into account environmental limitation, suggested growth model and another factors); migration strategy (determines the law of individuals movement).

The DEC software package is implemented using C++. It has been adapted for use on MPI clusters. The method is still being verified on the classic problems of population genetics. In particular, it has been shown that Fisher's fundamental theorem is satisfied in our models of natural selection for various population growth models. The population modeled contained 100-100 000 individuals, which had diploid genome of 10-20 chromosomes; chromosome contained 5-10 loci; locus contained 1-3 genes; individual had 1-10 traits.

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EVOLUTION OF TRANSLATION TERMINATION FACTORS

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Termination factors have arisen by the duplication of genes encoding elongation factors

Comparison of amino acid sequences in the family of elongation factors raised speculation that the progenitors of EF-G and EF-Tu arose as a result of duplication and subsequent divergence of a gene encoding an ancient GTPase, and further duplications led to the emergence of modern elongation and termination factors [1,2]. RF1, RF2 and RF3, as well as eRF1 and elongation factor eEF-2, are assumed to have been derived from the bacterial elongation factor EF-G [2], while eRF3 arose from the duplication of the gene encoding eukaryotic elongation factor eEF1-A [1]. eRF3 may have arisen in the early stages of eukaryotic evolution, since neither bacterial nor archaeal genomes contain homologues of eRF3 [1]. Recent studies have shown that the functions of eRF3 can be performed in archaea by EF1A [3]. The termination factor eRF3, preserving the functions typical of elongation factors (GTP-ase activity and interaction with the A-site of the ribosome), lost the capacity to bind tRNA but acquired the capacity to interact with eRF1. From this standpoint, elongation factor EF1A of archaea is functionally intermediate between elongation and termination factors: it acquired the ability to stimulate aRF1 while maintaining all the properties of an elongation factor [3]. Termination factor eRF1 is a striking example of neofunctionalization, because it has acquired a variety of functions absent in elongation factors, including the ability to decode stop signals and to catalyze the release of nascent peptides from eukaryotic ribosomes in response to stop codons.

Subneofunctionalization in a family of termination factors gave rise to proteins participating in mRNA quality control

Eukaryotic cells possess a mechanism known as nonsense-mediated mRNA decay (**NMD**) that recognizes and degrades mRNA molecules containing premature termination codons. NMD is mediated by the trans-acting factors Upf1, Upf2 and Upf3, all of which directly interact with eRF3; only Upf1 interacts with eRF1 [9,10]. In addition to NMD, eukaryotic cells contain two additional mechanisms of mRNA quality control. No-go decay (**NGD**) releases ribosomes that are stalled on the mRNA [11]. In yeast, NGD involves the proteins Hbs1 and Dom34 (Pelota in mammals). Another mechanism, non-stop decay (**NSD**), leads to the release of ribosomes that have read through the stop codon instead of terminating [12]. NSD has only been found in *S. cerevisiae* and involves the Ski7 protein [13]. A common feature of these processes is that all involve the termination factors eRF1 and eRF3 (NMD) or their paralogs (Dom34/eRF1 and Hbs1/eRF3 in NGD; Ski7/eRF3 in NSD).

Conclusion

Successive duplications of genes encoding elongation factors for translation led to the emergence of several protein complexes with different properties. The eRF1-eRF3 complex terminates translation, and the Dom34-Hbs1 complex is involved in the quality control of mRNA. Both eRF1 and eRF3 interact not only with each other but also with additional proteins. Some of these interactions are possibly mutually exclusive, and some of the proteins interacting with eRF1/eRF3 can be components of the complex terminating translation.

Acknowledgments

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OP-31

WHY WE NEED NEW EVIDENCES FOR DEEP ARCHAEA EVOLUTION: THE LESSON FROM STUDY OF HORIZONTAL TRANSFER HIGHWAYS

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Horizontal gene transfer (HGT) is an important factor of prokaryotic evolution. However, HGT events can affect significantly on the reconstruction of the phylogenetic relationships between species (Figure 1). We analyzed the influence of the HGT on the phylogenetic inference in Archaea. Research is based on reconstruction of the phylogenetic trees for each archaeal strict orthologous protein groups (SOPGs) from MetaPhOrs database [1] using CAT model [2] and comparing them with the species tree for 14 Archaea species groups (including or excluding Nanoarchaeota and/or Korarchaeota). We used the minimal number of subtree prune-and-regrafts (SPRs) to estimate the number and direction of HGT events (using SPRIT program, algorithm with Linz correction [3]).

The results allowed us to explain deviations from consensus Archaea phylogenetic tree topologies represented in two recent papers [4, 5]. We also conducted the functional analysis of SOPGs under study using annotations deposited in GO, eggNOG and ProtClustDB databases. Functional analysis showed that about two-thirds of SOPGs in all samples belongs to “translation, ribosomal structure and biogenesis” group.

The analysis of SPR values demonstrates that both Archaea consensus trees are far from explanation of information transmission processes during Archaea evolution. For example, if we analyze phylogenetic relationships in 62 SOPGs including Nanoarchaeota we need for 352 SPRs for reconciliation of gene/protein trees with consensus tree in [4] and 367 SPRs for reconciliation with tree in [5]; if we test 99 SOPGs excluding Nanoarchaeota we need for 521 SPRs for reconciliation with tree in [4] and 544 SPRs with tree in [5]. Comparison of SPRs values needed for gene/protein trees reconciliation showed that Archaeal phylogenetic tree published in Proc. Biol. Sci., 2011 [4] is slightly more parsimonious but insufficient for description vast majority of our data.

Using reconstructed sequences of subtree prune-and-regrafts for each of the gene/protein trees from a consensus trees we found close phylogenetic associations (sibs relationship) which are most frequent in evolution and not found in both consensus trees.

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The most frequent associations are Desulfurococcaceae-Thermococcaceae, Pyrobaculum-Desulfurococcaceae, Pyrobaculum-Sulfolobaceae, Caldivirga-Sulfolobaceae, Thaumarchaeota-Thermococcaceae, Thaumarchaeota-Thermoplasmatales. These associations could be interpreted in light of longtime co-existence of bacteria in the course of Archaea evolution.

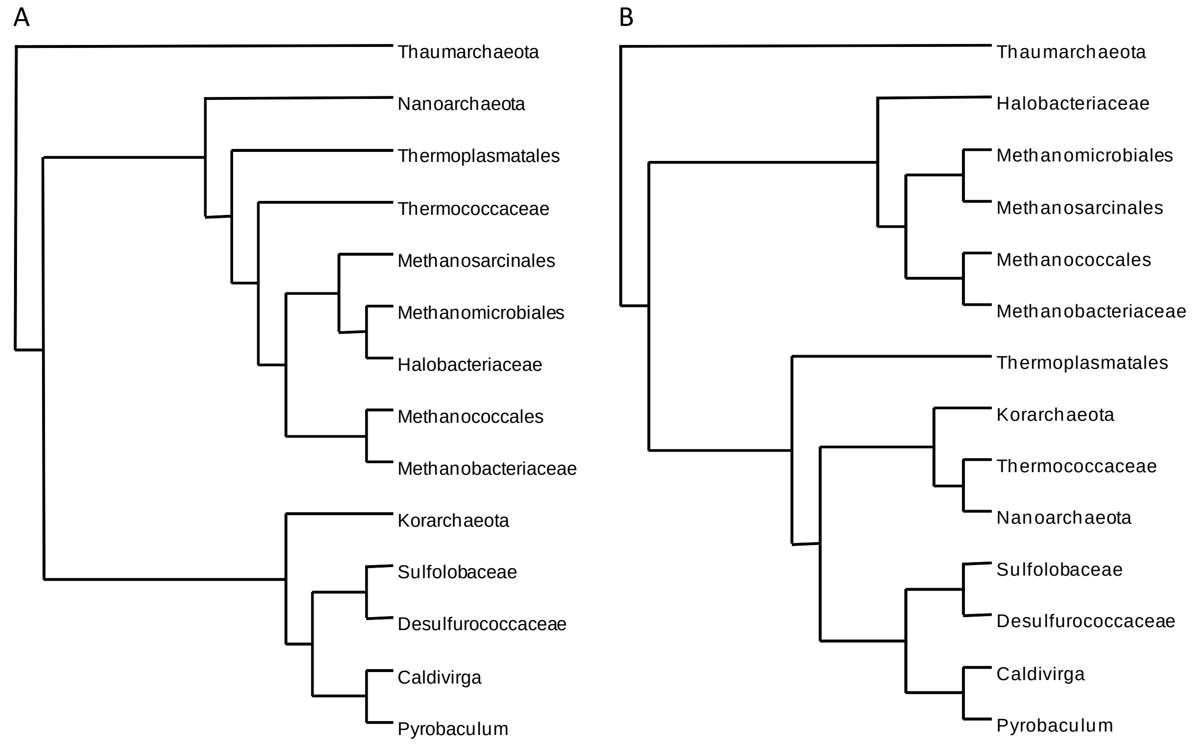

Figure 1. Consensus phylogenetic trees of Archaea published in (A) Proc. Biol. Sci., 2011 [4] and (B) Proc. Natl. Acad. Sci. U.S.A., 2010 [5].

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ENDEMIC GENERA IN LATITUDINAL FAUNISTIC ZONES AND POSSIBILITY FOR A HISTORIC MODEL BASED ON LIVING BRACHIOPODS

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When we see the geographic distribution of living brachiopods in the recent seas and oceans it is evident that the species of these animals are forming very clear faunistic zones which are characteristic for the other marine Invertebrates.

Now when "Part H Brachiopoda" (Treatise on Invertebrate Paleontology, 1997-2007) and the Check-List of the Recent brachiopods (Zezina, 2008) were published we can understand the time when the species and genera of living forms had appeared. Only 16% of living species have their paleontological history and 50% of recent genera are known also as paleontological objects.

The oldest genera of living brachiopods are known in the low latitudes (=in the tropical faunistic zone) with endemic genera which had been appeared in Mesozoic. The highest latitudes (= in boreal-arctic and antarctic faunistic zones) are characterized by younger endemic genera. But the more interesting are so cold "transition" zones (warm-temperal and cold-temperal in both Hemispheres): subtropical and low-boreal faunistic zones in the North and subtropical and notal faunistic zones in the South.

Subtropical (or warm-temperate) zones are similar to the tropical one. The southern subtropical endemic genera appeared in Maastricht. The subtropic waters could be refuges for the tropical forms at the borders of their geographical rages. Endemic genera of brachiopods in the low-boreal and in the notal faunistic zones (or cold-temperate one) appeared in Oligocene-Miocene. These were the times when Circumpolar Antarctic Current was formed. The other half of endemic genera appeared in Holocene after the last glaciation.

Ages of the endemic genera allow to reconstruct a history model for recent marine fauna with the steps depending on the global hydrological changes in the World Ocean.

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OP-33

TAXONOMICAL AND ECOLOGICAL DIVERSITY OF THE FAMENIAN (UPPER DEVONIAN) NONAMMONOID CEPHALOPODS

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The Late Devonian was one of warmest periods and unique stage in the Earth history.

As a result of the uniformity of the global climate could be expected biotic uniformity too.

However a faunal assemblage differs substantially by the highest taxa even in no distant regions.

The Famenian was unprecedented stage in the cephalopod evolution, when their biodiversity reached the maximum in the Earth history.

At the present times more than 200 genera belonging to 11 order (including ammonoids) were described from the Famenian. Nonammonoid cephalopods were represented the orders Oncocerida, Discosorida (not less 70 genera), Tarphycerida, Nautilida (subclasses Nautiloidea), orders Orthocerida and Pseudorthocerida (Orthoceratoidea), and only few genera known from Actinoceratoidea and Bactritoidea.

The main goal of the work is to compare the taxonomic features and ecological structure (proportion of different life forms) in the nonammonoid cephalopod communities from 7 regions of the Northern Eurasia (central part of European Russia, South Urals, Kazakhstan, Azerbaijan, Armenia, Turkmenistan and Poland),

In these regions it is known about 80 genera and 170 species from the three main group: oncocerids, discosorids and orthoceroids. This is approximately 70-75% from all nonammonoids described from the Famenian.

Comparative taxonomic analysis had shown some uncommon and even paradox results. For example Polish community has the general similarity with long distant communities of the South Urals and Western Kazakhstan caused by presence of common benthic, benthopelagic discosorid and oncocerid genera, whereas similarity of the pelagic orthoceroids from this regions was in two and more times less. Similarity of the communities of two adjacent areas: South Urals and Western Kazakhstan was considerably less.

Taxonomic structure (alpha diversity) testifies on the high degree of endemism of all communities. All of the communities could be examined as the very high rank biokhories. Furthermore the communities are characterized by the ecological structure, which reflected the adaptation to some specific adaptive zone. Five morphotypes of cephalopod shells (life forms) can be recognized in Famenian taxocenosis independently from their taxonomic positions. Their similarity reflected their adaptation to the same adaptive zone and niches.

In different regions the proportions of morphotypes (or ecological structure) were various and were not coincided with taxonomic diversity.

The special features of the ecological structure of the communities reflect the distribution and taxonomic content of the basic adaptive zones in basins of different regions. By this parameter the communities of Poland as the associations of central Devonian field are characterized by the similar balanced ecological structure whereas the systematic composition of genera is very differ. The South Urals and the Poland communities have most genera similarity, which is not explained by geographical proximity and migrations, but by similarity in the ecological structure. It is caused by similar area and landscape features in the distribution of the main adaptive and oceanographic zones of these basins. West Kazakhstan taxocenosis is more similar to distant Poland community than to close South Urals community. It could be explained by different ecological environment. The South Kazakhstan community is differed from all studied communities both taxonomically and ecologically. This is evidence of the unique distribution of adaptive zones in this region, of the independent origin this community, and of the probable belonging to separate and the more cold-water basins than in other regions.

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MICROEVOLUTIONARY PROCESSES IN THE THERMAL POPULATIONS OF HYDROBIONTS SUBARCTIC REGION

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Institute of Ecological Problems of the North, Ural Division, Russian Academy of Sciences Review of literature and original data on the structure of hydrothermal communities in Northern Eurasia and Iceland showed that the greatest biological progress in hydrothermal systems reach taxa, whose formation was going on the way to adapt to the development of extreme environments (Friberg et al., 2009; Woodward et al., 2010; Demars et al., 2011). Above all, this small ponds and flooded organic substrates, in which low levels of oxygen, increased concentrations of organic and mineral substances, and not uncommon in the summer heating up to high temperatures, even at high latitudes. Therefore, the fauna of the hydrothermal systems of the Subarctic and Arctic initially be regarded as allochthonous and migration, formed of representatives of different taxa set of pre-adaptation to the development of hydrothermal vents, was originally purchased outside the thermal anomaly. Hydrothermal vents with their constant temperature and hydrochemical regime, judging by the high-density populations of individual taxa, represent a more favorable habitat for them in comparison with the zonal variations. The various high-latitude hydrotherms formed similar benthic communities, which include those on the abundance and biomass dominate certain types of gastropods (family Lymnaeidae and Planorbidae) (Biota, ... 2009; Tahteev, Sitnikova , 2009). In populations of molluscs and insects that inhabit hydrotherms, have developed and consolidated a range of additional physiological and biochemical adaptations that allow them to successfully live in high temperature conditions (Berezkina, Starobogatov, 1988; Khmeleva et al.. 1985; Angiletta , 2009; Garbuz et al., 2008). Meanwhile, the brevity of the existence of hydrotherms in geological time scales, their evolutionary "ephemeral", led to low levels of endemism of their fauna, linked primarily to the intraspecific taxa and species level. The systematic status of many of these forms is not completely clear, since populations of different species and intraspecific systematic categories of molluscs, populating the inhabitation terms can independently acquire similar morphological, physiological and biochemical characteristics, ie have convergent similarity. Thermal populations of different gastropods characterized by small size of the animals, year-round breeding and apparently greatly reduced life expectancy (Khmeleva et al., 1985).

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OP-35

THE STEPS OF VASCULAR PLANT AND LAND ECOSYSTEM EVOLUTION

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Basal steps of vascular plant evolution are reflected by the structure of conducting tissues and transport fluxes. Historically, transport networks are derivatives of buffer zones for symbiotic exchange of prokaryotic pro-cursers. Two symbiogenetic acts (prochlorophytes + protists → algae; marine algae + fungi → land vascular plants) are presented in plant body by two networks for water transport. Descending phloem arises in phylogenesis from membrane capsule of prochlorophytes. Rising xylem is the special part of the apoplast. It starts from mycelium channels of fungi. Conducting elements of phloem and xylem are formed by transport fluxes which are not homologous. Cyanobacteria photosynthesis is the source of phloem flux, fungal proteolysis is the same for xylem flux. In spite of similar form of the conducting elements of phloem and xylem, they are differed by the cell compartments and topics of movement, pH, ^+K and ^+Na concentration. These differences are rising to ancestral environments and buffer zones of symbiogenesis. It is the theoretical base for anatomical reconstruction of the origin and history of vascular plant migrations.

Prochlorophytes and protists entering into symbiogenesis can be existed in freshwater reservoirs before World Ocean appearance in Procambrian. New saltwater environment could be extreme, inaccessible for independent inhabitance. Algae invasion of littoral for the depth of fifty meters becomes the result of endosymbiogenesis. First plasmodesmata are found in Volvox colonies. First plants with sieve-like cells are remarked in Laminariaceae family.

Back migration, from the water to land, are started by symbiogenesis of marine algae and fungi in Devonian. Land was unfit environment for both groups of organisms. It becomes inhabited by their symbiogenesis. Fungi mycelium and plant xylem channels continuality is enough evident. The origin of vascular plants, land colonization by them, and terrestrial ecosystems development in results of algae and fungi symbiogenesis are prepared the realization of gigantic plant and animal life form diversity.

The top of plant evolution is their woody forms which are given multiple-storey forest ecosystems under "green-house" climate conditions in the Paleogene ("megatermal tropical rain forests"). To the end of Eocene they are covered the all of continents up to poles. Ecological niches at that time are most favourable, and plants themselves are high effective on the rate of photosynthesis and growth. The structure of their conducting networks is the most optimal and economic by energy.

The transfer from warm climate of Paleogene to cold climate of Neogene causes a reduction of bioforms and biomes. One variant of land decolonization is related to plant return into water. Secondary water plants are lost the contact with fungi. The next steps are the roots reduction to rhizoids, the disappearance of root nutrient, xylem vessels, stomata apparatus, cuticular covers and transpiration. Vascular plant return to water environment can be considered as a particular revert to ancestral forms.

The season vegetation and dislocation of multiple organs under ground are an another indicators of land discomfort for vascular plants. Vegetation pauses are the result of adaptogenesis in cold or arid climate of the Neogene. The functioning and growth can be blocked on long time. Growth and dormancy periodicity is reflected by season rings of conducting tissue structure.

Fragmentation and compensatory interchanges of transport channels of phloem and xylem are the next features of vascular plant degradation in the Neogene. Forest biomes were displaced by herbaceous on large spaces in relation to higher resistance of herbs to cold, water deficit, and high intensity of light. The sum of these factors is similar with high-mountain conditions of taxa formation. Herbaceous cryophites of Neogene generation could be formed in alpine belt of young mountain systems and then expanded along cold plates to polar areas. That pattern of herbs origin and distribution is supported by comparative researches of their genesis and radiation in mountain systems of Middle and Central Asia, in Alps and Andes. The appearance and fast expanding of meadow and steppes in Eurasia, savanna in Africa, and prairies and pumps in America, instead of forests, are dated by the Miocene and Pliocene. The prolongation of climate cooling and aridisation along this scenario would be led to development of continent desertification. Land colonization by vascular plants in the Devonian developed from shore line to continent deepness. Opposite process of decolonization starts from inner regions and spread to coasts.

Genome enlargement is a clear trend of adaptive strategy during vascular plant evolution in the Cenozoic. DNA amount in the herbs of Neogene generation is a fourfold higher then that in the trees of Paleogene. Step to step cooling was documented as the total tendency of climate changes in the Cenozoic. Genome growth and particular decrease of plant specialization are going on each step. Modern polar deserts are the illustration of the final of land decolonization.

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CAMBRIAN CALCAREOUS ALGOFLORA – RELICT ASSOCIATION DIFFERENT GROUPS THE MICROORGANISMS

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Calcareous algae have appeared and spread around the world much earlier than is recorded on the schemes the major events in the Precambrian history of the Earth at around 1.2 billion years (Wood, 2001; Taylor and all., 2009 and others), despite the fact that older findings were found D.Grotzinger and P. Hofmann (1983) in Canada, in the Rocknest Formation with absolute age 1.9 billion years.

The reason for the mass distribution of calcareous algae that form the reef built at the boundary of the Vendian – Cambrian, was the transition from the cyanobacterial (stromatolitic) ecosystems to the algae – the event had a great response in the biological history of Earth and predetermined cambrian “explosion" small shelly organisms with rapid diversification throughout the world. “The explosion” was caused by a large amount of organic matter in reef space, the main producers of whom were cyanobacteria, calcareous algae and macroscopic elastic representatives of algae that inhabit the coastal areas. By analogy with modern algaeworld can assume that the Cambrian algaeflora cells were surrounded by a polysaccharide envelope permeable to water and dissolved low molecular weight substances, easily overlooking the sunlight. The composition of the shell consisted of proteins, glycoproteins, minerals, pigments, lipids, stored them intracellularly and within the body in large quantities to survive in adverse conditions. The composition of the shell consisted of proteins, glycoproteins, minerals, pigments, lipids, stored them intracellularly and within the body in large quantities to survive in adverse conditions. After the death of algae-bacteria destructors implemented mortmass destruction not only algae, but cyanobacteria that covered their surfaces, thus releasing organic compounds and influencing the cycles of calcium, phosphorus, silicon, and forming a high-carbon rocks (Rozanov and Zavarzin, 1997). At the same trophic scheme Cambrian reefs remained close to stromatolitic, ie producers and consuments continued to be in direct contact until the Ordovician period. Thalli of calcareous algae is an ideal substrate for bacterial and cyanobacterial communities and, as in the case of stromatolites, have contributed to the deposition of calcium carbonate in the reef frame, thus increasing the area of the substrate for the settlement of invertebrates. Not excluded, and symbiotic calcareous algae and archaeocyatha with endozoic photoautotrophic eukaryotic algae, as many times wrote the researchers. For information about this group of algal flora in the majority of the reviews about the initial stages of the evolution of the biota were either ignored or contained conflicting data, especially concerning the nature and systematics of Vendian-Cambrian calcareous algae, typical representatives of which were *Epiphyton, Renalcis, Proaulopora*, *Girvanella,* united in the scientific literature in the formal group under a variety of names: microbialites, calcimicrobs, dendrolites, calcibionta.

Finds unique preservation of cellular structure and other morphological elements made in recent years, allowed to audit the most common worldwide delivery genera *Renalcis* and *Epiphyton.* As it turned out, the development of genus *Epiphyton* vary depending on environmental conditions: in a supportive environment adult acquired form of the bush, in a hostile – or slowing the growth of branches is not advancing at all, and then the genus was described as *Renalcis.* Consequently, symptoms, previously served as the basis for the allocation of various genera, in fact, characterized by different stages of development of one genus *Epiphyton*. Previously, we proved the genus *Epiphyton* belonging to the division of Red algae (Terleev, Luchinina, 2000). Such revision will sooner or later must refer to and some other Cambrian "genera", for example, a morphological series as *Bija* Vologdin – *Botomaella* Korde – *Garwoodia* Wood – *Hedstroemia* Rotpletz.

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OP-37

THE DAWN OF THE AEROBIC BIOSPHERE: ECOLOGY OF NEOPROTEROZOIC AND EARLY PALEOZOIC BIOTA

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The history of the Proterozoic biota is characterized first of all by replacement of anaerobic communities with aerobic ones in many habitats and by massive incorporation of eukaryotes into prokaryote ecosystems. The evolution of the aerobic biosphere was spatially and temporally intermittent. The modern ocean contains 1% of all free oxygen on Earth, while the atmosphere contains the remaining 99%. During the early Proterozoic the distribution of free oxygen was different. The oxygen content of the sea water varied widely between habitats, while small fresh water bodies could have been completely oxygenated. The oxygen content in the atmosphere increased in discrete steps. Each sharp increase was associated with an abrupt change in the homeostatic feedback loop between the rate of oxygen release into the atmosphere and the rate of fixation of atmospheric oxygen. During the Paleo- and Mesoproterozoic the oxygen content of the atmosphere fluctuated at the level not exceeding one percent. This resulted in a strong UV radiation at the surfaces of both sea and land, which allowed existence of the phototrophic zone only at depths greater than 1-10 m, while the contact zone between the ocean waters and atmosphere, where organics was quickly mineralized by UV-generated superoxide radicals, was oxygen-depleted. This zone acted as a barrier considerably impeding diffusion of water oxygen into the air. The Neoproterozoic biota was characterized by glaciations and sharp fluctuations in the abundance of producers. During interglacials waters from melted ice transported large amounts of nutrients from the land into the oceans, causing mass development of producers. The benthic fauna of the Vendian serves as an indicator of oxidizing conditions in the corresponding habitats. Producers at that time period were represented by algal-bacterial mats, multicellular algae, and bacterial-algal plankton. During the day time the algal-bacterial mats saturated the bottom water with oxygen, enabling the existence of multicellular eukaryotic benthic fauna. The distribution of benthic communities of multicellular eukaryotes during the Vendian was determined by the mosaic distribution of oxygen in water and by its diurnal fluctuations, resulting from the low oxygen content of the atmosphere. These conditions determined the biology, physiology, and morphology of consumers. Multicellular consumers at that time had low metabolic rate and their activity was low, which was an adaptation to the extremely low oxygen levels during the night. This is reflected in the morphology of Vendian multicellular organisms: bodies with large surface area, often flattened, without appendages suitable for vigorous locomotion, feeding via extracorporeal digestion. Planktonic producers lived at some distance under the water surface, avoiding exposure to UV light. They produced most of the oxygen, saturating the surrounding layer of water during the day time. In the habitats where there was no thermocline some of the dying plankton sank to the bottom, forming part of the food ration for benthic consumers. There where the thermocline was present the microbial loop remained closed and the entire nutrient cycle took place above the thermocline. Oxygen from this layer diffused partly into surrounding water and partly into the low-oxygen atmosphere. Therefore the upper layer of water did not uptake oxygen from the atmosphere, as presently, but instead was depleted by the loss of oxygen into the atmosphere. This disrupted the balance of the microbial loop because there was not enough oxygen to completely decompose organic matter. As a result, the conditions at the lower part of the photic zone, above the thermocline, were anaerobic and not suitable for eukaryotes. The uppermost photic layer was also oxygen-depleted, because UV radiation here generated superoxide radicals, quickly reacting with organic matter. As before, this zone impeded diffusion of oxygen from the ocean’s photosynthetic zone into the atmosphere. The new equilibrium, established by the Early Cambrian, maintained the oxygen concentration in the atmosphere at the level of a few percent. This was sufficient for establishment of the ozone layer, colonization of the entire photic zone by producers, faster diffusion of oxygen into the atmosphere and its more even distribution in the upper layer of sea water. These conditions made possible the existence of pelagic filtrators, particularly arthropods, and facilitated rapid diversification of multicellular consumers and increase of their metabolic rate and activity. Because pelletized organic matter can penetrate the thermocline, the appearance of pelagic filtrators lead to disruption of the microbial loop. This resulted in a dramatic enrichment of bottom waters with organic matter, sharp increase of diversity and abundance of benthic fauna, and, simultaneously, in the increased amount of buried organic material and, correspondingly, higher oxygen level in the atmosphere (the Cambrian evolutionary explosion and Cambrian “agronomic revolution”). The establishment of a new level of atmospheric oxygen caused intensive development of sea biota in epicontinental seas during the Ordovician evolutionary radiation and to massive colonization of wet and aquatic land habitats by producers. During the early Devonian vascular plants began spreading out of water into land habitats, which was made possible by the evolution of their internal water transport system. If this system evolved as a result of symbiosis with fungi, the prerequisite of such symbiosis must have been a considerable amount of buried organic matter on the land. The organic matter that was buried during previous geological periods and became part of land masses could become re-exposed by erosion, thus determining a new equilibrium level of atmospheric oxygen.

OP-38

THE OLDEST EVIDENCE OF BIOTURBATION ON EARTH

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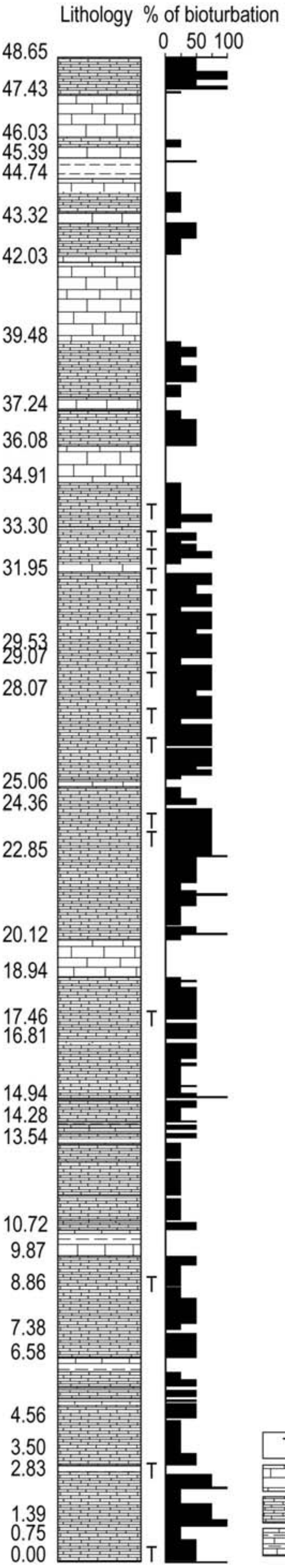
We documented intensely bioturbated ichnofabric and associated discrete, identifiable trace fossils in the Khatyspyt Formation cropping out on the Olenek Uplift in the north-eastern part of the central Siberia. Stratigraphic sections of the Khatyspyt Formation were logged for ichnofabric indices (percentage of original sedimentary fabric disrupted by biogenic reworking). The upper part of the Khatyspyt Formation appears to be moderately to intensely bioturbated (see Figure). There are two styles of ichnofabric preservation in the Khatyspyt Formation: three-dimensional and compressed. Three-dimensional preservation is attributed to early diagenetic silicification of discrete sedimentary layers and provides insights into the structure of both individual burrows and the entire ichnocoenosis. Each burrow demonstrates a terminal backfill structure which is a result of active displacement of a tunnel within the substrate and emplacement of the material by an animal posteriorly as it progressed through sediment. There is no trace of wall lining in the tunnels. Branching burrows have never been observed. Backfill menisci are composed of little-altered substrate sediment. Intervening menisci consist of early diagenetic microcrystalline silica (with dispersed grains of dolomitic mudstone) that could be selectively replacing areas with elevated levels of organic matter. In compressed preservation the intervening menisci consist of silicified mudstone with dispersed pyrite globules; the color contrast in these menisci can be greatly enhanced by diagenetic processes during fossilization. The appearance of ichnofabric can be severely disturbed by diagenetic overprint. For example, the menisci can be connected with each other by a string of silicified material or pyrite globules. In other specimens the original saucer-like shape of the menisci has been exaggerated and transformed beyond recognition, or the entire burrow is surrounded by a halo of microcrystalline quartz. Most burrows have width 0.5–3.0 mm, with the maximum reaching 6.5 mm. Depth of bioturbation measured from silicified sedimentary layers that were subject to minimum sediment compaction reached 5 cm. Meniscate backfill represents a locomotion structure (repichnion). The lowest stratigraphic occurrence of the ichnofabric is at the base of the Khatyspyt Formation 185 m below the first appearance datum (FAD) of *Cambrotubulus decurvatus* and 335 m below the FAD of *Treptichnus pedum*. By all means, the Khatyspyt ichnofabric is of late Ediacaran age which makes it the oldest reliable paleontological evidence of bioturbation. This study was supported by RFBR grants no. 09-05-00520 and 10-05-00953, RAS Program “Biosphere Origin and Evolution” and National Geographic Society.

OP-38



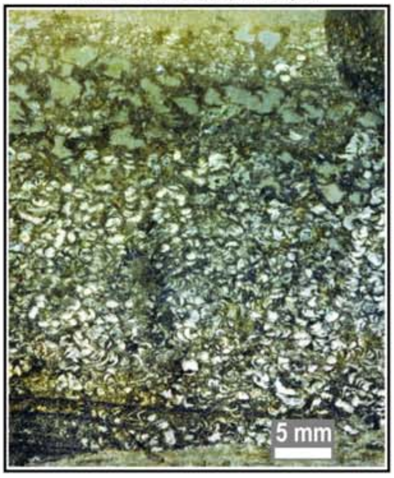
T volcanic tuff

▦ coarse-bedded limestone

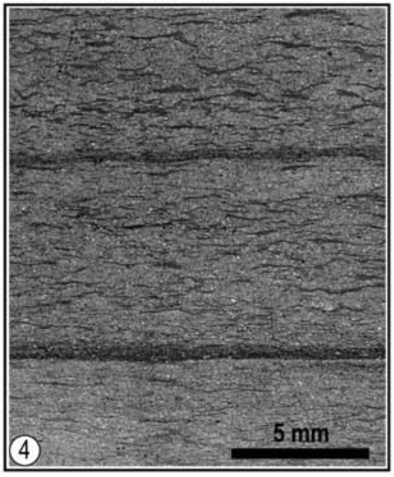
▤ thinly laminated limestone

▥ alternating limestone and shale

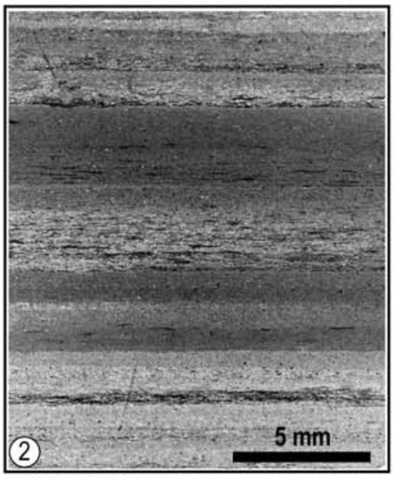
Silicified bioturbated layer



Examples of ichnofabric indices (1–5) in the Khatyspyt Formation

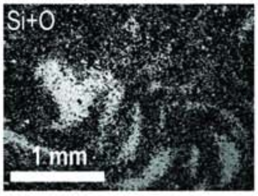


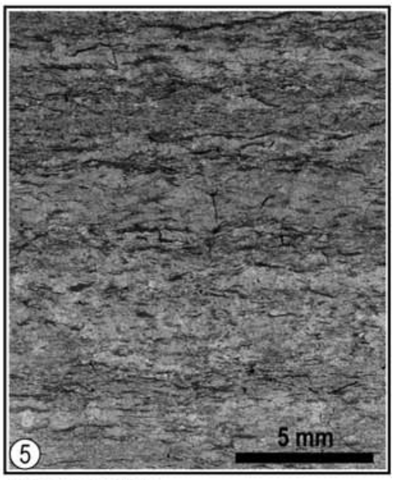
0603-2 (75-100%)



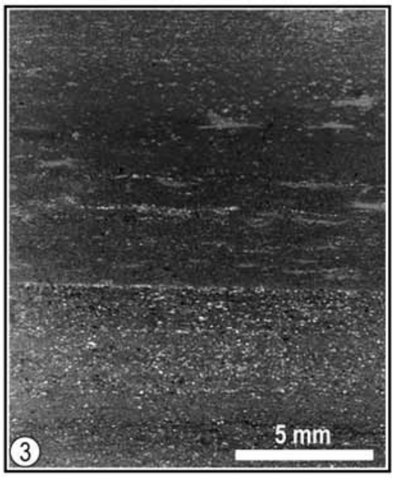
0603-6 (25-50%)

Elemental map of meniscate backfill

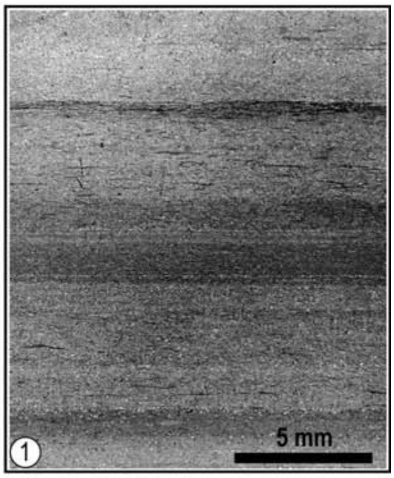




0603-3 (100%)



0603-9 (50-75%)



0603-5 (0-25%)

OP-39

SCIENTIFIC SURVEY ON LAKE BAIKAL – AS AN EXAMPLE TO STUDY AND DEMONSTRATE THE ORIGIN AND EVOLUTIONE OF LIFE ON THE EARTH

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Lake Baikal is one of the most ancient water reservoirs of our planet, but as compared with beginnings of the primary living matter on our planer the lake is relatively young.

A new exposition «Evolution of life during abiotic changes on the Earth» is created is being developed at the Baikal Museum. It includes the materials devoted to studies of the origin and evolution of the Universe, Solar system, and our planet. The evolution of life on our planet is demonstrated as a result of the changes occurring on the Earth. In this exposition the more emphasis is given to the origin of Lake Baikal, its biota resulting from local and global changes. The distribution of this knowledge amongst various groups of people is extremely important from the viewpoint of extending natural-scientific knowledge and a correct understanding of the processes occurring in the nature, increase of standard of culture of the population. People should know what processes were responsible for the origin of Lake Baikal or another natural site as well as the time of the origin and evolution of this or that natural site. We believe that it should affect the careful attitude to the nature, rational use of natural resources, perfection of "know-how" technologies. In the monograph «The Baikal Go» (scientific excursion across Baikal) the lake is considered as a uniform natural object [1].

Lake Baikal is a unique object in which geological evolution of the earth and evolution of climate are reflected, and where endemic flora and fauna are represented in their diversity. The latter were formed in this area as a result of comparatively long isolation. Lake Baikal is one of the well-studied water bodies on the planet. Therefore, it is necessary to use data on nature of Lake Baikal in the educational process at biological, geological, geographical and other departments for demonstration of natural processes and as an example of studies of natural phenomena. It is proposed to prepare and introduce a curriculum (training course) at natural-science departments of universities. The aim of this course is to acquire theoretical and methodological fundamentals on complex studies of natural objects. This course may be one of the major generalized subjects in the training system of biologists, environmentalists, geographers, and hydrologists.

The main advantage of this course is that it is possible to gain knowledge on natural phenomena and processes of a wide spectrum at one place and in one water body: to acquaint students and postgraduates with the results on origin and evolution of some elements of the Lake Baikal biota (algae, invertebrates, fish and fish parasites, seals, birds); to demonstrate how using the results of many areas of science (geology, paleontology, morphology, botany, algology, zoology, ichthyology, parasitology, and ornithology) it is possible to define fundamental hypotheses on the origin of some organisms relying on indirect and direct evidences of their evolution. Similar interdisciplinary approach allows us to enhance the significance of natural-science studies, to raise the level of knowledge of students and to stimulate their interest to scientific-research work.

[1]. The Baikal Go (scientific excursion on Lake Baikal). Novosibirsk: GEO, 2009. 244 pp.

OP-40

PERMAFROST ASTROBIOLOGY: TERRESTRIAL ANALOGUES OF MARTIAN ECONICHES AND INHABITANTS

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The terrestrial permafrost is the only wide spread and rich depository of viable ancient microorganisms on the Earth. From an exobiological point of view, the terrestrial permafrost, inhabited by cold adapted microbes and protecting the microorganisms against unfavorable conditions can be considered as a model of possible extraterrestrial cryogenic ecosystems on the Earth-like planets. Most intriguing are the traces of past or existing life on Mars; these are of interest due to upcoming missions. The cells and their metabolic end-products found in the Earth's permafrost provide a range of analogues that could be used as a bridge to possible Martian life forms and shallow subsurface habitats where the probability of finding life is highest.

'Mars-Odyssey' observations of neutron fluxes that found water in the subsurface layer indicated Mars as a "water-rich planet". Since there is a place for water, the requisite condition for life, the analogous models are more or less realistic. If life ever existed on frozen extraterrestrial bodies such as Mars, traces might have been preserved and could be found at depth within permafrost. The age of the terrestrial isolates corresponds to the longevity of the frozen state of the embedding strata, with the oldest known dating back to the late Pliocene in Siberian Arctic and late Miocene in Antarctic Dry Valleys. Permafrost on Earth and Mars differ in age: ~3-5 million years on Earth, and ~3 billion years on Mars. Such a difference in time scale would have a significant impact on the possibility of preserving life on Mars. This is why the longevity of life forms preserved within terrestrial permafrost does not contradict the panspermia theory, but can only be an approximate model for Mars. Therefore, the main goal is to reconcile the age of permafrost on Earth and Mars by increasing the age of terrestrial permafrost or decreasing the Martian one.

1. A number of studies indicate that the Antarctic cryosphere began to develop on the Eocene-Oligocene boundary, soon after the break-up of Gondwana and isolation of the continent. Permafrost degradation is only possible if mean annual ground temperature, -28°C now, rise above freezing, i.e., a significant warming to above 25°C is required. There is no evidence of such sharp temperature increase, which indicates that the climate and

geological history was favorable to persistence of pre-Pliocene permafrost. These oldest relics (~30Myr) are possibly to be found at high hypsometric levels of ice-free areas such as Dry Valleys, along the Polar Plato and Trans-Antarctic Mountains, and on Northern Victoria Land. It is desirable to test the layers for the presence of viable cells. The limiting age, if one exists, within this ancient permafrost, where the viable organisms were no longer present, could be established as the limit for life preservation at subzero temperatures. Any positive results obtained will extend the geological scale and increase the known temporal limits of life preservation in permanently frozen environment.

2. Even in this case, the age of Martian permafrost is still 100 times older. Only one terrestrial environment is close to Mars in age – active volcanoes in permafrost areas. The age of volcanic deposits frozen after eruption is much younger than the age of surrounding permafrost. Culture- and culture-independent methods show the presence of viable thermo- and hyperthermophilic microorganisms and their genes within pyroclastic frozen material on Deception Island (Antarctica) and Kamchatka peninsula. These bacteria and archeae have never been found in permafrost outside the volcanic areas. The only way for thermophiles to get into frozen material is through deposition during eruption, i.e. the catastrophic geological events transport microbes from the depths to the surface, and they survive at subzero temperatures within the permafrost.

The past eruptions of Martian volcanoes periodically burned through the frozen strata and formed the thermal and water oases. Simultaneously, products of eruptions (lava, rock debris, scoria, ash) rose from the depths to the surface and froze. Images taken by the High Resolution Stereo Camera on board the ESA Mars Express discovered young volcanoes 2-15Myr old on Mars. This is why terrestrial volcano microbial communities might serve as a model for Mars, particularly for young Martian volcanoes that date back to ages close to those for permafrost on the Earth.

3. Free water on Mars only has the opportunity to exist in the presence of high solute content, probably as overcooled brine lenses within permafrost, formed when Mars became cold. These brines, like their terrestrial analogues, may contain microorganisms adapted to subzero temperature and high salinity. This is why the halo/psychrophilic community preserved hundreds of thousands of years in Arctic in cryopegs - mineral-enriched water lenses, sandwiched within permafrost provide the plausible prototype for Martian extant or extinct biota.

OP-41

LOOKING FOR LIVE IN HIGH TEMPERATURE WORLDS

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Looking for habitable planets is based on notions of the Earth' physics. The Earth possesses a unique combination of physical properties needed for the evolution of amino-nucleic-acid form of life. Physical conditions that an Earth-like planet should possess produce very narrow intervals of many physical parameters that are required for the existence of our form of life. First of all, it is the temperature condition. A large number of discovered exoplanets orbits their host stars at very low distances. Even if many other parameters would be favorable or suitable for existence of life they differ in temperature conditions. One may accuse us of a certain Earth's chauvinism, not admitting the existence of non-amino-nucleic-acid living forms (despite having no proves for their existence). Strictly speaking, there is evidence that life would even adapt to the temperatures exceeding the ones in the interval $273 < T < 340$K and the hard radiation level. The known rhizobia use the high energy of pi-bonds reaching 10 eV and more in their metabolism without damaging themselves. If one considers such energies to be a result of equivalent temperatures influence on the action on these bacteria, one may conclude they could exist at very high temperatures. However, even if admitted that such metabolism is possible, the nucleic acids may not resist high temperatures. If high temperature life exists would its nature based on carbon or not? One may suppose that at the high temperatures another reaction types suitable for life could exist. Similar to conditions on some possible extrasolar Earth-like planet is the ambient temperature on the surface of Venus, 740 K. This parallel is considered in the paper. Strange black strikes can be seen amid stones on the first panoramas transmitted by the Venera-9 and Venera-10 landers from the Venus surface in October, 1975. The strikes are of more or less regular shape and are very dark, even in comparison with the dark Venusian surface (albedo 4-11%). May these strange strikes be living creatures, plants? Their details are blurred due to the picture's low resolution. Once it allowed me to put a question, if plants could exist on Venus, in the dense, incandescent atmosphere (Ksanfomality, 1978). This question seems rather fantastic. Impotant for life is availability of chemical sources of energy, for example chemical sources, as an oxidizing medium and oxidized materials. This is not the case for Venus-like planets. However, the illuminance 5-7 klx at the Venusian surface (Ksanfomality, 1985) is enough for the photosynthesis. For a Venus-like world, the photosynthesis is the most probable sources of energy for these hypothetic creatures.

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"BUTTERFLY EFFECT" IN PLANETESIMAL FORMATION OR STUDYING THE OUTCOME OF GRAVITATIONAL INSTABILITY IN MULTIPHASE PROTOPLANETARY DISC

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One of the most intriguing stages of matter self-organization in biosphere evolution is abiogenic synthesis of primary prebiology substances, preceding RNA-World. According to astrocatalysis hypothesis, most of Earth biosphere primary organic substance was synthesized before Earth formation, under the conditions of circumsolar protoplanetary disc.

Circumsolar disc evolution goes via growth of solid bodies – from nanometer dust grains to kilometric-sized planets. "Astrocatalysis" as a stage of chemical evolution coinsides with formation of large bodies (planetesimals and planet embryos) from metric size boulders – major bottleneck in the planet formation process. Planetesimal on the stage of its emergence is considered as a clump of gas and solids whose gravitational field preserves its mass when the clump moves. These self-gravitating clumps can be suggested as chemical reactors for efficient synthesis of prebiotic substance.

Gravitational instabilities can play a key role in formation of collapsing clumps of gas and solids. Although computer simulations show that development of gravitational instability often resulted in global spiral structure formation without triggering to self-gravitating clumps formation. Several regimes of such clumps formation is described yet. In all described modes collapsing object formation goes only under stiff (sometimes contradictory for real discs) limits on medium and physical process parameters. For evolving systems the probability to strike the target of such conditions is nearly equal to zero.

In our investigation we found new regime of self-gravitating clumps formation. Self-gravitating clumps can be formed by the development of "two-phase" Jeans instability of gas and primary bodies medium. This instability reveals so-called "butterfly effect" in two-phase discs when dynamics of the system is determined by collisionless collective motion of **low-massive** subdisc of primary solids.

This implies that the possibility of clump formation is determined both by the rate of gas cooling and its density redistribution and by the rate of large (over 1 m) primary solids concentration and decrease in dispersion of their velocities (cooling of primary solids). Thus we managed to expand the area of sufficient conditions for collapsing clumps formation.

OP-43

RISE AND FALL OF THE Y-CHROMOSOME OR CRONICA DE UNA MUERTE ANUNCIADA

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Mammalian sex chromosomes are believed to originate from an ancient pair of autosomes.

The first step of their divergence was an occurrence of *SRY* gene involved into control testis determination and, consequently, male development of the embryo. *SRY* is a truncated variant of an ancestral transcription factor *SOX3.* It controls the testis determination indirectly by interfering with the binding of another chromatin remodeling proteins.The chromosome carrying the male specific allele of SRY became the Y, while its homolog became the X chromosome.

The second step of divergence involved an accumulation at the Y chromosome the sexually antagonistic alleles, i.e. the alleles which were beneficial for males and harmful or neutral to females. This was achieved by a selection for such mutations in such genes at the Y chromosome and from translocations transposing such genes from the autosomes to the Y. At this stage natural selection was directed against recombination between the portions of the X and Y chromosomes containing sexually antagonistic genes.

At the third step of the divergence this selection led to accumulation of various epigenetic, genetic and chromosomal suppressors of recombination at the Y chromosome, while X chromosomes kept recombining normally in female meiosis. The non-recombining portion of the region Y chromosome grew generation by generation. Now in most placental mammals synapsis and recombination between X and Y chromosomes are restricted by a very small (about 5% of chromosome length) region.

Suppression of recombination led to inevitable degradation of the non-recombining part of the Y chromosome due to mutational meltdown. The Y chromosome as any non-recombining chromosome has been doomed to extinction. The human Y-chromosome has lost 1,393 of its 1,438 original genes over the time of it divergence from the X chromosome (about 160 mln years). If it will keep degrading with this speed, it gets extinct in about 10 mln years.

A hopeful insight into the future of the human Y chromosome may be gained by the analysis of the species which overrun us in rate the Y chromosome degradation. In some species of the grey voles studied in our laboratory the X and Y have completely lost their ability of pair and recombine. In my report I will discuss the causes and consequences of independent losses and acquisitions of the X-Y pairing regions in the evolution of the grey voles.

COEVOLUTION OF MAMMALIAN FAUNAS AND LANDSCAPES

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Several large stages are clearly discernible in the evolution of the land mammal communities. The Early Cenozoic stage of development of the Northern Hemisphere zoochores has started since the total isolation in the Paleocene. The mammalian faunas of North America, Europe and Asia were developed independently as three zoogeographic regions of the Holarctic Kingdom. The North African fauna was a part of the Afrotropical Kingdom. In this region the endemic placental mammal groups (hyraxes, aardwarks, tenrecs, golden moles, elephant shrews, proboscideans, sirenians) had evolved. The first Cenozoic great faunal interchange between north landmasses was occurred at the Paleocene–Eocene boundary. As a result, some close representatives of several mammalian orders (artiodactyls, perissodactyls, condylarths, creodonts, carnivores, tillodonts, pantodonts, and rodents) appeared in all parts of Holarctic. The faunal interchange between Europe and North America via North Atlantic land bridge occurred in Early and Middle Eocene. The faunal interrelationships between North America and Asia via the Bering land bridge continued until latest Eocene. The independence of the zoogeographic regions was preserved due to the existence of marine barrier between Asian and European landmasses (Popov et al., 2009). North Alpine Strait was the main marine barrier, which prevented faunal interchange between continental Palearctic and Western Europe archipelago. In the Late Eocene, the mammalian faunas of South Eastern Europe, Lesser Caucasus and Asia Minor were closely related to Central Asian mammalian fauna, being included in the North Asian Subregion of the Asian Zoogeographic Region. The disappearance of the West Siberian Basin and Turgai Strait, and the consolidation of the major parts of European land at the Eocene–Oligocene boundary resulted in a marked decrease in the faunal distinctions between the European and Asian zoogeographic regions. The beginning of the Oligocene in Europe was associated with the so-called Grande Coupure, the greatest rearrangement of the West European Fauna. At least 20 mammalian families migrated to Europe from Asia at the Early Oligocene. Of 15 endemic European families of the Late Eocene mammals, only 2 survived up to the end of the Early Oligocene. In the Late Oligocene the mammal fauna from Western Europe became even more similar to faunas from other Palearctic areas. More than 30 families were in common with Asia. Some rodent and ruminant groups typical for the Oligocene of Asia became widespread in Late Oligocene faunas of Europe.

With the gradual contraction of the Eastern Tethys in the Early Miocene, the faunal contacts between Africa and Eurasia were established. As a result, proboscideans had penetrated into Eurasia, and many Holarctic groups (carnivores, rhinoceroses, chalicotheres, suids, bovids, and giraffids) had entered Africa. In the second half of the Early Miocene the integrated European–Siberian Subregion was formed in the Eurasian Zoogeographical Region (Popov et al., 2009). The emergence of the Sub-Paratethyan Province was determined by the formation of so-called Sahara–Gobi desert belt, the extremely large ecological corridor of open habitats within a vast area from the East Mediterranean Europe through Asia Minor, Near East, and northern Arabia to Afghanistan and China. Apparently, it was just this province which provided the major faunal interchanges between Eurasia and Africa.

The influence of landscape changes on the structure and composition of the land biota is noticeable in the dynamics of the sedimentation, vegetation, climate and transformation of the small mammal communities of the Plio-Pleistocene of the Russian Plain (Agadjanian, 2009). The analysis of taphonomy and composition of the small mammals from 49 Plio-Pleistocene localities made it possible to trace the habitat and dynamics of the small mammal communities of the Russian Plain and adjacent territories over the past 3.5–3.0 million years. The relationship between the major paleogeographic events on the Russian Plain during the Late Cenozoic and dynamics of the transformation of the small mammal communities is demonstrated. A new model for the evolution of arvicolids, the most important group of rodents in the Northern Hemisphere, is proposed. The schemes of the correlation of small mammal faunas of the Russian Plain, Siberia, Transbaikalia, Central and Western Europe are proposed (Agadjanian, 2009).

Thus, it is shown that the development of mammal communities in different periods of the Cenozoic in Northern Eurasia occurred with the same patterns and was associated with large-scale landscape changes. One of the most important factors to be considered is the biogeographical one, providing the interoperability of local faunas. The crucial factors in this process are geographical conditions and community structure of the recipient region (Agadjanian, 2009). In general, the landscape restructure increases the efficiency of the introductions. Examples of feedback is a formation by vertebrates of local or regional landscapes by direct effects on plant associations (eating up by large gregarious ungulates, proboscideans, and social rodents; seed dispersion by mammals and birds), disintegration of the soil surface (burrowing by social rodents), changes in hydrological and other landscape characteristics of the territory (beaver dams, human activity).

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FRAMEWORKS OF LIFE ORIGIN RESEARCH AND CORRESPONDING DEFINITIONS OF LIFE

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There is no unified opinion concerning the necessity and usefulness of a general definition of life for efficient resolving of life origin problem. Analyzing publications on life origin shows that all studies in the field can be separated into two big groups:

a) studies attempting to find out the conditions and stages of the origin of **life** on the Earth, **life as we know it**;

b) studies examining the conditions and stages of the emergence of **any** conceivable scientifically **life form**.

These groups correspond to the accepted frameworks of research, which can be conveniently denote as Earth Life Origin (ELO) and General Life Origin (GLO), respectively. The difference between these frameworks is a critical issue, since it concerns fundamentally different approaches to the problem of the origin of life.

A researcher working within the ELO framework does not have to answer the question "What is life?" [12]. Practically, the ELO approach defines life as something composed, in a certain way, of proteins, RNA, DNA, phospholipids, and father on a modern textbooks of biochemistry and molecular biology. This simple definition of life, however, severely complicates understanding general principles of life origin and organization. In order to explain the origin of our specific form of life, one has to construct a cause-and-effect chain of conditions and events that inevitably lead to the form of life as we know it. This objective seems very difficult or even unsolvable. The analysis of the literature shows that most of the studies on the origin of life have been conducted within the ELO framework. The objectives that they address are stated quite clearly, they involve a large number of researchers, and recent results are highly interesting [8,9].

In contrast to ELO-framework studies, the GLO-framework approach cannot work without defining life in general terms. Some scientists think that life in general cannot be defined scientifically and that this definition is not a scientific objective [6,7]. Yet other scientists [4,5,10] believe that life can be defined in general terms, which would apply both to life of Earth and possible extraterrestrial life forms, and that this definition will mark the birth of true biology [4]. Studies of the origin of life within the GLO framework are closely related to practical objectives of astrobiology, since the probability of finding extraterrestrial life forms grows with the widening of the range of search, which is determined by the concept of life and its manifestations [3,11].

Possible approach to creating a general definition of life can be based on selecting some property (or properties) which is/are inherent only to living beings. However it seems natural that developed ("mature") life can have another dominant property than life during the formation period. Really it is possible to suggest some necessary (supporting existence itself) property which is inherent to initial probiont system –a precursor of living beings – and some property, which is as an attractor where the vector of living beings phylogenesis and ontogenesis are directed. The first one is ability to autocatalysis, which later transforms and divided into self-maintenance and self-reproduction. Second one is ability to make choice on the base of signal perception, or in other terms – information processing [1]. Namely information processing is immanent and specific property of living beings among other natural objects. It has to be emphasized that we consider only natural objects, and artificial ones can not be included in our consideration since they are created by living, and more, intelligent beings and "bear the prints of life".

The principle of graduality has to be satisfied over all stages of chemical evolution, transient to biological evolution, and biological evolution itself. In the paper key steps of chemical evolution from beginin to the transient period are discussed. The hypotheses of the multivariate oligomeric autocatalytic system is suggested as possible scenario of chemical evolution [2] and transforming dominant property of life during it.

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FLUCTUATING HYDROTHERMAL ENVIRONMENTS FOR PREBIOTIC CHEMISTRY

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According to the author’s approach to the origin of life, conditions in the maternal medium should be changeable (Kompanichenko, 2009). From this point of view, hydrothermal systems and their discharges in ocean or terrestrial groundwater aquifers characterizing availability of thermodynamic and/or physic-chemical fluctuations should be considered as the most appropriate environments for life to emerge. To get some experimental data in this way, fluctuations of pressure, temperature and availability of organics in fluid were investigated in several hydrothermal fields in Kamchatka. Temperature and chemical composition of the thermal discharges in are variable: pH is within the interval 2.5-8.5, temperature of hot springs ranges from < 60 to 98 °C, steam-gas jets - up to 380 °C. Concentrations of Cl^-, SO_4^{2-}, HCO_3^-, Na^+, Ca^{2+}, Mg^{2+}, NH_4^+ are prevalent in the liquid phase. The gas phase contains CO_2, CH_4, H_2S, H_2, N_2 as major components. Data on pressure and temperature monitoring in 27 deep (600-2000 m) bore holes was processed. Most of the bore holes open water-steam mixture with the temperature varies from < 100 to 239 °C and pressure from < 1 to 35 bars at the wellheads. The estimated vertical gradients of pressure and temperature are within the intervals 2.5-5 bars and 11-15 °C per 100 meters. Correlation coefficient between pressure and temperature ranges from 0.89 to 0.99 (average 0.96). Pressure monitoring at the depth 950 meters in the bore hole № 30 (Mutnovsky field) reveals high-amplitude (amplitudes up to 1-2 bars) irregular macrofluctuations, and low-amplitude quite regular microoscillations of pressure (amplitudes 0.1-0.3 bars) with the period about 20 minutes. The periods of pressure oscillations at the wellheads of several boreholes in Pauzhetsky and Mutnovsky systems ranges from 10 to 60 minutes. So, macro- and microfluctuations of the thermodynamic parameters are wide-spread phenomena in the explored hydrothermal systems.

To analyze moderately volatile organic compounds in the hydrothermal fields, the gas chromatomass spectrometer Shimatsu (GCMS-QP20105) was used. Samples of water and condensate of water-steam mixture were taken from hot springs and bore holes (60-2000 meters in depth). Then organics was extracted from water into the cartridges OASIS and C18 to run the analysis. Lifeless condensate of water-steam mixture (t = 108-175 °C) contains 18 organic compounds that belong to 5 homologous series: aromatic hydrocarbons (naphthalene, 1,2-methylnaphtaline, biphenyl, phenathrene, fluorene, squalene, 1,3-diethylbenzene, and trichlorobenzene), n-alkanes (decane, dodecane, tridecane, tetradecane, pentadecane, hexadecane, and heptadecane), aldehyde (oktadekanal), ketone (2-heptadekanon), and alcohol (2-undetsenol-1). 10 homologous series have been found in hot solutions (t = 60-99 °C) inhabited by thermophilic and hyperthermophilic microorganisms: aromatic hydrocarbons, n-alkanes, alkenes, aldehydes, dietoxyalkanes, naphthenes, fatty acids, methyl ethers of fatty acids, monoglycerides, and steroids. Investigating gas-steam jets in 7 hydrothermal fields in Kamchatka, Isidorov et al (1992) discovered 64 volatile organic compounds of the following homologous series: n-alkanes, alkenes, cycloalkanes, aromatic hydrocarbons, terpenes and terpenoids, alcohols, ketones, ethers, esters, thiols, disulfides, halogenalkanes, halogenalkenes. Mukhin et al (1979) detected glycine of probably abiotic origination in the lifeless condensate, and 12 amino acids of biological genesis – in hot solutions of 4 thermal fields in Kamchatka. Availability of the abiotic contribution is supposed at least for the following series/compounds: aromatics, alkanes, Cl-alkanes, glycine.

Summary. The explored hydrothermal environments characterizes by: a) spatial gradients and temporal fluctuations of the thermodynamic parameters in rising fluid; b) availability of various biologically important organic molecules (simple amino acids, lipid precursors, hydrocarbons) that could be involved into self-assembly/synthesis of prebiotic microsystems on the early Earth. Basing on this data, laboratory experiments on prebiotic chemistry under *changeable* conditions can be carried out.

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PRE-TRANSLATIONAL ORIGIN OF THE GENETIC CODE

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The major challenge to the understanding of the genetic code origins is the archetypal "key-lock vs. frozen accident" dilemma (Crick, 1968). Recently we have re-examined the dilemma (Rodin et al., 2009, 2011) in light of modular structures of tRNAs and aminoacyl-tRNA synthetases (aaRS) (actually bringing the code into action), and the updated library of amino acid-binding sites of RNA aptamers selected *in vitro* (Yarus et al., 2009; Yanus et al., 2010).

The aa-binding sites of arginine, isoleucine and tyrosine contain both their cognate triplets, anticodons and codons. We observed that this puzzling error-prone simultaneous presence is associated with palindrome-dinucleotides (Rodin et al., 2011). For example, one-base shift to the left brings arginine codons CGN, with CG at 1-2 positions, to the respective anticodons NCG, with CG at 2-3 positions. Technically, the concomitant presence of codons and anticodons is also expected in the reverse situation, with codons containing palindrome-dinucleotides at their 2-3 positions, and anticodons exhibiting them at 1-2 positions. A closer analysis reveals that, surprisingly, RNA binding sites for Arg, Ile and Tyr "prefer", ***exactly as in the actual genetic code,*** anticodon(2-3)/codon(1-2) tetramers to their anticodon(1-2)/codon(2-3) counterparts, despite the seemingly perfect symmetry of the latter. However, since *in vitro* selection of aa-specific RNA aptamers apparently had nothing to do with translation, this striking preference provides a new strong support for the notion of the genetic code emerging before translation, in response to catalytic (and possibly other) needs of ancient RNA life.

Consistent with the pre-translational origin of the code are our updated phylogenetic study of tRNA genes (Rodin et al., 2009) and a new model of gradual (Fibonacci iteration-like) evolutionary growth of tRNAs – from a primordial coding triplet and 5'-DCCA-3' (D is a base-determinator) to the eventual 76 base-long cloverleaf-shaped molecule (Rodin et al. 2011). The pre-translational genetic code origin is also consistent with the partition of aaRSs in two structurally unrelated classes with sterically mirror modes of tRNA recognition (Eriani et al., 1990; Delarue, 2007). This partition seems to have protected proto-tRNAs with complementary anticodons from otherwise very likely confusion, the only "exception" being the pairs of the "very first" (Miller's) amino acids, such as Gly and Ala with the acceptor- more than anticodon-sensitive risk of wrong recognition (Rodin & Rodin, 2006, 2008; Rodin et al., 2009).

Taken together, our findings (Rodin et al., 1993-2011) question many dogmas of the code and translation origins. First and above of all, primordial tRNAs, ribozymic precursors of aaRSs, and (later) the translation machinery as a whole seem to have been co-evolving to "fit" the (likely already defined) genetic code rather than the opposite way around. Coding triplets in this primal pre-translational code were similar to the anticodons, with second and third nucleotides being more important than the less specific first one. Later, when the code was expanding in co-evolution with the translation apparatus, the importance of 2-3 nucleotides of coding triplets passed on 1-2 nucleotides of their complements, thus distinguishing anticodons from codons.

The statistically compelling bias to anticodon(2-3)/codon(1-2) tetraplets in aa-binding sites of RNA aptamers points to a fundamental interconnection between the primordial RNA operational code (hence the genetic code itself) and a chiral selection of its components. Indeed, in model ribooligonucleotides-assisted aminoacylation of RNA minihelices, selection of L-amino acids was determined by a pre-selected D-ribose, and vice versa (Tamura & Schimmel, 2004, 2006). An intriguing question would be: what if, with a fascinating mirror symmetry, the chiral-mirror RNA world (with L-ribose and D-amino acids) is just the anticodon(1-2)/codon(2-3) biased? The mirror "selexed" RNA aptamers could provide an answer. The experiments that might test the possibility of such a mirror symmetric life are outlined.

All of the above make the following key hypotheses in the area – (1) stereo-chemical affinity between amino acids and anticodons (Woese, 1965; Orgel, 1968, Yarus, 1998), 2) coding coenzyme handles for amino acids (Szathmary, 1990, 1993), 3) tRNA-like genomic 3' tags (Weiner & Maizels, 1987, 1994) implying that tRNAs originated in replication, 4) the "second" (operational) genetic code of proto-tRNA aminoacylation (De Duve, 1988; Schimmel et al., 1993), in its ancient ribozyme-mediated version, and 5) SAS (sense/anti-sense) origin of two aaRS classes (Rodin & Ohno, 1995) and the yin/yang-like internal code for their sterically mirror modes of tRNA recognition (Rodin & Rodin, 2006, 2008) – not mutually contradicting but co-existing in harmony and essentially add to the fundamental premise: ***Translation without code does not make sense, but code without (and before) translation does!***

COULD CHRONIC STRESS INDUCED BY POLYCYCLIC AROMATIC HYDROCARBONS HAVE IMPLICATIONS FOR HOMINID EVOLUTION?

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Comparisons of the entire genomes of primates, including man and chimpanzee, demonstrated that the genetic pattern of adaptive evolution in man is the same as that in other primates, so they form homological series[1]. The genes evolving are largely those controlling interactions with the environment (signal reception and transduction genes, immunity genes, reproduction genes and genes controlling trophic and energy processes), while the genes controlling the cell cycle, cytoarchitectonics and ontogenesis are less involved. Importantly, most of these genes are expressed in many tissues, including the brain (except reproduction genes) [1, 3], while brain-specific genes are surprisingly rare (ASPM, microcephalin, FOXP2 [1]) and whether they undergo adaptive evolution is still an open issue [3][2].

Genetically, man is close to chimpanzee; however, behaviorally, it is also close to the most eurytopic primates in the Old and New World. Species like these do not depend much on their econiche: highly stress-resistant, they can travel in the ecocoenotic space and have their survival strategies changed as required. The first to indicate the involvement of stress in hominid evolution was Belyaev, who pointed out an association between domestication stress-driven selection in fox (domestication is tolerance towards man, self-domestication is tolerance towards neighboring conspecifics) and a change in some psycophysiological characteristics, including complex exploratory behavior [4]. We propose that the vector of evolution that optimizes stress response (prolongation of the cross-resistance phase, dampening down distress in the anxiety and exhaustion phases) is beneficial for eurytopic species, no matter what stress inducers operate (their list can be extended far beyond domestication stress and its derivatives). Hominization is associated with the Great Rift Valley (GRV)[3] [2], where some of exotic stressors could be such xenobiotics as polycyclic

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[1] This is consistent with data from comparative primatology [2]: behavioral and physiological elements typical of man apparently emerged in parallel in different Old and New World species.

[2] The growth in the share of non-synonymous substitutions in them is easier explained by an attenuation of stabilizing selection [1].

[3] In the hominid lineages that either have never been to GRV or once abandoned it, encephalization rates used to be slowing [2].

aromatic hydrocarbons (PAHs) and their derivatives. GRV accommodates their natural sources, volcanism and oil deposits [5]. A high level of PAH accumulation in trophic chains could, too, become a factor of hominid evolution as soon as the hominids reached the upper levels of the trophic pyramid. The toxic and teratogenic effects that PAHs have on mammals are due to the interactions between PAHs and AHR, after which the resulting supramolecular complex begins to regulate the expression of some genes responsible for non-specific resistance (stress genes, genes for xenobiotic metabolism), some immune system genes, some genes for the cell cycle and apoptosis and some genes for differentiation of some tissues (including neurogenesis) and some genes controlling ontogenesis. As is known, human neural progenitor cells are insensitive to PAHs because of lack of AHR [6]. In the adult human brain, AHR expression, the set of co-expressing transcription factors and the pattern of interaction between these factors and AHR are strongly altered [7] as compared to the chimpanzee.

Thus, selection for resistance to PAHs can have managed the evolutionary trends of genes that are expressed in a broad variety of tissues, including the brain, which had a correlative effect on its evolution, and the adaptive evolution of such nonspecific systems as xenobiotic metabolism and stress not only turned out beneficial for the eurytopic species, but also preadapted man’s ancestors for consistent use of fire. Even with the controlled use of fire, man beyond GRV was still stressed by xenobiotics, the variety whereof was growing on as the civilization advanced.

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A UNIVERSAL TREND OF NUCLEOTIDE ASSYMETRY IN TRNAS SUGGESTS A COMMON THERMOPHILIC ORIGIN

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Introduction. The origins of the Last Universal Common Ancestor (LUCA) of life beings have been covered by a secret veil. Most studies indicate that LUCA was a (hyper)thermofile.

Transfer RNAs (tRNAs) are the ancient nucleic acid molecules that can be found in all taxa. They charge specific amino acids, bind to 16S rRNA and recognize mRNA codons, establishing a genetic code that translates mRNA into protein. Since tRNAs are central to translation their sequences are fundamentally delimited by their structure and function. Slowly varying tRNA sequences can carry deep evolutionary signatures that were left behind when the living world diversified.

tRNA nucleotide substitutions have been extensively studied earlier to uncover the structural make-up of the molecule which is critical to perform multiple tRNA functions. In this paper I used well-established phylogenetic methods to detect tRNA single substitutions for each of 20 iso-acceptor tRNA families in 123 taxa and found that tRNAs slowly accumulate adenine and uracil and correspondingly lose guanine and cytosine nucleotides. A similar work [1] has compared sets of orthologous proteins and revealed a universal trend of amino acid gain and loss but the underlining mechanism is still under debate [2, 3].

Methods and Algorithms: tRNA aligned sequences were drawn from http://www.uni-bayreuth.de/departments/biochemie/trna/. From them 20x123=2460 tRNAs were extracted, each corresponding one amino acid of one taxon of 123 taxa representing all three domains of life - Bacteria, Archaea and Eukaryota.

To reveal favored nucleotide substitutions I calculated fluxes for each of 20 tRNA families as well as Jordan and colleagues have analyzed amino-acid fluxes in proteins [1] (Fig. 1).

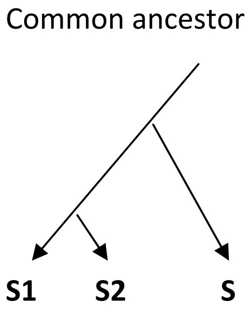

Figure 1. A maximum parsimony evaluation of simple 3-taxon trees. All 123 taxa were splitted into closest triples, in each of them S1 and S2 were two closer taxa and S was more divergent taxon. The nucleotides shared by S1 and S2 were assumed to exist in the common ancestor and if nucleotide in S was different a single substitution occurred along the branch leading to S. Positions differing in all 3 taxa were deemed non-informative and were excluded from consideration. By these means the transition matrix was calculated: its asymmetry defines the directions of substitution rates.

Results: Considering the changes between the ancestor and the descendant taxa at branching nodes 1972 non-informative positions and 24415 single substitutions have been detected: the difference reflects the well-known fact of tRNA sequence conservation. Transitions G↔A and C↔U were the majority (56%) of found substitutions. More importantly, forward and backward rates of transitions were unequal and differed by 14% and 12%, correspondingly. Asymmetry of fluxes of reciprocal substitutions means that tRNAs are not at evolutionary equilibrium. Nucleotide changes are time-irreversible and directed towards nucleotides of weaker Watson-Crick base-pairing.

To infer the qualitative evolutionary trajectory of nucleotide frequencies in tRNAs it is instructive to recalculate the nucleotide changes into the transition matrix of two-letter (S-W) code and to apply the simplest substitution model [1]. Within the model it is assumed that substitutions occur uniformly in time and independently of each other. Then the nucleotide frequency evolves under the following kinetic equation:

$$\frac{\partial n}{\partial t} = k_{to}(1-n) - k_{from}n$$

Using this equation and the forward and backward substitution rates, k_{to} and k_{from}, the steady-state nucleotide frequencies can be readily estimated (Table 1). Difference between the observed and the stationary frequencies of nucleotides corresponds to the expected loss of two S-S pairs per one tRNA in the distant future.

Table 1. tRNA nucleotide content evolution: gain and loss rates, current and equilibrium frequencies calculated from the model of independent stationary substitutions.

Nucleotide	Nucleotide gain\loss rate per substitution	Current frequency	Asymptotic frequency
S (G+C)	-0.024	0.61	0.58
W (A+U)	0.024	0.39	0.42

Conclusion: I show that tRNAs are not in detailed evolutionary equilibrium, consistently losing strong (G\C) and accumulating weak (A\U) nucleotides. This may reflect under-representation of A and U in early tRNAs or, in other words, relaxed selection constraint favoring G-C pairs compared to A-U pairs in helical regions of secondary structure. This may also suggest G-C abundance in the prebiotic environment, where weak nucleotides were rare. It is well-known that the taxon nucleotide content depends on its environmental temperature: therefore a universal trend found in this work supports the earlier observations that LUCA was more thermofilic than currently living beings.

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ADAPTATION OF THE PYROCOCCUS SPECIES TO DIFFERENT ENVIRONMENTAL CONDITIONS: ANALYSIS OF THE EVOLUTION AT THE PROTEOMIC AND STRUCTURAL LEVELS

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Deep sea hydrothermal vents represent extreme habitats with high temperature and pressure. It is assumed that these conditions were common for early life at the Earth [1]. Thus, studying the evolution of the microorganisms from deep sea hydrothermal vent biotopes can shed light on the life origin. From the other hand, such analysis can provide important information about adaptation of microorganisms to extreme environments in the course of evolution.

We investigated the evolution of three archaeal species of the Pyrococcus genus from hydrothermal vents: deep sea P. abyssi and P. horikoshii and shallow-water P. furiosus [2]. It was demonstrated that the function of proteins that have been subject to positive Darwinian selection is closely related to abiotic and biotic conditions to which archaea managed to become adapted. It was shown that the pressure is important environmental factor in the course of evolution. Nevertheless, adaptation to pressure does not appear to be the sole factor ensuring adaptation to environment. For example, at the stage of the divergence of P. horikoshii and P. abyssi, an essential evolutionary role may be assigned to changes in the trophic chain, namely, acquisition of a consumer status at a high (P. horikoshii) or low level (P. abyssi).

We present results of the comparative analysis of the molecular dynamics simulation of Nip7 proteins from the P. abyssi and P. furiosus species. These proteins are involved in ribosomal biogenesis, participate in 27S pre-rRNA processing and 60S ribosomal subunit formation [2]. We investigated changes of the polypeptide chain conformation and solvent accessibility at different pressures (0.1 - 300 MPa) and temperatures (300 and 373 K).

Obtained data suggested that the RNA-binding domain of the P. abyssi Nip7 protein is more resistant to the effects of high pressure. Our data also suggests that the interactions of these proteins with solvent are different and could be important for adaptation to high-pressure conditions at the protein structure level.

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GROWTH OF MICROORGANISMS IN MARTIAN-LIKE SHALLOW SUBSURFACE CONDITIONS: LABORATORY MODELLING

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Low atmospheric pressures on Mars and the lack of substantial amounts of liquid water were suggested to be among the major limiting factors for the potential Martian biosphere. However, large amounts of ice were detected in the relatively shallow subsurface layers of Mars by the Odyssey Mission and when ice sublimates the water vapour can diffuse through the porous surface layer of the soil. Here we studied the possibility for the active growth of microorganisms in such a vapour diffusion layer.

Our results showed the possibility of metabolism and the reproduction of non-extremophile terrestrial microorganisms (Vibrio sp.) under very low (0.01–0.1 mbar) atmospheric pressures in a Martian-like shallow subsurface regolith.

COMPLEX HETEROTROPHIC EUKARYOTES AT THE MESOPROTEROZOIC–NEOPROTEROZOIC BOUNDARY

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Although the late Proterozoic record of biotic evolution is resolved in very general terms, it has become evident that the rise of biodiversity and morphological complexity of microorganisms was very nonuniform. One of the greatest transformations in the history of biosphere occurred in late Mesoproterozoic and early Neoproterozoic: morphological diversity of large complex microfossils in contemporaneous rocks suggests diversification of eukaryotes and their incorporation into prokaryotic ecosystems. Phylogenetic affinities of extinct eukaryotes are difficult to establish based on morphological criteria only; however, when taphonomic features of fossil preservation are taken into account, it is possible to elucidate probable role of the extinct organisms in trophic structure and test the morphological criteria.

The Lakhanda fossil microbiota in the east of the Siberian Craton provides the best paleontological record across the Mesoproterozoic–Neoproterozoic boundary. Morphological and taphonomic features of the microfossils suggest that the Lakhanda microbiota included saprotrophic eukaryotes:

1. Caudosphaera expansa Hermann – organisms that formed mycelia with outgrowing vertical long multiseriate filamental stipes ending with spherical sporangia. Preservation on several bedding planes indicates that in life the mycelium was embedded in the sediment, with sporangia protruding above the sediment surface. Most likely, the organisms were heterotrophs.

2. Organisms that formed procumbent (two-dimensional) netlike thalli with diverse cellular structure and growth strategies.

2.1. Coenocytic thalli growing by expansion; first, ringlike structures form by fusion of the ends of elongated juvenile cell, then processes form and anastomose in the space enclosed by the ring, and finally the ring expands and is divided into two new ringlike structures.

2.2. Coenocytic thalli growing by dichotomous branching and anastomosis of claviform processes.

2.3. Cellular thalli (or colonies?) Eosaccaromyces ramosus built of filament-like structures each consisting of 1–2 series of elliptical cells.

3. Mycelium-forming organisms with elliptical sporangia (usually preserved as hollow structures) connected to the filamental mycelium by short relatively dark holdfasts.

4. Organisms forming a plasmodium-type thallus.

Fossils of first three groups possess morphological features similar to mycelium of modern eukaryotes that belong to fungi-like protists or true fungi. Sporangium morphology of Caudosphaera expansa resembles that of true fungi, but the absence of cellular septa in the hypha does not allow making direct comparisons. The second group of the studied organisms comprises morphologically similar fossils (two-dimensional netlike structures) suggesting a similar life style and feeding strategies. This type of morphology is optimal for extracting dispersed organic matter and distinctive of saprotrophic organisms. Coenocytic mycelium (fossils of groups 2.1 and 2.2) occurs in Zygomycota and other groups of fungi-like protists, but the overall morphology does not have direct counterparts among modern heterotrophic eukaryotes. It is possible that these organisms, including Caudosphaera expansa, were representatives of stem groups (not crown groups) of heterotrophic eukaryotes. Morphology of the third group of fossils resembles oogonium of representatives of genus Saprolegniales of the class Oomycota, a large group of aquatic heterotrophic fungi-like protists. The third group, therefore, could be referred to as possible oomycetes. The fourth group includes fossils that are characterized by absence of visible cell walls (thalli become thinner along the edges) and significant morphological variation while maintaining the same body plan. These features are indicative of plasmodium stage of modern heterotrophic protists Myxomycetes. All described fossils were obviously eukaryotic, because their morphological elements exceed the size of hypha in Actinobacteria, the only group of prokaryotic organisms that form mycelium.

MOLECULAR DATA IN THE STUDIES OF EVOLUTION AND SYSTEMATICS: USAGE AND INTERPRETATIONS

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After a period of insolence to phylogenetics in general and to numerous phylogenetic trees drawn manually, phylogenetic studies and systematics became very popular. It will be not an exaggeration to say that nowadays these studies experience a period of “renaissance”. No secret that this wave of popularity is related to a wide application of molecular methods to the studies of phylogeny and systematics. The success of molecular phylogenetics and systematic is evident, the number of publications devoted to various groups of animals and plants grow in geometric progression and it is impossible to imagine further development of botany and zoology without the application of molecular techniques. Molecular data turned out long lived ideas and concepts on phylogenetic relationships and systematics even within such well studied groups as mammals and angiosperms. New findings inspired for new search and developments of more and more rigorous techniques both in experimental design and mathematical analysis of data and all this produced an impression of a serious breakthrough or even revolution in this field of biology. However, such wide penetration of molecular data in these classical and descriptive fields brought a lot of controversies and was ambiguously met by scientists working with morphological and paleontological data and experts in the groups under study. In this communication I would try to analyze the most common reasons why the results of molecular studies do not please everybody. Naturally within the frame of short communication it is impossible to pretend on comprehensive review of such topical question so I will highlight the most general reasons but nevertheless they are not so evident for those who are unfamiliar with analysis of molecular data but enforced to take in account its findings.

The reasons why the results of molecular phylogenetics and systematics may not satisfy advocates of classical approach may be divided into three main groups: methodical mistakes, wrong interpretation of results and psychological reasons. I will not touch the last group of reasons as these are outside scientific field.

Under methodical mistakes I mean first of all a set of mistakes at the very first step of analysis of sequencing data which inevitably will lead to a wrong result. The key moment here is the analysis of alignment. The backbone of multiple alignment is the hypothesis on homology of nucleotides/amino acids and the hypothesis on homology is the keystone in any kind of phylogenetic analysis. Noteworthy that very often while comparing molecular and conventional approaches as a main distinctive feature propose the objectivity of results in molecular studies independent of the researcher prior ideas, while conventional approach is highly subjective and require an expert knowledge. It is interesting that this argument often use both proponents and opponents of molecular data in phylogeny and systematic in order to strength their point of view. However, it is important to underline that there is not less subjectivity in establishing homology in molecular data (alignment) than in morphology. Alignment is a mathematical process totally independent from biological reality and the question always rises to what extent mathematically optimal alignment is optimal biologically? Alignment of sequences is no doubt one of the most hard and disputable tasks in molecular analysis due to insertions, deletions, sometimes it is even better to refute from aligning ambiguous sequences what is often the case when the taxa are too distant. There are a great number of papers on alignment and here I want only to underline in the context of all said above that this first procedure of molecular analysis does not lack subjectivity and require an expert knowledge not less than in any other kind of research.

The other issues producing ambiguity of solutions in molecular phylogenetic studies are related to multiple substitutions in one site leading to high phylogenic noise. This issue quite corresponds to the homeoplasy in morphological characters. Specific issues to molecular data are bias in nucleotide frequencies and codon usage. These issues are well known and well described in literature; there are certain ways to deal with but one need to keep it in mind while using molecular data.

Beside methodical mistakes quite often one may come across the case when the analysis itself was carried out properly, the alignment, model of nucleotide substitution and algorithms of analysis are appropriate and the obtained tree is robust but interpretation is incorrect. Generally this is related to the simple fact that gene trees and organism trees are not the same. Wrong conclusions on phylogenetic relationships despite the correct data analysis more often happen when only one gene is analyzed. Results obtained from the analysis of mitochondrial genes should be treated particularly careful. As an example of such wrong interpretation I can refer to the own experience of working with a widely used molecular marker – cytochrome b. While analyzing the phylogeny of Asian mountain voles of the genus *Alticola* (Lebedev et al., 2007) we tried to take in account all possible methodical issues listed above and obtained quite robust tree with good statistical support, so that inferred phylogeny seemed to be reliable. The phylogenetic relationships thus recovered showed that the genus *Alticola* is paraphyletic. However the analysis of a number of nuclear genes carried on later convincingly indicates the monophyly of the genus (Bodrov, Abramson, 2011). The wrong interpretation of the results in the given case evidently was due to introgression of mitochondrial genes caused by past hybridization.

Alongside with phylogenies inferred from the use of single gene wrong ideas may be deduced from analysis based on incomplete taxa sampling.

In conclusion I would like to emphasize that “the danger of generating incorrect results is greater in computational molecular phylogenetics than in many other fields of science” (Hillis, Moritz, Mable, 1996) and phylogenetic analysis require thorough thought whereas quite often it viewed as a black box where one put the data and take the result.

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A FRACTAL SPATIOTEMPORAL STRUCTURE OF AN OPEN LIVING SYSTEM AND FRACTAL PROPERTIES OF DYNAMIC SYSTEMS ON COSMIC SCALES

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The experimental data described in papers [1–25] are theoretically analyzed to construct an adequate model for dynamics of an open nonequilibrium living system. In addition, we have attempted to provide a generalized description of the properties of living and nonliving matter. Relevant published data were used to demonstrate a fractal structure of the space in the vicinity of centrally gravitating bodies with satellites revolving around them along closed trajectories and serving as a kind of testers of the neighboring space. A local violation of its discontinuity is likely to be a necessary (yet not sufficient!) dynamic characteristic of the spatiotemporal continuum for self-organization of molecules into a living, i.e., self-replicating, system.

Introduction

Over 50 years ago, two Moscow microbiologists, V.A. Elin and V.O. Kalinenko, independently from one another discovered a paradoxical phenomenon, namely, the ability of organotrophic microbial *E. coli* cells after a certain pretreatment to reproduce in the saline solutions completely deprived of any organic substances. Independently of the composition of this saline solution (be it physiological solution or phosphate buffer) and the initial concentration of viable cells (10^3–10^5 cm^{-3}), all populations over 1–2 days of incubation at 37°C reached the same limit concentration of about 10^6 cm^{-3} and retained a long-term viability in this state without any access to organics. Results of these experiments were published in the journal *Mikrobiologiya* (Microbiology) [1, 2]. This phenomenon has not been explained in any manner acceptable for microbiologists, being regarded as an artifact, and was forgotten for years.

Thirty years ago, our research team by a lucky confluence of circumstances discovered an analogous phenomenon of reproduction of an organotrophic microorganism, *E. coli*, under even more stringent conditions, in tetradistilled water. These experiments are described in [3–7]. There we also formulated a biophysical model for this phenomenon. Additional experimental data on the evolutionary drift of the *number of viable cells* (hereinafter, NVC), cooperative effects, quasiperiodic variations of the mean NVC value in a sample, as well as relative variance and biorhythms in the microbial communities under extreme conditions of absolute substrate starvation, i.e., in a superpure distilled water, are briefed in [8]. Below, we describe the results of further studies into the properties of microbial populations in a substrate-free medium.

Conclusions

From the standpoint of the author, in addition to the standard physiologically necessary conditions for sustainable existence of life, namely, “normal” pressure, temperature, and humidity of environment and the absence of pathogenic physical and chemical factors, polarization of the physical vacuum is a basically important factor for self-organization of molecules into a self-replicating system [18, 19]. The consequence of this is a fractal, i.e., noninteger, space–time dimensionality, which entails nonlinearity of all molecular processes eventually giving rise to a spatiotemporal ordering of the molecular processes that had led to formation of self-replicating informational structures. Note that the noninteger, i.e., fractional, dimensionalities of both space and time separately also gave in sum an integer, an invariant of four!

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POSTER PRESENTATIONS

ABIOGENIC SELF-ASSEMBLAGE OF THE SIMPLEST ELEMENTS OF LIVING MATTER IN THE FRAMES OF HYDRATE AND QUATARON HYPOTHESES OF THE ORIGIN OF LIFE

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The problem of the origin of life on the Earth finally comes to the problem of abiogenic assemblage of the simplest elements of living matter – DNA and RNA molecules. Because probability of their casual self-assemblage is negligibly small, there is necessity of search of corresponding mechanisms of synthesis and concentration of biomolecules. Unfortunately, not any of great number of hypotheses of the origin of life put forward till now is capable to explain processes of abiogenic assemblage of complex molecules. Moreover, the majority of hypotheses try to disregard or ignore this central problem.

Two new hypotheses of the origin of life suggested recently open ways for solution of the considered problem. We mean the so-called hydrate [1] and quataron [2] hypotheses of the origin of the simplest elements of living matter.

According to the hydrate hypothesis the simplest elements of living matter - N-bases, riboses, DNA- and RNA-like molecules, as well as protocells arise from CH_4, nitrates and phosphates inside cellular structures of hydrate of methane. This hypothesis suggests the mechanism, by which nature could go to simultaneously create, in the closed volume, conditions for occurrence of great number of various DNA and RNA-like molecules.

The quataron hypothesis proceeds from the fact that places of accumulation and conservation of biogenic elements and subsequent assemblage of elements of living matter are special nano-clusters formed in super-saturated medium (clusters of "hidden" phase or quatarons). The most probable quataron-forming molecules in atmosphere are CH_4 and H_2O molecules. For some reasons in the initial variant of the quataron hypothesis the preference was given to water molecules. Probably, quatarons of water are capable to form fullerene-like structures with large enough internal cavities which radius makes from 0,3 to 0,6 nanometers depending on vapour super-saturation. In particular, for quatarons of $(H_2O)_{20}$ or $(H_2O)_{24}$, forming, in condensed condition, liquid water with density about 1 g/sm^3 the radius of the internal cavity is equal to 0,384 nanometers. In these cavities not only separate atoms and molecules, but also their whole groups can be disposed. The scheme of abiogenesis in the quataron hypothesis looks as follows:

Formation of quatarons in atmosphere - capture and conservation (in cavities of quatarons) of H, O, C, N and P atoms necessary for formation of nitrogenous bases, phosphatic groups, D-riboze etc. - condensation of quatarons with "guest" atoms, molecules (possibly with already formed functional groups) - interaction and aggregation of "guest" atoms and molecules, nitrogenous compounds in condensed water medium, - polymerization and formation of DNA and RNA molecules.

Thus, according to these hypotheses abiogenic assemblage of complex biomolecules and the origin of life are not casual processes, but a consequence of quite real physical and chemical processes. Both hypotheses demand presence of three-dimensional cavities (nano-reactors) which sizes coincide with the corresponding sizes of functional groups of component parts of DNA and RNA molecules. Processes of usual assemblage of molecules in that or other case, possibly, begin in atmosphere from the moment of formation of methane or water quatarons.

The comparative analysis of hydrate and quataron hypotheses of the origin of the simplest elements of living matter testifies to their deep generality and possible parallel realization. Both hypotheses allow to propose ways of abiogenic assemblage of DNA and RNA and thus to reveal new ways to disclosing the secrets of the origin of life. At least, both these hypotheses partially remove the problem of extremely small probability of self-assemblage of such complex biopolymers as DNA and RNA during casual interactions of separate elements. According to these hypotheses the process of self-assemblage because of preliminary self-organization ceases to be completely casual. This is already the assemblage not from separate chemical elements, but from ready "bricks" and "blocks" - functional groups. As a result the formation of molecules of DNA and RNA type obtains the characteristics similar to cluster growth of crystals.

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FLUID INCLUSION IN QUARTZ FROM THE ALIGUDARZ GRANITOIDS, NW IRAN

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Abstract: The Aligudarz granitoid Plutons have intruded into meta- sediments in the sanandaj – sirjan zone, north west of Aligudarz city (west Iran). Based on petrography and geochemistry, the Aligudarz granitoid have been classified into granite, granodiorite, pegmatite S–Type with the mineral assemblage of quartz, plagioclase, K – Feldspar, Biotite and moscovite. The intrusion has thermally metamorphosed the country rocks up To Albite – epidote hornfels fasies. Fluid inclusion study on quartz vein in Aligudarz granitoid sow Four Type of Fluid inclusions, 1- low salinity aqueous inclusion 2-high salinity inclusion 3- CO_2 – H_2O inclusion 4- carbonic inclusions. The density data of Fluids in Aligudarz granitoids indicates entrapment temperature of 580 To 636 °C at pressures of 3.9 to 5.1 bars. This data nearly coincides with the mineral P–T estimates. There are Partial melting processes during the formation of S–Type Aligudarz granitoids.

Keywords: Fluid inclusion, Aligudarz granitoids, salinity, S-Type

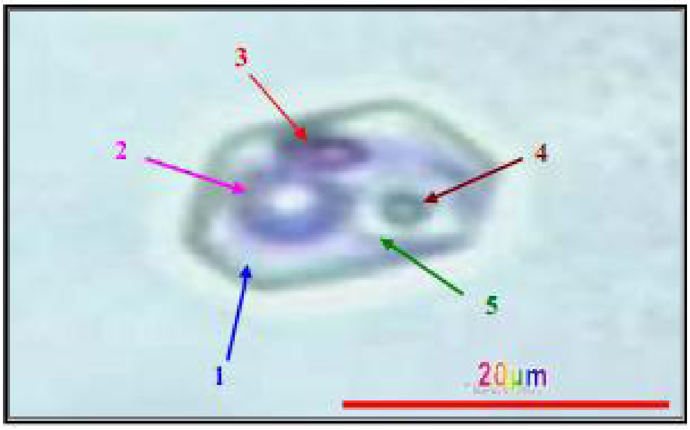

Figure 1: Fluid inclusion in Quartz vein in Aligurarz Granitoid (high salinity inclusions)

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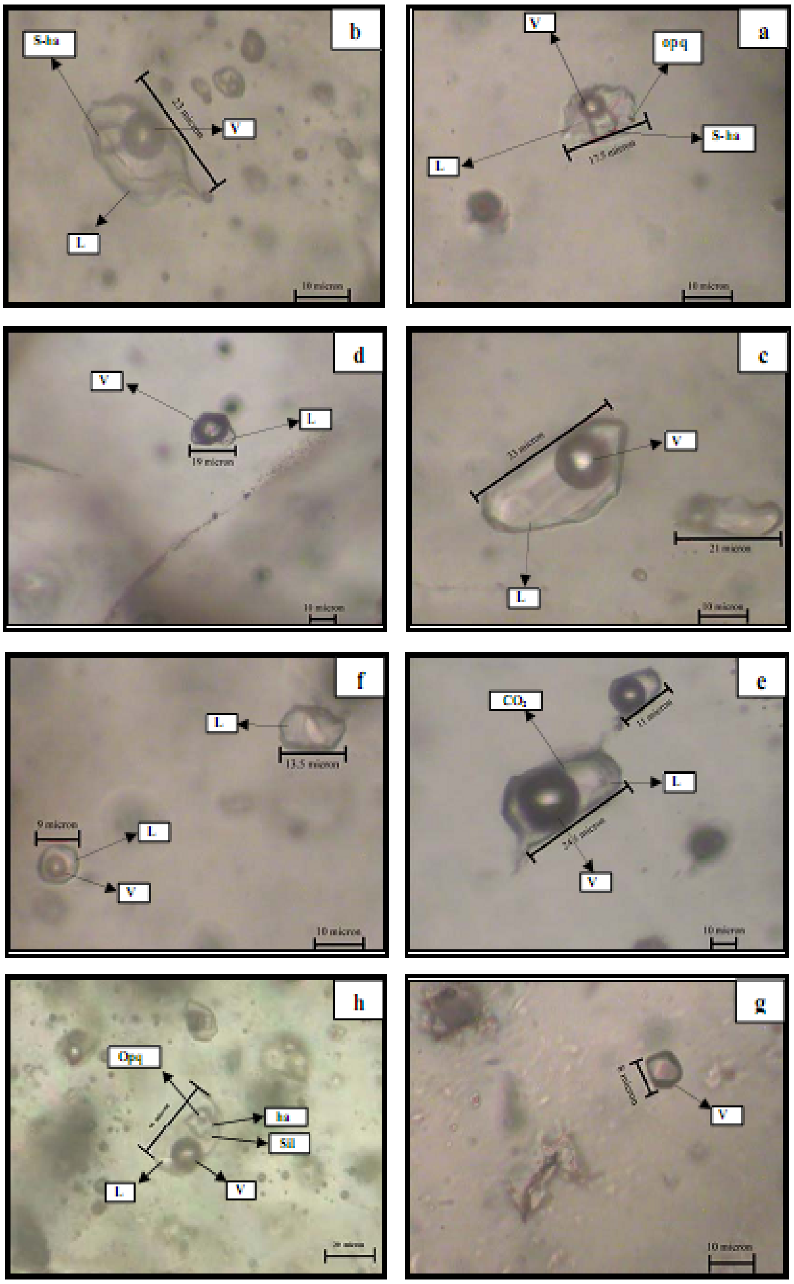

Figure 2: a, b: three-phase fluid inclusions (L+V+S); c: two-phase fluid inclusions (L+V), rich from liquid phase; d: two-phase fluid inclusions (L+V), rich from vapor phase; e: two-phase fluid inclusions (L+V), including two phase of the non-mixed vapor; f: liquid single phase of fluid inclusion (L) and two phases (L+V); g: gases single phase of fluid inclusion (V); h: multi-phase of fluid inclusion (L+V+ha+sil+opq)

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PALEOZOIC APOCALYPSE: WHAT CAUSES?

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On the Paleozoic-Mesozoic boundary, 251.0±0.4 Ma, there was the largest in history of the Earth mass extinction of organisms. The end-Permian mass extinction eliminated 96% of all marine species and had a significant impact on land species as well. Marine species biodiversity was reduced from ~250 thousand species to less than 10 thousand. What were the causes of this catastrophe, which has received the name a Paleozoic Apocalypse?

As the causes of biota extinction many factors are offered: disappearance of ecological niches during connection of continental plates in Pangaea; hypersalinity; an anoxia; increased CO_2; poisoning by H_2S; sea level lowering; transgressions; volcanism; warming and acid rains as a result of volcanism; warming owing to methane discharge from gas-hydrates; short-term cold episodes; impact events, i.e. collisions with large asteroids or a combination of these mechanisms. All these factors which have reduced a biodiversity are proved by paleontological, geological, geochemical, isotope, and other data. It is very important to note, that some of these factors are in hierarchical relations, but others affected independently, and in limited time interval.

On changes of systems of a terrestrial surface, including biosphere, the changes occurred in internal geospheres influenced. Connection of a biodiversity with tectonics, geoid evolution, mantle convection, and the shifts of the Earth core caused changes of geopolarity is supposed. Causal relationships were carried out through volcanism, fluctuations of a sea level, methane discharge from gas-hydrates, strengthening of ocean stratification, and an anoxia.

Correlation of extinctions with volcanic eruptions is precisely revealed. Temporary correlations between the largest eruptions of Siberian traps, and the extinction are tracked.

Eruptions caused «the volcanic winter» with a global cold episodes because of aerosol shielding of atmosphere, outflow of harmful gases and the acid rains. After the main basalt outflow «the volcanic summer» followed, detaining restoration of a biodiversity and strengthening stratification of ocean.

Decomposition of gas-hydrates conducted to outflow of huge amounts of CO_2 and to occurrence of very strong greenhouse effect. Fast global warming caused changes of environment harmful to biosphere: weakening of upwellings, stagnation of ocean, falling of bioproductivity. Influence of volcanism of the Siberian trap province was very powerful. All the listed factors developed rather slowly and could not cause fast biotic catastrophe. Fossils distribution in sections of China has shown that extinction occurred during 3 Ma, however the most intensive (in an interval less than 500 years) it was 251.4 Ma (Jin et al., 2000).

The trigger of sharp changes on a background of gradually developing harmful ecological conditions were, possibly, impacts of large asteroids as it was on Cretaceous/Paleogene boundary (Barash, 2008). Influence of impact events is proved only last years. Crater Bedout (diameter 180-200 km) is found near Australia (Becker et al., 2006). Crater Araguainha (40 km diameter) is found in Brazil (Lana, Marangoni, 2009). Crater Arganaty in Kazakhstan (315 m diameter) is proved. Some probable impact structures demanding additional researches are found. Possibly, the largest impact event in history of the Earth was impact event in Antarctica, on Wilkes Land (Von Frese et al. 2006). Geophysical methods reveal here a 500-kilometer crater which is settling under the East-Antarctic glacial sheet. Its probable age is 250 Ma. Consequences of asteroid impacts are similar to consequences of volcanism. They caused global distribution of a dust, downturn of light exposure, change of temperature, acid rains, fires, etc.

The analysis of the materials available leads to one of the most important inferences that all the terrestrial processes, the biospheric included, develop in close and continuous relation with the extraterrestrial processes that occur beyond the solar system in the space to which our planet belongs (crossing by the Sun of spiral galactic sleeves, its fluctuations perpendicularly to galactic plane or others).

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BIOCHEMICAL REACTION OF EARLY PALEOZOIC BRACHIOPODS ON GEOBIOLOGYCAL EVENTS IN THE NORTH URALS PALEOBASIN

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In the European Northeast brachiopods are one of the most widespread and well studied faunal groups, which continuously occur through in various facial sediments of Early Paleozoic [1]. In connection with brachiopods served as a basis for defining the biochemical response of these organisms to external environmental changes and compositional changes of amino acids in brachiopod shells and host rocks through the Late Ordovician, Silurian, and Early Devonian.

The rock samples with brachiopod shells were collected from Silurian, Ordovician, and Devonian deposits of the North Urals, Subpolar Urals and Chernyshev Uplift. The samples are characterized by well defined stratigraphic and facies positions.

The amino acid contents are highly variable in shells (0.04 to 0.19 mg/g of the shell) and practically stable in carbonate rocks (0.03– 0.06 mg/g of the rock). In samples significant fluctuations of individual amino acid composition are observed that is quite characteristic for Paleozoic shells [2, 3]. Among individual amino acids are usually dominate glycine, serine, glutamic acid and leucine, while threonine, proline, and valine often are absent. The samples also contain D-alloisoleucine, which represents an amino acid forming under high temperatures.

The biochemical study of brachiopod shells reveals changes in amino acid concentrations: increase across the Ordovician–Silurian boundary (from 40 μg/g in the Ordovician to 50–80 μg/g in the early Llandovery (Rhuddanian)); decrease to 40 μg/g at the end of late Llandovery; abrupt growth to 100–190 μg/g in the Wenlock; reduction of values to 40 μg/g in the Ludlov and Pridoli; and increase up to 80 μg/g in the Early Devonian. The maximum of amino acids concentration exceeding 100 μg/g is fixed in samples selected directly above a level of paleontologically proved Llandoveri–Wenlock boundary [4].

As all the investigated samples are characterized by practically the same catagenetic heating level, differences in the concentrations of amino acids in brachiopod shells from a single stratigraphic interval may be explained by their different burial conditions. For example, the protein component in shells from the Wenlock and Early Devonian appeared to be practically unchanged at the initial stages of diagenetic transformation; only subsequent catagenetic heating resulted in destruction of the protein matrix. This assumption is consistent with the results derived from the study of *Spirinella, Protatrypa* and *Lenatoechia* burials, which include well preserved shell accumulations of different sizes and age stages (from young to old) with well-preserved ornamentation, thin spines at the surface (*Spirinella*), and elements of the inner structure, that is characteristic of life-time brachiopod burials or their burial in the same biotope during storms.

It was established, that amino acid contents in brachiopod shells substantially depend on primary conditions of sediments accumulation and facial confinement.

Comparing with the first results on amino acids with paleontological data [1, 4, 5] it was established, that the maximal amino acid concentrations in brachiopod shells are dated in periods of ecosystem reorganizations coincident with critical geological and biotic events in the history North Urals paleobasin: Ordovician-Silurian (Hirnantian Event), Llandoveri–Wenlock (Ireviken Event), Silurian-Devonian (Klonk Event).

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EDIACARAN SOFT-BODIED ORGANISMS AND MACROPHYTES: TWO SIDES OF ONE COIN?

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There are two fundamentally different types of Proterozoic macrofossil preservation: casts (molds) usually attributed to soft-bodied organisms and carbonaceous compressions interpreted as macrophytes. That some of the casts (molds) of soft-bodied organisms have morphological analogues among carbonaceous compressions has long been appreciated (Zhu et al., 2008), but the full scale of this phenomenon is revealed in a Konservat Fossil Lagerstätte discovered in the Arctic Siberia (Grazhdankin et at., 2008). The Upper Vendian Khatyspyt Formation cropping out along the Khorbusuonka River of the Olenek Uplift (northeast of the Siberian Platform) is characterized by two types of macrofossil assemblages: (1) casts and molds of soft-bodied organisms (about 600 specimens) and (2) carbonaceous compressions of macrophytes (about 250 specimens). The soft-bodied organisms are represented by rangeomorphs and frondomorphs, as well as microbial colonies, however the frondomorphs and microbial colonies can also be preserved as carbonaceous compressions, whereas the rangeomorphs are restricted to fossil assemblages with moldic preservation. Preservation of certain soft-bodied organisms in a style which is typical for macroscopic algae suggests that at least in frondomorphs their macrophyte nature cannot be entirely excluded. This has important implications for interpretation of the Avalon biota of Newfoundland, the oldest fossil assemblage of Ediacaran soft-bodied organisms, which is also represented by frondomorphs and rangeomorphs. The Avalon biota is interpreted as deep-sea communities that inhabited continental slope below the photic zone (Clapham et al., 2003); however, if frondomorphs are just seaweeds, then the Avalon biota is irrelevant to understanding the metazoan evolution. In any case, a possibility should not be excluded that casts, molds and carbonaceous compressions could represent different modes of preservation of the same organism, not necessarily a metazoan.

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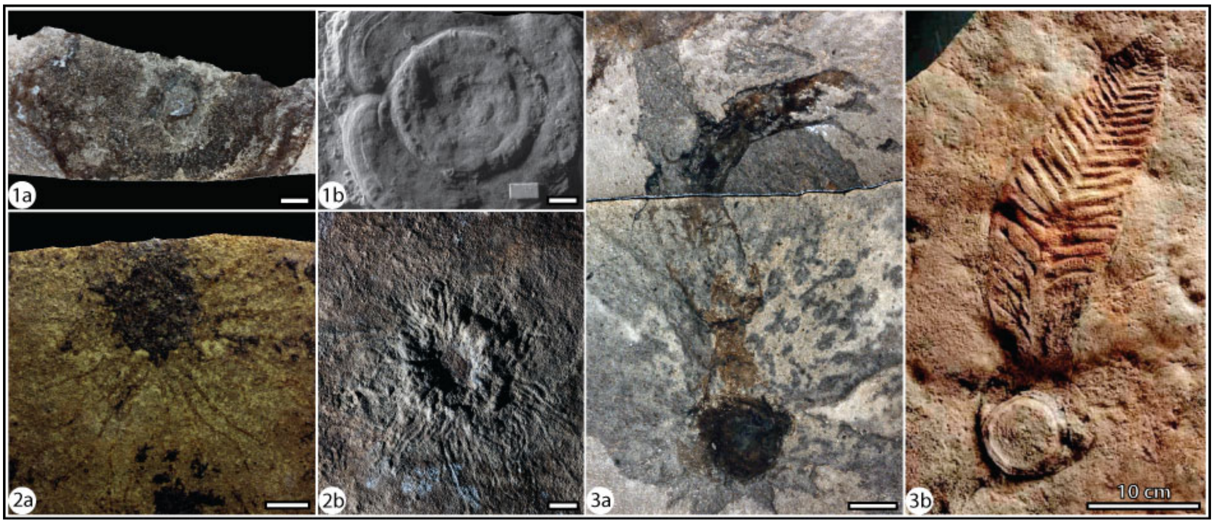

Two types of preservation of some soft-bodied organisms (1) Ediacaria, (2) Mawsonites and (3): Charniodiscus: a – preservation as carbonaceous compressions; b – preservation as casts and moulds. Scale bar 10 mm, except 3b.

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SOFTWARE MODELLER OF EVOLUTION PROCESSES

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Modeling of evolution processes of substance generates the problem of solving high dimension system of ordinary differential equations (ODE). This problem is typical for tasks of abiogenous synthesis of prebiotic compound and for tasks of modeling of biological hierarchical systems.

Modeling of chemical evolution of substance includes numerical integration of large system of time dependent chemical rate ordinary differential equations (ODE).

ChemPAK software package was created for solving these problems. Due to the rapid growth of the computing power, as well as the rapid development of computational mathematics and algorithms, a whole series of articles and software realizations appears in various fields of science. The areas of application of approximate formulas for the simulation of various processes are rapidly developing. Objects are approximated as a solution for equations and systems of partial differential equations. The usage of approximated formulas can be used accurately for guarantee the quality of the numerical results. The problem of computational linear algebra operation of calculating the scalar multiplication is a base for other operations. Therefore, all operations of computational linear algebra is necessary to be assessed for the guaranteed accuracy of calculations. It is also worth noting that the many modern libraries did not assess for the accuracy of calculations. For the summation of a large number of elements beyond the trivial sum has developed a number of algorithms, including the assessment guarantee the accuracy of the result. New version of ChemPAK software package will be presented with high accuracy and GPU optimized ODE solvers. This technology gives possibility to solve evolution model task with more than 1000 differential equations in a seconds.

PP-7

CHROMATO-MASS-SPECTROMETRIC ANALYSIS OF ORGANICS WHICH ARE PRODUCED DURING SIMULATED HYPERVEVOCITY IMPACTS ON TITAN

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Prebiotic synthesis of organic compounds at natural conditions is interesting for the problem of origin of life. The possibility of prebiotic synthesis and complexity of its products is defined by large number of physicochemical conditions in the system such as density and composition of atmosphere, presence of water, source of free energy etc.

The formation of organic compounds (OC) was studied by simulation of hypervelocity impact chemistry in the atmosphere, which simulates qualitative composition of the atmosphere of Titan. The impact vaporization was simulated by evaporation of peridotite sample by a specific laser pulse with total energy of about 600 J in gaseous medium under atmospheric pressure. The gaseous medium consists of clean methane or nitrogen and mixtures of methane with nitrogen of the volume ratios 1:1 and 1:9. Experiments were carried out in clean hermetic camera with the optical window of quartz glass.

Formation of significant number of volatile and high-molecular compounds (kerogens) was measured during hypervelocity impact simulation experiments in reducing atmosphere. OC in this case were mainly presented by the polycyclic aromatic hydrocarbons (PAH). Oxygen-containing OC were also present: carbonyl compounds and the unsaturated fatty acids.

PAH and kerogens are the most stable compounds at high temperature in the presence of various forms of chemically active oxygen, which is produced in impact vapor plums due to dissociation of petrogenic oxides. With decrease of the reducing nature of the atmosphere the variety and the amount of OC substantially decreases. It was impossible to reveal detectable quantities of OC (>1 ppm) in experiments in pure nitrogen atmosphere.

It is possible to expect formation of some important prebiotic OC at Titan's conditions due to hypervelocity impacts.

THE EARLIEST STEPS OF ORGANISMS SKELETONIZATION

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One of the most intriguing mysteries of biota evolution on the Earth is the initial origin of mineralized skeleton in the animal kingdom. It is impossible to underestimate the huge significance of hard skeletons for the morphological evolution of phyla and classes, as well as for changes in the entire biota and environment. Since Ch. Darwin times this explosive phenomena was attributed to the Precambrian-Cambrian boundary, but nowadays it is obvious that skeletonization was a more prolonged process, embracing several epochs and periods (Rozanov, 1986; McMenamin, McMenamin, 1990; Rozanov, Zhuravlev, 1992). Basing on the study of earliest skelatal fossils we can outline five major steps of this process through the Late Proterozoic – Early Cambrian time.

The first step of skeletonization occurred in the Late Riphean marked by the appearance of tentatively “annelid” genera *Sabellidites* and *Parmia* with organic skeletons (Gnilovskaya, 1998; Gnilovskaya et al., 2000), *Protoarenicola* with carbonate (?) skeleton (Lin et al., 2008). According to biomarker data (McChaffrey et al., 1994), sponges with organic skeleton are also known from the pre-Riphean strata (1.8 Ga).

The second step in skeletonization occurred in the Early Vendian, owing to presence of tubular problematic fossil *Cloudina* and cnidarian-like *Namacalathus* with carbonate skeletons, as well as agglutinate foraminiferan *Platysolenites* (Kontorovich et al., 2008). Riphean sponges with organic skeleton in the Vendian were changed by the sponges with organic, carbonate and siliceous skeletons.

The third step of skeletal mineralization, Latest Precambrian, i.e. Nemakit-Daldynian, is represented by the appearance of anabaritids (*Anabarites*, *Cambrotubulus*), hyoliths, mollusks (*Halkieria, Siphogonuchites, Purella, Latouchella, Anabarella*) and chancelloriids with carbonate skeletons (Khomentovsky, Karlova, 1993; Parkhaev, 2008). Supposed chaetognaths (*Protohertzina*) (Demidenko, 2006) and phosphate problematic tubular fossils (hyolithelmintes) also originated in the Nemakit-Daldynian. Therefore all chemical types of animal skeletons were already present in the Nemakit-Daldynian.

The fourth most significant step of skeletonization occurs in the earliest Cambrian Tommotian Stage. One can observe the mass appearance of numerous and diverse groups of skeletal animals. Archaeocyaths with carbonate cups, brachiopods with carbonate and phosphate shells, phosphate problematic tommotiids, radiolarians with siliceous skeleton have appeared along with already existed various pre-Tommotian groups.

The fifth step in skeletonization starts in the Early Atdabanian and marked by ‘arthropodization’ – origin and diversification of arthropods with organic and carbonate carapaces (trilobites, phyllocarids (*Isoxys*), anomalocarids, bradoriids, etc.) and lobopods with phosphatic skeleton (*Microdictyon*). In addition, during the Middle - Upper Atdabanian time the first echinoderms with the carbonate skeleton appeared.

Thus we can trace five main steps in skeletal mineralization lasting from the Late Riphean to the Early Cambrian. By the end of this time all main compositional types of animal skeletons have been formed, and further evolution went on in the structural way, but not in the compositional. Still we are far from precise determination of actual causes that triggered the process of skeletonization, guessing only that it was a complicated combination of a variety of biotic and abiotic factors. However, the study of ancient skeletal organisms can shed light on this mysterious phenomena of the biota evolution.

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MODELING THE CONFIGURATIONS OF WATER MOLECULES IN CLATHRATE HYDRATE CRYSTALS

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The various clathrate hydrates represent the class of solid supramolecular host–guest compounds. Their crystal structures are known as polyhedral cages built of water molecules connected with one another by strong hydrogen bonds while the polyhedral cavities are occupied by guest organic molecules, contacting with the host molecules by weak van der Waals forces. The methane clathrate hydrates occur in nature in huge amounts. The regions of their occurrence on our planet are sea floor deposits and permafrost zones grounds. In life sciences, the interest to the clathrate hydrates is connected with a hypothesis of life origin [1], which proposes clathrate hydrate water matrix to play the key role in self-assembling of primary DNA molecules from nucleotide units.

The experimentally observed structures of gas hydrates of cubic (-I and -II) and hexagonal type belong to high symmetry groups (*Pn*3*m*, *Fd*3*m* and *P*6/*mmm*, respectively). This symmetry, however, characterizes the structure of oxygen cage but not the arrangement of the hydrogen atoms, whose actual positions are smeared by crystal disorder.

In this work, we report global lattice energy minimization results of clathrate hydrate crystals. Interactions of water molecules were modeled with the TIP4P potential set [2], which involves a 6-12 LJ atom-atom potential, to describe van der Waals interactions of oxygen atoms, and electrostatic point charges accounting for the Coulomb interactions of the polar molecules. The water and guest methane molecules were treated as rigid bodies [3]. The starting models for minimization were built on lattice constants and oxygen atoms positions taken from experiment, while the staring sets of Euler angles were taken at random from the list of 1080 matrices corresponding to a nearly uniform distribution of molecular rotations in the three-dimensional space. For the three structure types, the calculations were performed in the frameworks of space group *P*1, assuming no crystal symmetry except lattice translations, and centrosymmetric *P*-1 group. All in all ten thousands of starting models have been sampled with this procedure for each of the three types of clathrate hydrate structures.

The principal results and conclusions of this work are as follows:

- Removing guest molecules from cavities does not collapse polyhedral water structure: it stays stable being a local energy minimum in the global configuration space. This is an argument to regard such a predicted guest-free host structure as a 'polyhedral ice' polymorph; its density is only about 10% less than the density of hexagonal ice.
- The lowest-energy structures demonstrate H-bond networks perfectly complementing the Bernal - Fowler 'ice rules' of with standard H-bond geometric parameters. The most stable polyhedral ice structure of the cubic-II type was found centrosymmetric and face centered (i.e., space group *F*-1), with energy E = –56.15 kJ/mol. It is 0.04 and 0.33 kJ/mol more stable than the lowest-energy *P*-1 polyhedral ice structures of the cubic-I and hexagonal-I types, respectively. For comparison, the hexagonal ice polymorph, as calculated by optimization of the Bernal–Fowler model [4], is of E= –56.99 kJ/mol, Though, we have to admit that the number of *P*1 starting models sampled by us is small as compared to the total number of proton configurations, amounting, e.g., for cubic-I to as much as 17 millions [5].
- In addition, the global search detects numerous less stable structures as local energy minima. They are characterized by the presence of one or more local 'defects', where significant deviations from normal hydrogen bond geometry take place resulting in local violation of the ice rules. Inspecting still less stable structures reveals one or more hydrogen bonds broken, thus opening 'windows' between the adjacent cavities.
- We conclude that the ability of water molecules for self-assembling into the polyhedral structures stems from the fine peculiarities of molecular structure and the intermolecular potential of the water molecule rather than those of guest one.

Generally, this work demonstrates clearly the prospects of our crystal-structure prediction technique [3] as an instrument to help understand poorly resolved experimental structural data, such as those where crystal disorder is inevitably present. Moreover, it gives a possibility to compare different experimental structural observations on theoretical grounds and look further beyond the experiment to predict yet undiscovered phases.

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PP-10

FUNGAL-LIKE ELEMENTS IN THE CONSTRUCTION OF THE RIPHEAN UNICELLULAR MICROFOSSILS

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Precambrian microfossils are useful in comparative studies of such fundamental aspects as the transition from unicellular to multicellular organization. The specific population of the Riphean unicellular organisms has been described from ~1Gyr sediments (Lakhanda Group, Uchur-Maya region, SE Siberia). They have been recorded in shales and consistently associated with water-deposited sediments. Unicells having a hollow shell of highly varied shape (spherical, ellipsoidal, elongate or sometimes polygonal) are composed of an organic substance and show net-like distribution.

A considerable number of Precambrian genera remained of undetermined affinity and genera defined on morphology only, without implication as to relationships, it is undesirable that they should be classed into the Linnaean hierarchy of orders and families. It is clearly preferable that any classification, adopted should give no false impression of any natural relationship and should facilitate the easy transfer away of genera when their affinities came to be determined. The lakhandinian microfossils were interpreted as probable yeasts that have evidence in growth habit, general morphology, mode of reproduction commonly can be discerned features that provide a basis for comparison of extant and fossil taxa. Riphean unicells display the coincidence of their morphology, the mode of typical multilateral budding of Saccharomyces and give additional evidence of the very early existence of such biological organization. These organic-walled fossils have been described as Eosaccharomyces ramosus Herm. (Hermann, 1979). Precambrian unicellular organisms extremely numerous and show innovations in biologic organization involved in the evolutionary transition from a single cell to multicellular pseudo tissue-like microcolonies.

Adjacent or loosely connected cells in these colonies tend to be similar texture and color, but differ in their diameter and shape. The connection between adjacent cells in colonies is usually with indication of cytoplasmic connection. Within an array fossils are equidimensional, but more often with one of the cells two to three times longer than its neighbor and resemble sack-like body called an ascus. There are some spheroidal structures that are much darker (probably thicker walled). The occurrences above mentioned cells suggest the presence of reproductive structures of microfossils.

Unicellular organisms have an entirely distinct habit and mode of the formation of numerous multicellular branching colonies that have been organized into asymmetrical, sectorial-type clusters with different number of budding or divided unicells.

Fungi are protists by far the most metabolically diverse eukaryotes that can preserve some diagnostic features of life cycle and morphology. Fossil records give an opportunity to suggest Ascomycota radiation events in the Proterozoic era.

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PP-11

COSMIC PERIODICITY IN PHANEROZOIC GEOLOGY

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There is cyclisity in many processes, such as the changes in mainlands' structure, variation in biodiversity of species, galaxy influence, impacts of cosmic bodies. The problem of an establishment of the cyclicity and correlation of all those processes discovering has been performed for 50 years.

In the present work we search for interrelation of events in biosphere and geospheres of the Earth from comparison of the data on mass extinctions and impacts and data on geological activity for the same period (Phanerozoic). Phanerozoic history contains all extinction events of the “Big Five” (major extinction events by Jack Sepkoski and David M. Raup) — End- Cretaceous (65.5 Ma), Late Devonian (205 Ma), End-Permian (251 Ma), End-Triassic (360-375 Ma), and End- Ordovician (440-450 Ma). In addition, we examine data on Phanerozoic climate change, which kept data on the glacial periods. There are four major periods called glacial periods with lowest average temperature on the Earth defined by ^{18}O parts per thousand.

The results of spectral, wavelet and correlation analysis of data series representing those processes are shown in the report. The conclusion is made that most of them are cyclic, some of the periods are present in all the processes. The galactic causes of the cycles with duration in tens and hundreds millions years are discussed.

PP-12

GTF2I DOMAIN: STRUCTURE, EVOLUTION AND FUNCTION

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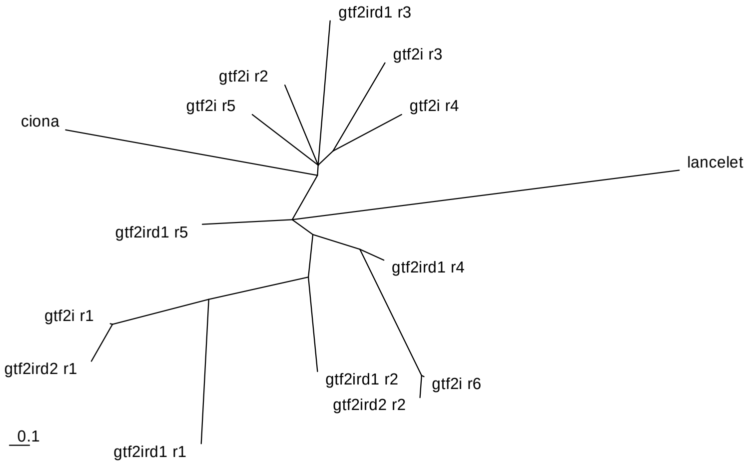
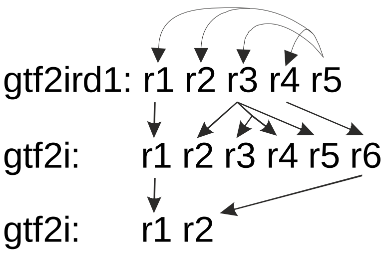
The GTF2I gene family consists of *gtf2i*, *gtf2ird1* and *gtf2ird2* genes encoding transcriptional factors and the first two of them involved in Williams-Beuren syndrome if mutated [1]. The main characteristic of this gene family is the presence of several so called GTF2I repeats. There are 5 such repeats (R) in *GTF2IRD1*, 6 in *GTF2I* and 2 in *GTF2IRD2*. Our aim was to study the molecular evolution of these repeats.

We collected the GTF2I repeats from about 20 chordate species from *Branchiostoma floridae* to *Homo sapiens* using the information about gtf2i-like genes from databases and retrieving information from genomes, assemblies and EST collections. Then we reconstructed the phylogenetic networks using Bayesian, maximum likelihood and distance methods, and found that R5 (*gtf2ird1*) could represents most probable ancestor of all GTF2I repeats.





We also found that amplification of *gtf2i* gene repeats (R2, R5, ancestor of R3 and R4) and duplication of *gtf2ird1* gene repeats (R4, ancestor of R2 and R1) occurred before Gnathostomata origin. Based on our hierarchical classification of GTF2I repeats and recent research [2] we hypothesize that GTF2I gene family have raised from the two genome duplication events early in vertebrate evolution.

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Comparison of molecular evolution model of the GTF2I family with real data using method implemented in SAMEM [3] discovered several types of statistically rare aminoacids replacements ($p \leq 0.01$) which characterized by greatest physicochemical changes. These replacements related with: 1) the divergence between *gtf2ird1* R4 and *gtf2i* R6, 2) the origin of *gtf2ird1* R1 and R2 ancestor, and 3) the origin of *gtf2ird1* R1 and *gtf2i* R1 ancestor. We used the program package PDB3DScan for structural alignment to find the differences in the 3D structure of GTF2I repeats in *gtf2i*, *gtf2ird1* and *gtf2ird2* genes and identified that those statistically rare substitution mostly situated in loop regions or in the beginning or in the end of helices. We showed that the helix in structure of the first repeat of *gtf2i, gtf2ird1, gtf2ird2* is much less conservative then in the other repeats. We also found the unique mutational pattern for each GTF2I repeat that could be caused by their functional specialization (for example, DNA-binding [4]).

This work was supported by RFBR grant No. 09-04-01641-a and Biosphere Origin and Evolution program.

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DEEP INSIDE INTO VERTEBRATES AND INVERTEBRATES MACROEVOLUTION: THE MOLECULAR EVOLUTION MODES OF STRICT ORTHOLOGOUS PROTEIN SEQUENCES

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The molecular evolution modes of 752 orthologous protein groups (OPGs) of vertebrates and of 1736 OPGs of invertebrates were analyzed. In our analysis the OPGs were taken from MetaPhOrs database [1]. The OPGs containing at least one strictly confirmed orthologous sequence without ambiguous characters from each of 20 vertebrate species groups and 9 invertebrate species groups were taken into analysis (Figure 1). Cnidaria and Tunicata were served as outgroup taxa. The ancestral protein reconstruction in each internal tree node of OPG was made using PAML 4 CODEML program [2] (marginal reconstruction) on the basis of the known tree topology (Figure 1) and amino acid replacement matrices calculated by MODELESTIMATOR [3] program. These ancestral sequences were used to calculate the number of observed amino acid substitutions. For each amino acid replacement type we compared the observed number of changes with expected ones under the assumption of a stationary Markov process of protein evolution. Expected replacement numbers were calculated using 1000 computer simulations of OPG molecular evolution by the INDELible program [4], taking into account the peculiarities of the investigated OPGs. Comparison of expected and observed numbers of each replacement type was performed using permutation tests (10^5 permutations). We count the number of random samples, M, in which the frequency of expected changes of a certain type higher than the frequency of observed ones. Thus, the value $M/10^5$ is the occurrence probability, p, of a certain amino acid replacement type observed by chance.

The analysis of R value, the proportion (%) of OPGs with atypical amino acid replacements ($p \leq 0.01$), showed that internal tree branches of vertebrate tree with $R \geq 20\%$ strictly correspond to aromorphoses in the vertebrate evolution (Figure 1): 1) the full genome duplications in early stages of vertebrate evolution and actynopterigian fish evolution, 2) the adaptation to terrestrial environments, 3) the origin of Amniota, 4) the divergence of primitive mammals and placental mammals. It is of big interest that the molecular evolution of insects and nematodes were characterized by significant increase in R

value in comparison with its mean value for vertebrates (Figure 1). The absolute maximum of *R* value is typical for nematodes. It was shown that the divergence of Insecta and Diptera accompanied by increasing of *R* (Figure 1) may be due to the emergence of insects-angiosperms ecosystems and to the formation of the characteristic Diptera morphology. This study we also conducted the functional comparison of OPGs containing atypical amino acid replacements that allowed us to uncover various features of gene networks molecular evolution on each internal branches of vertebrate and invertebrate trees (Figure 1).

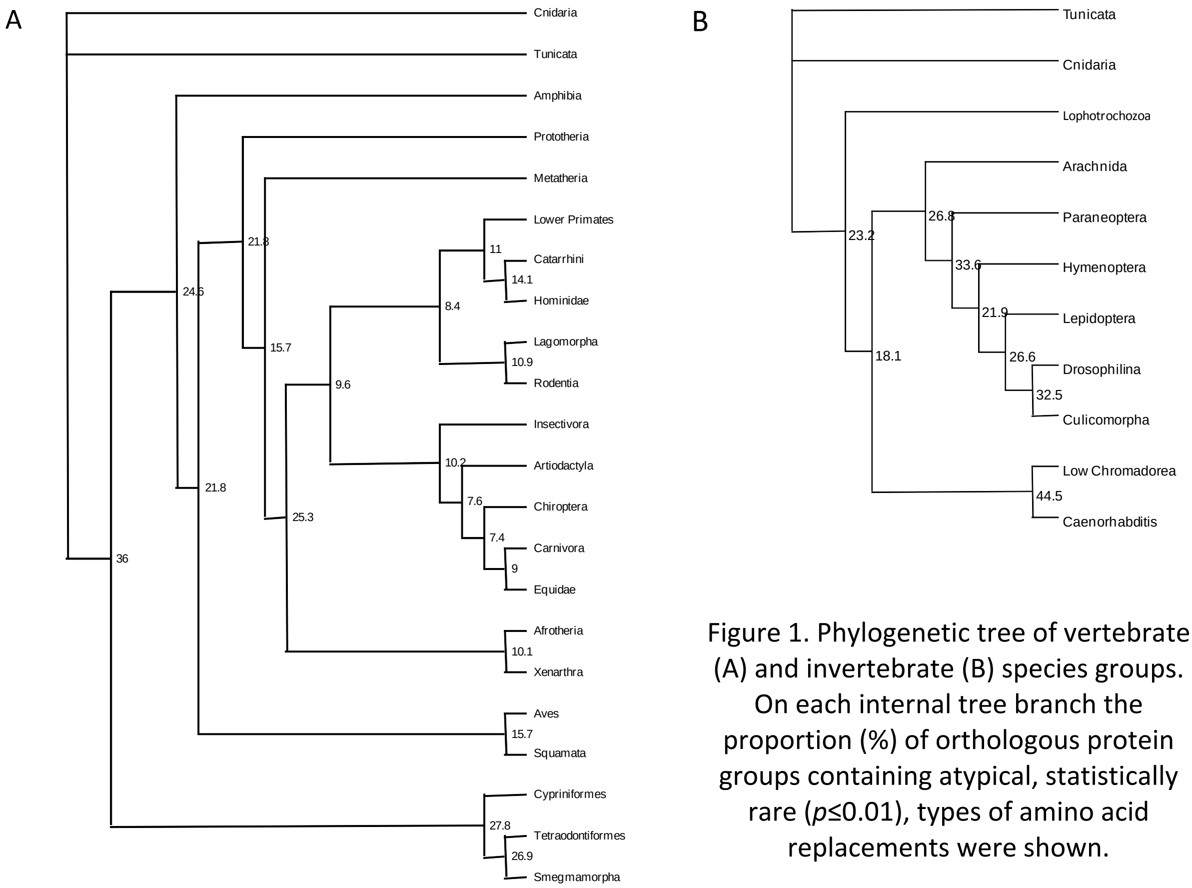

Figure 1. Phylogenetic tree of vertebrate (A) and invertebrate (B) species groups. On each internal tree branch the proportion (%) of orthologous protein groups containing atypical, statistically rare ($p \le 0.01$), types of amino acid replacements were shown.

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GENERATION OF MODERN MINERAL-BIOLOGICAL SYSTEMS UNDER CONTINENTAL CONDITIONS

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In contrast to the biostagnated systems developed in water basins, the mineral-biological systems localized on the land are more irregular, show a greater degree of fortuity, not stable exchange of matters inside the system and with the environment. These properties require specific methods of investigations. In particular, the point-counter microanalysis will provide more reliable information about chemical processes than a classic analysis of media.

The paper presents the results of research of interaction of epilithic and epigenous lichens with ore and ore-free rocks of the scheelite-sulfide deposit dumps. Fragments of the oxidized ore are populated with bushy lichen *Stereocaulon sp.* and crustose lichen, ore-free area being ignored. Study of the samples, using the electron scanning microscope EVO-50 XVP with spraying of samples, revealed *Stereocaulon sp.* growing on hypergene ferruginous crusts and films. More precisely, algae are localized exclusively on crusts, and fungus hyphae occur on crusts and under them and penetrate between mineral fragments. Microanalysis showed that in addition to Fe, S these crusts contain carbon and W. Other admixture elements vary depending on the primary ore composition.

On the ore-free dumps, mainly on the granodiorite fragments, another genus of lichen – *Cladonia sp., Cladonia gracilis (L.)Wild)* – grows. Here fine fragments of rocks are entangled with fungus hyphae, and algae appear above this boundary layer. In the podetium body there were found the rounded ferruginous inclusions of 1.5-2 mkm in size. In their morphology they look like pyrite framboids [1]. This can be suggested to be is a result of vital activity of thiobacteria, reworking the sulfides [2].

Minerals, intergrown with lichens, are diverse: quartz, feldspars, pyroxenes, scheelite, and rarely sulfides. Intergrowth is very firm at a macro- and microlevel. In the mineral spectra, carbon is present, and their composition stoichiometry is usually destroyed. This indicates the chemical exchange, including a probable treatment of the mineral base by the biota ferments. The latter provide the firm “cementation”.

So the epilithic lichens use a rock not only as a support for settling. A biomineral system is formed where the chemical interaction of minerals and lichen take place: enrichment of ferruginous films with carbon and thalli with elements of Fe, S, and Si, and in certain cases with Mg, Al, K, and Mn. Heavy metals (W, As, Zr, Ag, Ir) are not used by a growing organism. They are toxic for it, so scheelite, silver, and some sulfides are preserved even through the treatment of them with ferments, and under appropriate conditions they can be accumulated and redeposited to some degree by the lichens. The reported interactions of minerals and lichens characterize the generation of isolated elements of future biogeocoenosis with the individual thus far chemical processes.

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ADSORPTION OF RIBOSE NUCLEOTIDES ON MANGANESE OXIDES WITH VARIED Mn/O RATIO: IMPLICATION IN CHEMICAL EVOLUTION

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Transition metals are significantly more important as catalyst in the formation of biopolymers during the course of chemical evolution and origin of life. (Arora and Kamaluddin, 2007; Arora et al. 2007; Arora and Kamaluddin 2009). Manganese exists in different oxidation states under different environmental conditions with respect to redox potential. Various forms of manganese oxides, namely, Manganosite (MnO), Bixbyite (Mn_2O_3), Hausmannite (Mn_3O_4) and Pyrolusite (MnO_2) were synthesized and their role in chemical evolution studied. Adsorption studies of ribose nucleotides, namely, 5'-AMP, 5'-GMP, 5'-CMP, and 5'-UMP on the above manganese oxides at neutral pH. Results of our studies suggest that highest binding if ribonucleotides occurred with Manganosite (MnO) as compared to other manganese oxides. Oxides of Manganese having a lower Mn-O ratio showing higher binding affinity towards the ribonucleotides implies indirectly that such oxides may have provided their surface onto which biomonomers could have concentrated through selective adsorption; thereby stressing upon the concept that activities of chemical evolution were pronounced when the redox potential of the earth atmosphere was low and the atmosphere was less oxidized. Purine nucleotides were adsorbed more in comparison to that of the pyrimidines nucleotides under neutral conditions. Adsorption data obtained followed Langmuir adsorption isotherm, X_m and K_L values were calculated. The nature of the interaction and mechanism is elucidated by the infrared spectral studies conducted on the metal-oxide and ribonucleotide-metal-oxide adducts.

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PP-16

FROM PRIMARY DNAs TO CELLS: LIFE ORIGINATION HYDRATE HYPOTHESIS (LOH-HYPOTHESIS)

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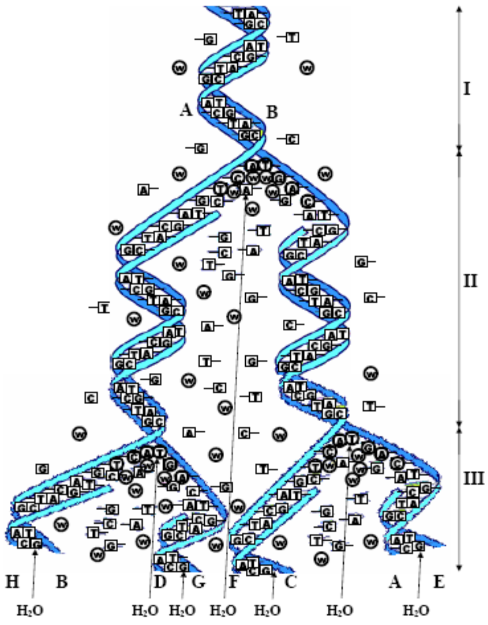
1. Introduction

We believe that the DNA origination and replication is governed by a physicochemical process of the same nature, namely, by the formation–destruction of the honeycomb hydrate structures around each N-basis. Cells are no more than the chambers that protect DNAs from the rivalry for the nutrients and space. The main differences between DNAs origination and replication consist in the occurrence, during replication, of inoculating DNAs in each cell, in the specificity of the nutrient soup composition, and in somewhat enhanced temperature, which is, however, so low that it doesn't allow disruption of the thermodynamically-caused sequence of chemical reactions; and the main similarities between these processes consist in the disutility of any agitation, in the occurrence of carbon, quinquivalent nitrogen, and quinquivalent phosphorous mixture in the soup composition, and in a rather low temperature.

2. From primary DNSs to replicating cells

According to the LOH-hypothesis [1–8], the N-bases, riboses, nucleozides, nucleotides (living matter simplest elements (LMSEs)) and also DNA- and RNA-like molecules formed within the CH_4-hydrate structural cavities. Then, as H_2O, NO_3^-, and PO_4^{3-} diffused into the system, the structure liquidized and transformed into a structured soup (super-cytoplasm) [2, 8], in which the simplest living organisms began the long history of their development and expansion over the world. In the super-cytoplasm, all the substances, necessary for the existence and development of the primary DNA- and RNA-like molecules, and amino-acids, could be synthesized on the basis of CH_4 and of NO_3^-, and PO_4^{3-} that diffused from the environment [1, 2, 8]. Nucleic acids were shown to self-replicate [9–12]; we proposed a possible mechanism of this process. Under appropriate conditions, these processes led to an increase in the concentrations of nucleic acids and organophosphorous substances within the super-cytoplasm. Increasing in their concentrations to a certain critical level led to precipitation of phosphor-containing membranes around DNAs with origination of protocells. Thus, in addition to the super-cytoplasm, intracellular cytoplasm appeared. Ever since, DNAs developed and replicated inside the cells and the cells began to break down similarly to the present ones. This assumed mechanism is detailed in [2, 8].

According to the LOH-hypothesis, living matter originated repeatedly. Within any one localization, a multitude of different but similar DNA- and RNA-like molecules and proto-cells originated simultaneously, and, in different localizations, multitudes of other but similar DNA- and RNA-like molecules originated in different time periods. The lengths and degrees of perfection of the DNA-like chains that originated within a hydrate structure were directly dependent on the period of their growth within the underground "incubator". Therefore, the first ancient prokaryotes appeared earlier than the eukaryotes which have longer and more complicated DNA chains [2, 8]. Thus, the conclusion made in [13] on the repeated originations of new species obtains a natural explanation. The LOH-hypothesis explains the occurrence of numerous species of prokaryotes and eukaryotes without Darwin's theory of evolution resulted from interspecies variations and natural selection as the leading causes of the species diversity. It is not impossible that living matter originates somewhere in our time.



DNA replication scheme [2, 8] will be detailed in the presentation. The "branchy" chromosome sections adjoining to one of the ends of the centromere: ⓦ are water molecules; $\boxed{A}$-, $\boxed{T}$-, $\boxed{G}$-, $\boxed{C}$- are different nucleotides; ○ are H_2O envelopes of N-bases; II, III are the chromosome sections adjoining to one of the ends of centromere I.

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PP-17

ORGANIC UNIVERSE & SPONTANEOUS SELF-ORGANIZING SYSTEMS

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Universe has a tendency to evolve consistently into a better Organic playgrounds. Every aspect of Universe has the spontaneous tendency to evolve into a More Complex, High Ordered system. Elementary particles combined to form atomic particles, atomic particles to an Atom, Atom to Elements, Elements to Compounds Compounds to Complexes & Complexes to Organic Molecules. A journey from the least to the most developed system. According to most acceptable belief, Life arose out of chemicals due to High-Pressure, Mediocre Temperature & Electric Fluctuations due to continuous Lightning. However, this hypothesis requires certain conditions to take place in order to transform group of Organic chemicals to be transformed into an life-form. For upcoming this Fallacy, an unique theory was established named “Self Organizing Systems” theory. According to this theory, every system in the Universe, capable of having Selforganized nature leads to formation of life. A “Self Organized System” has an intrinsic tendency to create novelty & to thus promote formation of life. Further a “Self Organized System upgrades to Autopoiesis (Self-Making) and thus evolves from a basic system to Complex system.So the driving force of evolution, according to the new emergin theory, is not to be found in the chance of random muation but in life’s inherent tendency to create novelty, in the spontaneous emergence of ever-increasing complexity and order. As we see, Universe itself promotes every system to be a Self-Organized system, Universe promotes new avenues of Life. Hence Catastrophe, even after devouring most of the life; leaves a trace of more advanced life-form. Self-Organized system is a self-driven process & heads towards highest development, hence there is no need of Random mutations as discussed by Neo-Darwinism theory.One thing we can say about the universe is that the potential for life exists in abundance throughout the cosmos. Research over the last few decades has provided a fairly clear picture of geological & chemical features on ealy earth that made life possible. Observing the universe at large and our galaxy in particular, astronomers have discovered that the characteristic chemical components found in all life are present in abundance. We earthlings are the products of Organic Universe & maybe Self-Organization must have created some of our distant cousins in neighbouring galaxies as well. My recent experiments on self-organizing photosynthetic pigments in micelles have given a worthwhile proof of how chemical & biological systems have intrinsic tendency to evolve & be novel.

CONCLUSION

Universe is spontaneously evolving into a More complex, High ordered system; eg. Elementary particles gradually combined & evolved to form life. Universe promotes Self-Organized System which has intrinsic tendency to create novelty & promote formation & evolution of life. Self-Organized System along with Autopoiesis, promotes transition of Basic System to Complex System. Universe thus behaves a "Organic Playground" with spontaneously increasing effective area & avenues of Intelligent life.

KEYWORDS

Self-organization, Autopoeisis, Catastrophe, Neo Darwinism, Universe

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PP-18

TUNGUSKA IN THE LIGHT OF NEC: COMETS & VERNADSKIY MISSION TO NEA2005NB56

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The abstract was not presented for the publication.

YOUNGEST OIL OF PLANET EARTH

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Authors selected and examined oil shows from the caldera of the Uzon volcano (Kamchatka). The hydrocarbon type content of oil shows is dominated by hydrocarbons (HC) (90-93%). The concentration of saturated hydrocarbons by weight in them is two times as much as that of aromatic ones. The concentration of heterocyclic compounds is 7-10%. Few asphaltenes are present in the examined samples (< 0,3%). The composition of saturated and aromatic hydrocarbons of oil shows in the Uzon volcano caldera shows that they have been derived from lipids of land plant remains brought into sediments (the ratio of sterane concentrations $C_{29}/C_{27}>2,5$, tricyclane index $2(C_{19}+C_{20})/\Sigma C_i$ ($i = 23, 24, 25, 26$)>1,5, relatively high concentration of triaromatic steroids), aquabionts, inhabitants of caldera sediments and bottom waters (the ratio $n\text{-}C_{27}/n\text{-}C_{17}<0,2$, $Pr/Ph<0,5$), and bacterial living matter (hopanes). This source of lipids of the initial living matter is also confirmed by isotope carbon composition of the fossilized organic matter ($\delta^{13}C = -28.3‰$). The obtained data on the composition of the caldera oil are in agreement with geochemical investigations performed previously [Bazhenova et al., 1998, Simoneit et al., 2009].

Judging from the composition of biomarker hydrocarbons of oil, the level of initial organic matter maturity corresponds to the very beginning of the main phase of oil formation. This is also indicated by the ratio of odd to even n-alkanes (close to 1), high concentrations of αα-steranes, and, at the same time, the absence of biohopanes higher than C_{27}, the predominance in homohopanes of S-isomers over R isomers, the low values of Ts to Tm hopane concentration ratio, the low values of of phenanthrene and dibenzothiophene indices (0.6-1.1 and 0.3-1.2, respectively). The caldera of the Uzon volcano is a natural system where owing to the discharge of high-temperature hydrotherms, the sediments almost near the very surface are heated to temperatures, characteristic of depths of 2-3 km and more in classic petroliferous basins. Under these conditions, in the real time scale, in Pliocene-Lower Quaternary sediments of the Uzon volcano caldera, the destruction of organic matter and formation of hydrocarbons and heterocyclic compounds of oil occurs. The peculiarity of forming HC because of short time of this unique experiment of Nature and relatively low temperatures is that hydrocarbons of oil from the Uzon volcano caldera inherit the carbon skeleton and stereochemistry of lipid of the initial living matter. In these “young” formations, saturation with biomarkers becomes more apparent than in “normal” oils. The young age of the examined caldera oil is indicated by the presence in the composition of its compounds of carbon isotope ^{13}C, determined by the methods of isotopic geochronology – the time of formation of living matter of Uzon oil is 940±40 Ma (calibrated-conventional) [Simoneit et al., 2009]. In other words, caldera of Uzon volcano represents a natural laboratory of the modern generation of oil from organic matter from Pliocene-Lower Quaternary sediments. The attempts to consider compounds, forming these oil shows as a product of abiogenic synthesis of hydrocarbons, are absolutely unfounded [Simoneit et al., 2009]. The above study confirms the previously stated hypothesis by M.K. Kalinko (1975) that at the present moment of geologic time, owing to hydrotherm impact, oil is being formed from the recent organic matter buried in the sediments of the Uzon caldera.

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PP-20

MID-CHAIN BRANCHED MONOMETHYLALKANES IN THE UPPER PROTEROZOIC AND CAMBRIAN OF SIBERIAN PLATFORM

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Mid-chain branched alkanes or 12-, 13-monomethylalkanes (12-, 13-mmas) present in high concentrations (up to 18% of the total alkanes) in Upper Proterozoic oils of the Siberian Platform and Oman [1-4 and others], as well as in the Neoproterozoic dispersed organic matter from Oman [3] and the East European Platform [5] represent well the biochemistry of lipids from the Precambrian specific biota (eukaryotes?) dominating some ecological niches. Until recently, the 12-, 13-mmas were unknown from the Upper Proterozoic dispersed organic matter of the Siberian Platform.

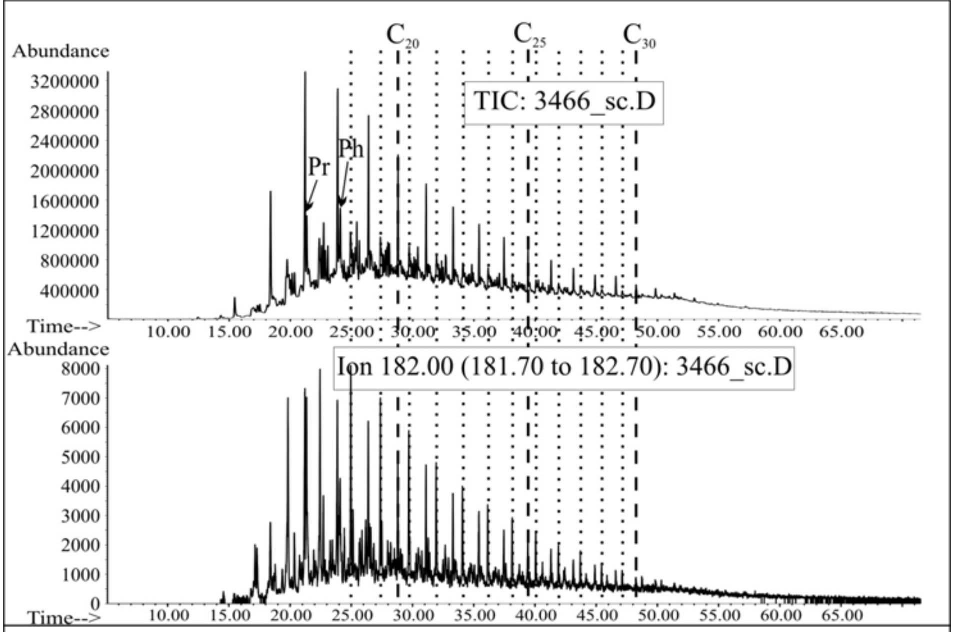

Fig. 1. Chromatogram (TIC) and mass fragmentogram (m/z 182) of chloroform-extractable bitumen from mudstone in the Kumakha Formation of the Upper Proterozoic Lakhanda Group, Maya depression in the SE Siberian platform (n-C_{20} - number of carbon atoms in normal alkane molecule, Pr - pristane, Ph - phytane, dashed lines - location of n-C_{20}, n-C_{25}, n-C_{30} normal alkanes, dotted lines - location of 12- and 13-monomethylalkanes).

In 2010, these hydrocarbons (fig. 1) were first identified by the authors in mudstones from the Kumakha Formation of the Upper Proterozoic Lakhanda Group, Maya depression in the Southeastern Siberian platform (7.3-9.0% of the total alkanes), in mudstones from the Lower Cambrian Kuonamka Formation in the Northeastern Siberian Platform (18%), and in Middle Cambrian marls and mudstones encountered in the Nizhneimbakskaya-219 well (about 7%) drilled in the Bakhta mega-salient, western Siberian platform. This allowed identification of a possible source for specific Precambrian oils of the Siberian Platform. This is the first report of 12-, 13-mmas identified in Cambrian rocks, which allows us to extent the stratigraphic range of organisms that contained precursor structures for the mid-chain branched alkanes.

This work was supported by RFBR (10-05-00705) and the Earth Sciences Department Program N 15.

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BIOMARKER HYDROCARBON COMPOSITION IN UPPER PROTEROZOIC OILS OF SOUTHWESTERN SIBERIAN PLATFORM

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Crude oils from the Kuyumba and Tera-Kamov blocks of the Yurubchen-Tokhomo field (YTF) and Shushukskaya prospect of the southwestern Lena-Tunguska province have acyclic biomarker distributions similar to those reported for previously studied oils [1, 2] typical of the Upper Proterozoic and Lower Cambrian in the Nepa-Botuoba and Baykit (Yurubchen block of the YTF) anteclises. Several samples analyzed are revealed to lack cyclic biomarkers.

Oils from Tersko-Kamovskaya and Shushukskaya wells (Fig. 1) differ from previously studied Riphean and Vendian oils of the Siberian Platform [1, 2] by the homohopane ratios ($C_{35}/C_{34}<1$).

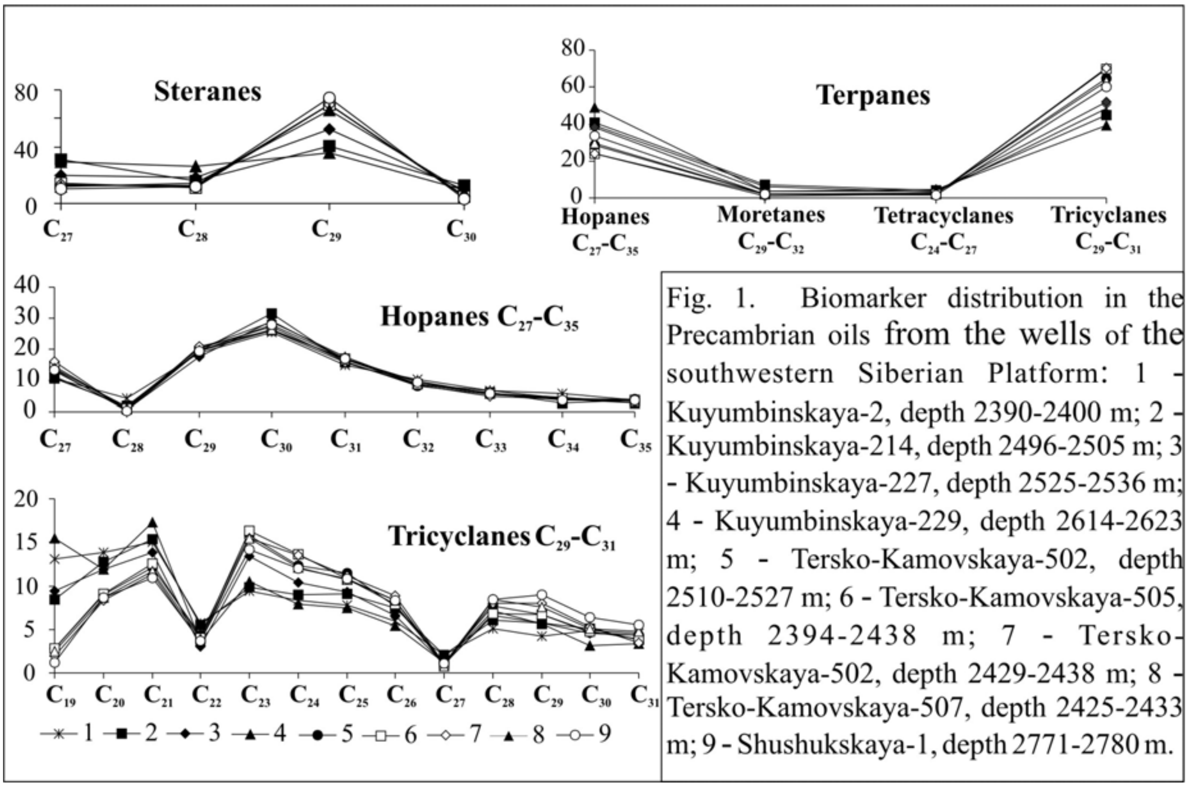

Fig. 1. Biomarker distribution in the Precambrian oils from the wells of the southwestern Siberian Platform: 1 - Kuyumbinskaya-2, depth 2390-2400 m; 2 - Kuyumbinskaya-214, depth 2496-2505 m; 3 - Kuyumbinskaya-227, depth 2525-2536 m; 4 - Kuyumbinskaya-229, depth 2614-2623 m; 5 - Tersko-Kamovskaya-502, depth 2510-2527 m; 6 - Tersko-Kamovskaya-505, depth 2394-2438 m; 7 - Tersko-Kamovskaya-502, depth 2429-2438 m; 8 - Tersko-Kamovskaya-507, depth 2425-2433 m; 9 - Shushukskaya-1, depth 2771-2780 m.

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Oils from the Kuyumbinskoye field have the tricyclane index $2C_{19-20}/C_{23-26}>1$, atypical for marine oils, low C_{35} homohopane and C_{29} steranes concentrations, higher diasterane and hopane contents.

The decreased concentrations of C_{29} steranes in the Kuyumba oils were reported earlier in [3]. These variations are interpreted to result from admixture of hydrocarbon from other sources.

This work was supported by RFBR (10-05-00705) and the Earth Sciences Division Program N 15.

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BIOMARKER HYDROCARBONS IN KARELIAN SCHUNGITES

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Organic matter represented by shungites (C_{org} about 1.6-27.5%) from the 2100-1950-Ma-old Trans-Onega Formation encountered in Zazhoginskaya-175 well at the Onega synclinorium (Baltic shield) was found to preserve carbon isotopic signature typical of the mature polymerlipid aquatic organic matter ($\delta^{13}C$ ranging from —39.7 to —28.1‰).

The presence of steranes (fig. 1) in these rocks suggests that eukaryotes existed in Early Proterozoic times. Steranes with an equivalent distribution of C_{27} and C_{29} homologues are characteristic of marine black shales, which contain organic matter derived mainly from planktonic autotrophic (C_{29}) and heterotrophic (C_{27}) organisms [1]. Similar sterane distributions were previously reported for bitumens in rocks collected from several Lower Proterozoic exposures at the Baltic and Aldan shields [2] and Upper Proterozoic exposures in the Yenisei Ridge and Baykit anteclise [3], as well as in a number of Upper Proterozoic crude oils and bitumen extracts of the East European platform [4-6 and others], Upper Proterozoic and Lower

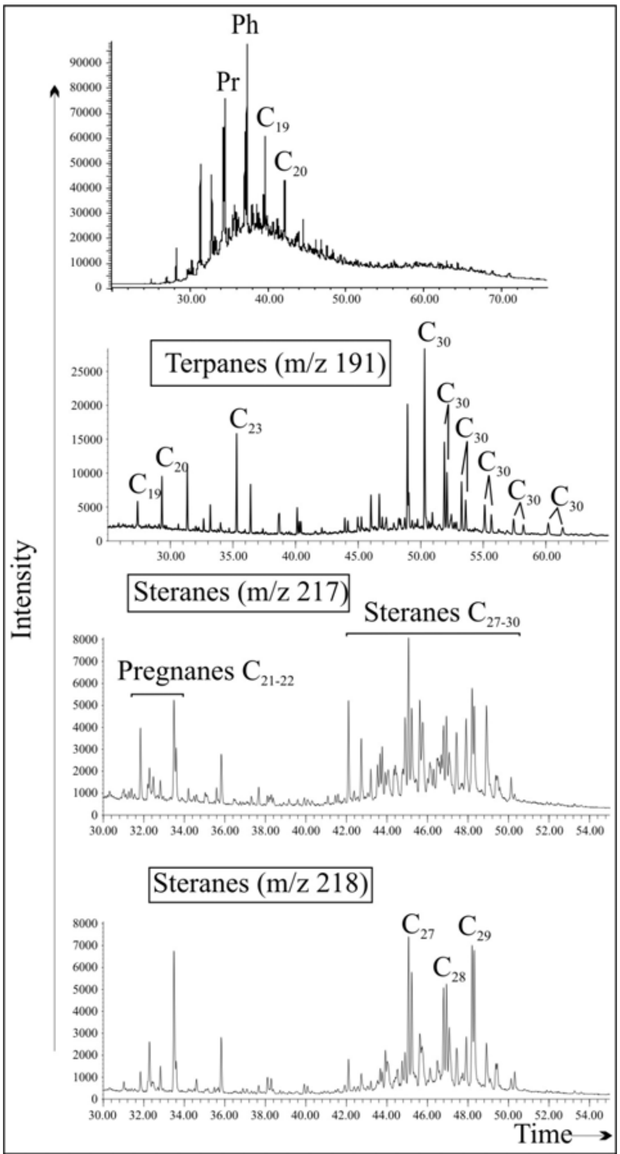

Fig. 1. Typical gas chromatogram (n-C_{20} - number of carbon atoms in normal alkane molecule, Pr - pristane, Ph - phytane) and mass fragmentograms of terpanes (C_{19}, C_{20}, C_{23} tricyclanes, C_{30} hopane, C_{31}, C_{32}, C_{33}, C_{34}, C_{35} homohopanes) and steranes (isosteranes C_{27}, C_{28}, C_{29}) of chloroform-extractable bitumen from shungites of Trans-Onega Formation (Lower Proterozoic) in Zazhoginskaya-175 well at the Onega synclinorium (Baltic shield).

Cambrian oils from the Angara-Lena step and Bakhta mega-salient of the Siberian platform [4].

The shungite-bearing rocks of the Trans-Onega formation have low carbonate contents (high diasterane concentrations), and diagenesis of organic matter in these sediments took place under anoxic condition without high content of hydrogen sulfide in bottom waters (for homohopanes $C_{35}/C_{34}<1$).

All of the samples analyzed contain no indicators of continental organic matter, such as oleanane, the higher-plant marker. The overall biomarker distributions (*n*-alkanes, steranes, tricyclanes) and some hydrocarbon ratios (Pr/Ph, T_s/T_m) reflect the predominance of marine biological precursors, thus indicating a lack of contamination by younger hydrocarbons.

This work was supported by RFBR (10-05-00705) and the Earth Sciences Department Program N 15.

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EVOLUTION OF TRILOBITE BIOFACIES IN EARLY AND MIDDLE CAMBRIAN (OUTER SHELF OF THE SIBERIAN PALEOBASIN)

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Trilobites associations lived in similar facies conditions are considered as Trilobite Biofacies. Studies of the Cambrian Trilobite Biofacies on the Siberian platform can be very useful for biostratigraphy, paleobiogeographical analysis, detection paleoecological features of habitats and the evolution of the basic elements of marine ecosystems of the Early Paleozoic, which played an important role in the Phanerozoic biosphere.

The Siberian platform is an ancient piece of continental crust that was an island continent in Cambrian time. Three distinct facies belts comprise the Early Cambrian and Early Middle Cambrian of the Siberian Platform: a western belt of restricted-circulation, evaporitic carbonate sediments (Turukhan–Irkutsk–Olekma facies region), a reef-shoal transitional belt of archaeocyathan-microbial facies (Anabar–Syn facies region), and an open-marine eastern and northern belt (Judoma–Olenek facies region).

Trilobites, which appeared in the Early Cambrian to Early Middle Cambrian widely dispersed in the territory of the Siberian platform. They had high rates of evolution and have become the most numerous and diverse group of organisms that time and existed in all three facial regions. There is a dependency of the trilobites associations from their place in the Siberian platform and the facial nature of rocks, which enclosed the remains of trilobites (Pegel, 2000). The main factors influencing the settlement of trilobites were salinity, depth and nature of substrate (Repina, 1977). In addition to the spatial variability observed change of a Trilobite Biofacies over time. Often these changes are associated with changes in facial conditions. But sometimes these changes occurred regardless of changes in facial conditions. The authors analyzed the trilobites associations from the Eastern part of the Siberian Platform, which existed in the Early and Early Middle Cambrian on the outer shelf of the Siberian paleobasin. Most of trilobites associations rigidly tied to facies, although some associations are found in different rocks.

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The oldest Trilobite Biofacies were common in the outer shelf of the Siberian paleobasin. Trilobite Biofacies Fallotaspidoidea has occurred in several areas (the Lena River, Aldan River, Kharaulakh mountains, etc.). The next Trilobite Biofacies Fallotaspidoidea – Eodiscoidea already found in all parts of the study territory. These Biofacies existed in Atdabanian (Early Cambrian). Protolenids trilobites (biofacies Protolenidae (*Bergeroniellus*, *Bergeroniaspis*) – Eodiscoidea) replaced Fallotaspids and Eodiscids trilobites communities in Botomian (Early Cambrian). Despite the facies differences in different parts of the platform, and some representatives Protolenids and Eodiscids trilobites held in a dominant position in the trilobites associations to the second half of the Toyonian (Early Cambrian). Although species composition was different in the trilobites associations, Protolenids still dominated in the first half of the Toyonian (*Biofacies Protolenidae (Lermontovia, Paramicmacca), Neopagetina*). But the dominant were the representatives of other genera. At this time in the Upper-Markha area trilobites associations was mixed, Protolenids trilobites it is not dominant (Biofacies Agraulidae – Jakutiidae – Utiidae – Paradoxididae). Differentiation of trilobites associations occurred in the study area at the Early Middle Cambrian. Trilobites associations, which occupy large areas, were replaced by complexes which prevalent in small areas of the Siberian paleobasin (Biofacies Paradoxididae – Dorypygidae – Dinesidae, Dorypygidae – Ptychopariidae – Dinesidae, Ovatoryctocara – Agnostida, Agnostida – Oryctocephalidae).

Agnostids and Oryctocephalids trilobites dominated on the area where accumulated organic-rich rocks. Representatives of the families Dorypygidae, Ptychopariidae, Corynexochiidae existed and dominated in other part of the Siberian platform at different times. The Eastern part of the Platform is populated Trilobites Biofacies Agnostida – Anomocaridae – Dorypygidae at the end of the Amgan (Middle Cambrian). But in the Upper-Markha area there is another Trilobite Biofacies (Anomocaridae – Corynexochiidae – Paradoxididae).

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COMPARATIVE ANALYSIS OF BIOMARKER HYDROCARBONS IN UPPER PROTEROZOIC, PALEOZOIC, AND MESOZOIC ORGANIC MATTER OF WEST SIBERIA

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It has been identified that the saturated fractions of bitumens (chloroform extracts) from Upper Proterozoic, Paleozoic (Є-C) and Mesozoic (J) deposits contain C_{10}-C_{37} n-alkanes, C_{13}-C_{25} acyclic izoprenanes, cyclic biomarker hydrocarbons (HC) of sterane (C_{21}-C_{22}) and C_{27}-C_{30}) terpane (C_{19}-C_{35}) series.

The following biomarker parameters were established for Upper Proterozoic OM (well Vostok-3): $n\text{-}C_{27}/n\text{-}C_{17}<0.2$, $1\approx Pr/Ph<1.3$; C_{29}/C_{27} steranes ≈ 1, tricyclane index = $(2*(C_{19}+C_{20})/\Sigma C_{23}\text{-}_{26}) \leq 1.7$, high concentrations of pregnanes and tricyclanes (to 74.6% of C_{19}-C_{35} total terpanes). Judging by the composition of biomarker HC, plankton-derived and bacterial organic matter (OM), buried in sediments of the Upper Proterozoic marine basin, contained biochemically similar lipid complexes. A slight change in biofacies in time is indicated by variations in the ratio of tricyclanes to hopanes (28-75 and 22-67% of C_{19}-C_{35} total terpanes, respectively).

The distribution of biomarker hydrocarbons in Paleozoic bitumen extracts of West Siberia was studied in most detail for Cambrian deposits (Pre-Yenisei subprovince, Stepnoi Altai) and Devonian deposits (Stepnoi Altai, Shchuchye salient of Polar Ural, the southeastern and central parts of West Siberia (Kontorovich et al. (2000, 2008, 2009), Sarayev et al. (2004), Sennikov et al. (2005), Kostyreva (2005), and oth.) [Kontorovich et al., 2010]. Recently, geochemical data have been acquired with the same degree of detail from the southwest of the area (Kurgan district) for predominantly Carboniferous deposits. Analysis of composition of relict saturated HC in Paleozoic deposits allows separation of the examined bitumen extracts into two groups. The first group (Є-C) is characterized by the following values of biomarker parameters: $n\text{-}C_{27}/n\text{-}C_{17}<0.5$; $Pr/Ph < 2$; C_{29}/C_{27} steranes ≤1, tricyclane index ≤1, high concentrations of pregnanes and tricyclanes (to 74.6% of C_{19}-C_{35} total terpanes). These parameters suggest that OM is of aquagene nature, which is also confirmed by $\delta\,^{12}C$ to $\delta\,^{13}C$ isotope ratio in OM (-35)-(-29) ‰. The second group of bitumen extracts (Є, D, C) shows the different values of biomarker parameters: $n\text{-}C_{27}/n\text{-}C_{17}\geq 1$;

Pr/Ph<1.5; C_{29}/C_{27} steranes >1; tricyclane index <1.5; concentrations of pregnanes and tricyclanes are not high and $\delta^{13}C$= (-30)-(-28) ‰). Prokaryotes and protozoan eukariotes with the same biochemistry originated as early as the Precambrian (Grantham (1986); Kontorovich et al. (1996, 2004, 2005 and oth.).

Based on the composition of biomarker hydrocarbons, several biogeochemical facies could be distinguished in Paleozoic complexes of West Siberia because of the complex relationship of carbonate reef, black shale pelagic and volcanogenic sedimentation in the Paleozoic basin as well as counterflows of terrigenous material of variable composition, directed both from near-platform island land and active volcanic arcs.

The aquagene OM of Bazhenovo genotype (J_{3v}-K_1) differs at molecular level from the Upper Proterozoic-Paleozoic OM only in lesser spread of values of biomarker parameters (ratios: n-C_{27}/n-C_{17}<1, Pr/Ph<1.5, C_{29}/C_{27} steranes <1, tricyclane index <1), $\delta^{13}C$= (- 33,9) ÷ (- 30,9) ‰ and in lower content of cheilanthanes (15-20% of C_{19}-C_{35} total terpanes). The terragene OM of Tyumen genotype (J_2a_2-bt_3) is characterized by a set of biomarker parameters different from the aquagene OM: n-C_{27}/n-C_{17}>1, Pr/Ph>1.5; C_{29}/C_{27} steranes>1.5; tricyclane index >1.5; cheilanthane content <15% of C_{19}-C_{35} total terpanes, and $\delta^{13}C$= (- 27.1) ÷ (- 22.6) ‰. In the OM of mixed genotype (terragene-aquagene or aquagene-terragene) of Mesozoic deposits, the spread of values may vary within the wide ranges. In some horizons, the Mesozoic OM, unlike the Upper Proterozoic-Paleozoic OM, is notable for the sharp predominance of odd normal alkanes over the even ones, very high content of biosteranes even from m/z 218 mass chromatogram, the predominance of R-isomers over S-isomers in homohopanes, the presence of biohopanes in m/z=191 mass chromatograms of terpanes, which is indicative of very low stage of catagenesis, also confirmed by the low values of R^0_{vt}<0.6 (Kontorovich et al. (2009) and oth.).

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CYANO-BACTERIAL MATS OF HOT SPRINGS IN BARGUZIN BASIN (BAIKAL RIFT ZONE) AS A MODEL FOR STUDYING EARLY ECOSYSTEM AND MINERAL FORMATION

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The oldest lithified cyanobacteria found in sediments date back to 3.6 Ga (Dobretsov, 2005). Well-preserved cyanobacteria older than 3.46 billion years were found in Western Australia (Brun and Lawrence, 2000). However biogenic origin of Australian stormatolites is still being discussed (Allwood et al., 2006). Today's cyanobacteria have been expelled to extreme habitats, such as hot springs where thermophilic communities can live. Based upon studying of hydrotermes microbial communities, one can get information about the processes which occurred in early prokaryotic world and its significance for the formation of rocks and ecosystem.

There are a lot of hot springs (more than ten) within the Barguzin river basin of the Baikal Rift Zone. Bacteria populations were found at all venting sites (Namsaraev et al., 2006). However carbonate agglomerates are only formed at three sites (Alla, Garga, and Gusikha) (Plyusnin at al., 2000). The largest carbonate body is formed on the Garga hot spring. The Garga hot spring stream has Na-SO_4 composition (TDS = 1 g/l, T=77°C, pH-8.2). Alkaline, alkaline-earth (Li, Rb, Sr, Cs, Ba) and anionogenic elements (Si (30-45 ppm), Ge, Mo, W) are prevailing in the solutions.The carbonate body thickness is 3-5 m. Cyanobacterial mat (T 54-49°C) grows at the surface of this body. *Phormidium, Mastigocladus* and *Oscillatoria* species are dominate in the microbial community. The Gagra microbial mat structure was studied by scanning and transmission electron microscopy. In the thermophilic cyano-bacterial community calcite precipitates in the form of well-faceted crystals ranging in size from 20 to 40 μm. Transmission electron microscopy studies showed the structure of microbial mat. A variety of morphology of the bacteria among the cysts or spores, and rests of lysed cells is found. Local analysis of elemental composition showed that silica is concentrated mainly in a thick layer of cellular slime surrounding the bacterial cells. Monocrystals of calcium carbonate were found in the intracellular space. Hollow nanosized calcium phosphate sphere were detected inside of the bacterium cells. The mineral formation processes in the cyanobacterial mat, mineralogical and structural features of the Garga carbonate body were thoroughly studied by complex of physical-chemical methods.

The result obtained allowed the conclusion about the history of formation of the Garga carbonate body. This carbonate structure was formed as a result both of the deposition of minerals from the hot spring stream and of the activities of cyanobacterial community.

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THE BIOGEOGRAPHICAL EVOLUTION OF THE PERMIAN AMMONOIDS

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The Permian period was a time of global climatic turnover, when the cold icy climate of the Late Paleozoic was replaced by the ice-free Mesozoic. The climate of the Early Permian showed prolonged episodes of glaciations, which to a large extent determined the evolution of the marine biota. The area covered by glaciers reached its maximum at the end of the Late Carboniferous-beginning of the Early Permian. The first significant warming episode occurred in the second half of the Sakmarian-beginning of the Artinskian. The second half of the Artinskian and Kungurian are considered as the warmest periods in the Early Permian epoch. The general regression of the Middle and Late Permian was complicated by smaller, relatively short-term transgressive-regressive cycles and warming and cooling episodes.

The data on the generic and familial content of assemblages in all localities, endemic genera, centers of diversification, and quantitative changes of the dynamics of generic changes in ammonoid communities allow to the recognition of five large realms: Uralian, North American, Arctic, Australian, and Paleotethyan.

The majority of all Permian genera are known from the Paleotethyan realms. At the beginning of the Early Permian 45% of all genera known from this interval (a.g.)come from the Paleotethys. At the end of the Early Permian over 60 genera, or 80% a.g.; at the beginning of the Middle Permian - 78-96% a.g., of these up to 60-70% a.g.at various times were endemic. In the Late Permian ammonoids were preserved only in this Realm (100% a.g.).

At the Uralian Realm three of the four typical Permian families appeared. At the Asselian and Sakmarian ammonoids constituted 71% and 61% a.g. The Early Artinskian ammonoids are the most typical in this region (78% a.g.). In the Late Artinskian diversity of these ammonoids decreased to 45% a.g., and to 6% a.g. in the Kungurian.

At the Arctic Realm (Northeastern Asia, Novaya Zemlya, Pai-Khoy, Vaigach Island, Volga-Urals, Canadian Arctic Archipelago, and Alaska) ammonoids were moderately diverse (22% a.g.in the Asselian, and 29% a.g. in the Sakmarian). There were fewer Early Artinskian ammonoids (14% a.g.). In the Kungurian the extent of endemism also increased, i.e., of 10 genera existing at that time, 7 were endemic. In the Roadian stage there existed 9 genera, whereas only 2 genera are known from the Wordian.

At the American Realm ammonoids were moderately diverse: in the Asselian - 31% a.g., in the Sakmarian - 26% a.g. Of 23 genera existing during that period, 8 appeared in the same region, whereas four are endemic. From the very beginning of the Middle Permian the relative diversity began increasing: in the Roadian it was 27% a.g., in the Wordian 38% a.g., and in the Capitanian 80% a.g. Almost all new genera were aboriginal.

At the Australian Realm ammonoid occurrences are known from the Sakmarian-Capitanian beds. The Sakmarian ammonoids - 8 genera (19% a.g.), all these were immigrants from other regions. 7 genera existed in the Artinskian (12% a.g.), Kungurian (6%). 4 genera are recorded in the Roadian; the composition of these assemblage is interesting: 2 cosmopolitan genera, 1 - Tethyan, and one is a characteristic taxon of the Arctic Realm.

In the Permian, there were several separate centers of morphogenesis within the Paleotethys Ocean (Pamir, Timor, Sicily, South China), which suggests that these basins were from time to time isolated within this realm. Basins of Pamir, Afghanistan, Southwest China, Thailand, Malaysia, and Timor were connected to each other throughout the Early Permian, with a more intense exchange in the second half. At the beginning of the Middle Permian basins of Sicily, Tunisia, Oman, Iraq, the Crimea, Greece, and Croatia could freely exchange their pelagic faunas, especially in the Wordian. Apparently, relatively stable connections existed between the above regions and Timor. A restricted exchange of faunas occurred between the eastern part of the Paleotethys and the American Realm. At the end of the Late Permian, the South China, Far East-Japan, and Iran-Transcaucasia basins were inhabited by related ammonoid communities, which apparently resulted from similar environments, close geographic location, and migratory pathways.

Climatic fluctuations of the Permian period were a significant factor influencing both morphological and paleobiogeographical changes. A wide distribution of ammonoid faunas at the end of the Artinskian coincided with an episode of global warming, whereas a sharp decrease in the ranges and increased provincialism at the end of the Permian coincided with the general trend towards aridization and prominent cooling. A considerable warming at the very end of the Permian significantly changed the morphological and biogeographical structure of the Triassic ammonoid communities, which essentially arose anew.

MICROBIAL COMMUNITIES OF OIL AND GAS BEARING DEPOSITS IN LAKE BAIKAL

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Lake Baikal is the oldest (25 million years) and deepest lake in the world (Grachev, 2002). Mud volcanos, methane, and oil seeps were identified in Lake Baikal using different methods (Klerkx et al., 2003; Kontorovich et al., 2007; Khlystov et al., 2007). Oil sampled from the lake surface is associated with oils which hadformed in sediments of deep freshwater basins during the Oligocene-Early Miocene (Kashircev et al., 2006). It was determined that the source of Baikal oil is an organic matter and remains of higher land plants (Kashircev et al., 2006). Khlystov et al. (2007) suggested that oil found on the lake surface is formed in sediments of Central Baikal with the most favourable thermobaric conditions (700 atm pressure, at >200°C) for oil and gas generation, rather than directly in sediments of an oil seepage site. Despite constant intrusion of oil into the water surface, the size of oil slick remains the same indicating oil biodegradation. According to the 2005-2007 observation data, at sites of natural oil seeps, there was a three order increase in aerobic hydrocarbon oxidizing microorganisms (HOMs) compared to the remote sits from the oil seepages. In 2008-2009 the number of HOMs stabilized which was evidence of an adaptation of microbial communities to oil coming to the water surface. The data on 16S rRNA nucleotide sequence obtained from bottom sediments at the sites of natural oil seepages have shown a similarity with ten phyla of the domain *Bacteria.* It has been detected that the nearest neighbors of the Baikal uncultured bacteria from different ecosystems of the world participate in oxidation of oil and its derivatives (Alfreider *et al*., 2002; Kasai *et al*., 2005; Kleinsteuber *et al*., 2008). To confirm theability of pure HOM cultures from the sites of natural oil seepages to oxidize *n*-alkanes of oil, screening of *alk* genes was performed. It has been indicated that Baikal HOMs contained *alk* genes oxidizing a wide range of *n*-alkanes. Comparative phylogenetic analysis has shown that nucleotide sequences obtained have the closest similarity with DNA of representatives of the genus *Rhodococcus* rather than with their own DNA. It may indicate an introduction of *alk* genes into genomes of different bacteria genera as a result of interspecies horizontal transfer, and *Rhodococcus* were probably donors of these genes. This fact correspond to the data obtained by J. V. van Beilen et al. (2001) and Tourova et al. (2008).

To detect microorganisms discharging together with oil, the experiment in methane atmosphere at high values of pressure (80 atm) and temperature (80°C) was carried out in laboratory conditions. Total DNA obtained during the experiment allowed the performance PCR analysis using the primer set of wide specificity for bacterial sequences. PCR product was prepared for cloning, thus, allowing the identification of microorganisms and comparison of its DNAs with those from bottom sediments of the observed site.

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MICROEVOLUTIONARY PROCESSES AND SPECIATION IN EXTREME BIOTOPES DEPEND ON SPECIALIZATION TO THE BIOTOPES: STUDIES OF HYDROTHERMAL VENT SHRIMPS

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Hydrothermal vents may be considered as model ecosystem reflecting biological processes on earlier Earth. Cairns-Smith et al. (1992), Russell et al. (1988; 1994) and Russell and Hall (1997), and other researchers proposed that life emerged in submarine hot springs in a Fe-rich ocean in Hadean Earth 4.4–3.85 billion years ago. Recent hydrothermal vent communities are interesting objects for studies of patterns of evolutionary processes. Vent biotopes are extreme ones from biological viewpoint and we can reveal a row of taxa that demontrates increasing specialization to the biotope. One of the best objects to study specialization to such extreme biotopes are vent shrimps of the superfamily Bresilioidea.

Bresiliid shrimps represent the key elements of hydrothermal communities of the Mid-Atlantic Ridge and they are members of the hydrothermal communities in other areas of the oceans. The present COI nucleotide divergence estimates reveal that recent species of vent- and seep-endemic shrimp constitute a natural (i.e., monophyletic) group that most likely radiated in the Miocene, 6.7 to 11.7 MYA (Shank et al., 1999). Vent shrimps give examples of almost unspecialized genus (the genus *Alvinocaris*), extremely specialized genus (the genus *Rimicaris*), and intermediate forms (the genera *Chorocaris, Mirocaris*, and *Opaepele*). We analyzed how degree of specialization determines speciation, biogeographic patterns, life cycles, and microevolutionary processes. All known species of vent shrimps were involved into analysis.

Phylogenetic analysis of the vent shrimps revealed two main clades and 26 species of vent shrimps. Species within each of these clades are randomly distributed throughout the World Ocean, thus making impossible to show the area where the group originated. Less specialized genus (*Alvinocaris*) was found to be much more divergent than more specialized. The most specialized *Rimicaris* is nearly monotypic.

Each species within less specialized genera inhabits 1-2 vent fields. Each species of the most specialized species occurs in numerous vent sites. Genera with intermediate specialization demonstrate intermediate pattern of geographic distribution.

More specialized species have distinctly different life strategy than less specialized species. They have larvae living in the water column for a long time and dispersed for a long distance. Yet conversely, less specialized species have larvae living in the vicinity of the vent site where they hatched. These dispersal strategies may account for different types of geographic distribution of the shrimp species.

Speed of the microevolutionary processes within vent shrimp populations depends on the degree of specialization. More specialized genera and species with wide-range dispersal strategy create a single metapopulation occupying vast areas. Gene exchange along this area makes both microevolutionary processes and speciation slow. Conversely, less specialized genera having narrow-range dispersal strategy are characterized by high speed of microevolutionary processes. Within one geographic region many distinct populations exist and speciation occurs much faster that is reflected in a number of distinct species.

Thus, evolutionary patterns in extreme biotopes are related to specialization of the shrimp species to the biotope. Moreover, evolutionary patterns may depend on the basic geological characters. In the relatively young Atlantic Ocean, with low-spreading mid-ocean ridge and prominent rift valley along the ridge, dispersal of larvae is more successful, gene exchange is high, and microevolutionary processes/speciation are slow. Conversely, in the relatively old Pacific Ocean with high-spreading mid-ocean ridge and absent rift valley along ridge dispersal of larvae is less successful, gene exchange is low, and microevolutionary processes/speciation are high.

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BIOGENIC AND ABIOGENIC BIOMORPHIC STRUCTURES IN OCEANIC IRON-MANGANESE CONCRETIONS AND THEIR EVOLUTION

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We investigated two types of the ferromanganese nodules (FMN). Among the first type are the deep-see (pelagic) nodules of the Clarion-Klippertone zone at the Pacific Ocean. This type of nodules is known for a long time. The deep-see nodules have been discovered at 1873-1876 during the expedition on Challenger boat and from that moment they are constantly investigated. Such a great interest to these natural (native) formations is connected with the fact that FMN are considered to be a potential source of raw materials (mineral products). Nodule reserves only at the Clarion-Klippertone zone are about 30 milliards of tons and it is very important that these reserves are constantly regenerative. The main feature of nodules is their enrichment by many ore elements. Concentrations of such elements in nodules are extensively higher than in continental manganese ores. For example, Mn, Co, Mo, Ti are concentrated in pelagic nodules at hundred times more than in ores; Ni, Ag, Ir, Pb from fifty to one hundred times more; Cu, Zn, Cd, W, Bi from ten to fifty times more and P, V, Fe, Zr – at ten times more than in continental ores.

Among the second type of FNM are the nodules of Baltic Sea shelf. This type of FMN has never been regarded as the object (material) for industrial using. However recent investigations let us to change our attitude to this ore type and (to try) to find it’s worth application.

There are great differences between the characteristics of these two types of the ferromanganese nodules such as:

- nodule size
- inner structure
- chemical and mineral composition.

Results of the XRD investigations displayed that the main part of ore matter of the ferromanganese nodules is roentgen-amorphous (uncrystalline). Among the ore minerals such phases are determined: 10Å-phase, 7Å-phase – birnessite and vernadite. Mineral stability under high-temperature treatment (heating) was studied for the 10Å-phase determination. The most common 10Å-phase in our nodules is todorokite. In smaller quantities asbolane and buserite are present. Ferruginous minerals of the nodules are uncrystalline. They were determined with the help of Mossbauer spectroscopy. On the picture there is Mossbauer spectra of the nodules both untreated and heated up to definite temperatures. According to the Mossbauer spectra of the heated nodules first of all γ-FeOOH and more slowly another Fe-Mn oxide mineral are transformed into a new Fe phases with the sextet magnetic spectrum structure. The end annealing products are hematite α-Fe_2O_3 and its Mn- analogue $(Mn,Fe)_2O_3$. Hematite determines magnetic structure of spectra and contains about 70% of Fe.

The detailed study of the nodule outer surface revealed that Fe-Mn oxides form either leakage structures consists from nanoscale flakes or micriglobules. Among the structures the most common are Fe-Mn spherulites with the addition of phosphorus in the composition (in wt.%): MgO –1.84; Al_2O_3 –5.96; SiO_2 –15.97; P_2O_5 –3.56; K_2O – 1.20; CaO – 2.20; MnO – 18.52; Fe_2O_3 –24.54; BaO – 0.77. The size of such flakes is not more than 2 microns. The nodule surface is also consisting of nanoscale flakes. Such surface structure is analogous (similar) to bacterial forms with the cover from mineralized glycocalyx. Similar types of bacteria have been discovered in the ferromanganese nodules of the Pacific Ocean.

Globular structures are typical not only for the surface of the nodules. We discovered numerous pyrite microglobules with the surfaces indistinguishable from the surfaces of ferromanganese nodules. The ability of biogenic pyrite formation is widely discussed and now is undoubted.

Inner structure of is quite different from the outer (surface) one. There are no globular forms at the inner parts of the globules. Fe-Mn oxides formed nanoscale “net”. At such conditions mineralization processes occur very fast. This resulted in the fact that we can observed only uncrystalline phases (not crystalline) what is typical for biogenic mineralization.

Recently the role of biogenic factor in mineral formation is discussed very wide from the different positions. Microorganisms are regarded as “accumulators” of some elements that are necessary for mineral formation at definite conditions; they can influence on the mineral substance during biofilm formation on the mineral surface; microorganisms can form some minerals at the processes of their vital functions.

The role of biogenic factor at the formation and growth of ferromanganese nodules is discussed since their revelation to our time from the different positions and now is undoubted. Nowadays only ideas about the forms of biogenic formation and range of it importance can be changed. Today biogenic factor is regarded in different aspects: as source of nodule nuclei, as element supplier for nodule growth and so on, up to the ideas about stromatolithic nature of the nodules. The most evident participation of biogenic formations in nodule building is their use as nuclei. This process is so widespread that the separate biomorphogenic type is separated among the nodule morphotypes. Into this morphotype are combine nodules forming an incrustation on worms-mudeaters excrements and tracks, on fish teeth, on whale helixes and auditory ossicles. Occurrences of microflora remains with layered localization are testified about active participation of microbiological processes in ferromanganese nodules formation. Microorganisms can to live on the nodules surface and create superstructure accumulating Fe-Mn oxides. It was mentioned that nodule layers with numerous organic remains are grow faster. On the pictures you can see planktonic remains found abundantly at the inner parts of nodules both Baltic and Pacific. Often we can observe replacing of this remains by Mn oxides in the form of covering films.

Uncrystalline phases of Mn oxides are one of the most common minerals in the ferromanganese nodules. Our investigations show that these phases are represented by mineralized glycocalyx. We diagnosed this phase as todorokite on the basis of results of high-temperature transformation experiments.We found numerous examples of rod-shaped and fusiform bacteria in Mn oxides of in the ferromanganese nodules.

Remains of bacterial structures consisting of mineralized glycocalyx are the typical structure forms of uncrystalline fine-dispersed Mn oxides. Nano-dimentionality of Mn oxides may be connected with the fact that they are products of vital functions of cyanobacteriae that are forming around covers of Mn-rich components. Nanostructures of Mn oxides are fibrous aggregates.

In the ore zones the ferromanganese nodules we found inclusions of native metals. In nodule samples inclusions of copper-red and brass-yellow metal formations in the form of plates, flakes, dendrites were determined as native copper and intermetallic compounds of copper and zinc (brass-yellow grains). Infrequently we met iron-copper compounds and native iron. Besides this we found single grains of native aluminium and zinc. Sulfide minerals in nodules (pyrite, chalcopyrite, pyrrhotite, troilite, covellite, bornite) are commonly associate with organic remains and forms as a result of appearance of reduction microcenters because of bacterial activity. Presence of nickel minerals in the nodules (buzerite, taenite, niccolite, violarite) is connected with the biochemical processes of organic matter transformation.

At the inner parts of Baltic nodules the inclusions of pyrite, monazite, zircon and thorite have been found.

Increased contents of some radioactive elements in nodules permit us to consider these formations as good adsorbents and to use them for the water purification.

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PP-30

AUTOCATALYTIC PRIMORDIAL METABOLIC SYSTEM WITH POSITIVE-PLUS-NEGATIVE FEEDBACK AND ORIGIN OF ANCESTRAL PROKARYOTES

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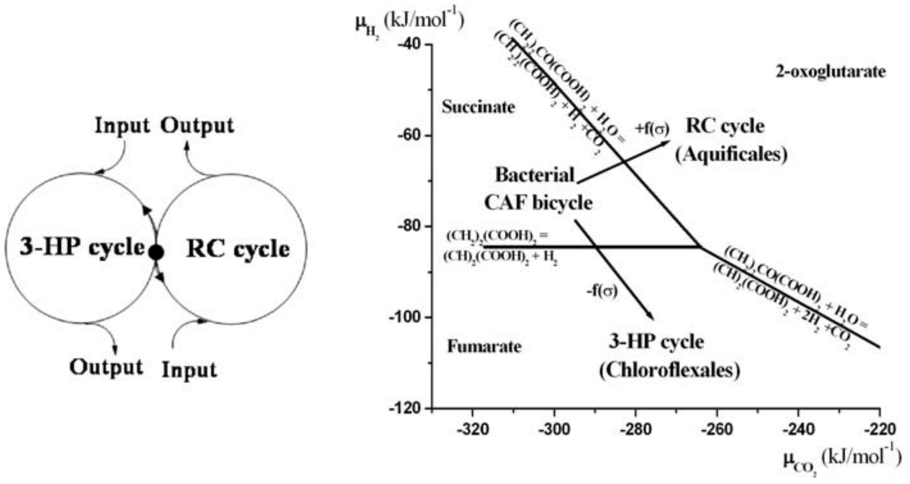
Autocatalytic systems possess the properties of the positive and/or negative feedback and are of fundamental importance for understanding of the primordial metabolism origin [1-3]. Reductive citrate (RC) and 3-hydroxypropionate (3-HP) CO_2 fixation cycles are the cores of autotrophic intermediary metabolism of Aquificales and Chloroflexales orders respectively, which located near the root of the bacterial ribosomal phylogenetic tree [4-6]. Biomimetic models of these metabolic systems represent the positive feedback loops, allowing them to function from cycle to cycle in a self-amplifying regime. Superposition of these cycles based on the general sequence of succinate-fumarate-malate components generates a self-regulating bicycle – primordial negative feedback loop in natural hydrothermal systems. In combinatorial (RC + 3-HP cycles) archaic bacterial bicycle the input signal, or homeostatic parameter σ, determines which of the two processes (succinate $\rightarrow$ fumarate+H_2 $-f(\sigma)$ or succinate+CO_2+H_2 $\rightarrow$ 2-oxoglutarate+H_2O $+f(\sigma)$) becomes realizable (fig. 1b). In the “chemical point of bifurcation” (fig. 1a) occurs the branching of the reactions direction.

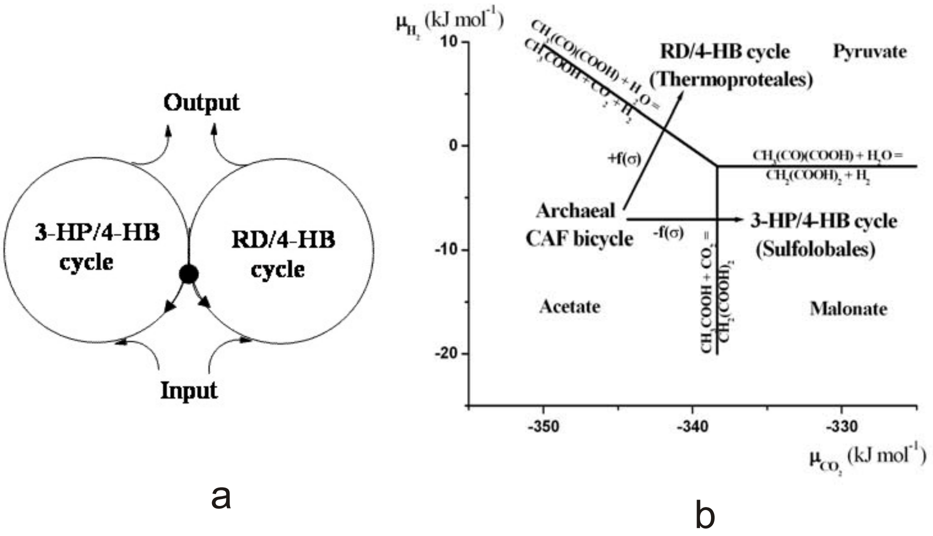


a b

Fig. 1. Negative feedback metabolic system of bacterial common ancestor (a). ● – point of bifurcation defining reactions (arrows) presented on the phase diagram chemical potential CO_2 (μ_{CO_2}) – chemical potential hydrogen (μ_{H_2}) (b). CAF – CO_2 autocatalytic fixation.

Depending on physical and chemical conditions of hydrothermal environment, metabolic cycles will develop adequately to these conditions (arrows). A competition between cycles and natural selection under the influence of hydrothermal environment of ancient Earth have led to divergence of last common ancestor of domain Bacteria, containing archaic bicycle, into ancestral orders Aquificales (RC cycle) and Chloroflexales (3-HP cycle).

In common with the above bacterial protometabolic systems, in the primordial archaeal autocatalytic chemical network [7] the splitting of function $f(\sigma)$ is determined by two reactions of acetate carboxylation with formation of pyruvate $+f(\sigma)$ or malonate $-f(\sigma)$, fig. 2.



a

b

Fig. 2. Negative feedback metabolic system of archaeal common ancestor (a), ● – point of bifurcation. Branching direction of bicycle reactions (arrows) on the phase diagram μ_{CO_2} - μ_{H_2} (b).

The last common ancestor of domain Archaea (subdomain Crenarchaeota) contained the integrated system of autotrophic carbon dioxide assimilation – 3-hydroxypropionate/4-hydroxybutyrate (3-HP/4-HB) + reductive dicarboxylate/4-hydroxybutyrate (RD/4-HB) bicycle, which became the metabolic basis of ancestral orders of Sulfolobales (3-HP/4-HB cycle) as well as Thermoproteales and Desulfurococcales (RD/4-HB cycle), fig. 2.

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PP-31

COMPARISON OF THE PALEOPROTEROZOIC STROMATOLITES WITH MODERN MICROBIAL BUILDUPS FORMING IN THE HYPERSALINE COASTAL LAGOON ENVIRONMENT

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Laminated carbonate sedimentary structures representing fossilized microbial mat or stromatolite development are remarkable organic remains from the early Earth and reflect microbial biomineralization processes, which have been operate from the Paleoarchean to the Recent. In modern microbial mats, a complex biological and biochemical organization leads to several zones of photoautotrophic organisms with layers of aerobic and anaerobic heterotrophs metabolizing within variable amounts of extracellular polymeric substances (EPS) (Spadafora et al., 2010). Modern lithifying microbial mats produce a range of carbonate precipitates resulting from the interplay of the biological activities of microorganisms and the environmental conditions. Microbial mediation is the only demonstrated mechanism to precipitate dolomite under Earth surface conditions.

Purpose of the research work was to compare Paleoproterozoic (2.2-2.1 Ga) dolomite stromatolites (fossilized microbial buildups) from Eastern Fennoscandian Shield, which are considered had been formed under evaporate conditions (Melezhik et al., 1999) with modern microbial mats forming in environment of the hypersaline coastal lagoons (e.g. Lagoa Vermelha in Brazil) by primary dolomite precipitation induced by microorganisms (Vasconcelos et al., 2006).

The main results obtained within the study are:

1. Light microscopy of the thin sections taken from Paleoproterozoic stromatolites, revealed clotted fabric, which resembles peloidal fabric of Lagoa Vermelha stromatolites (Spadafora, 2010).
2. Numerous traces of microbial activity preserved within the rock e.g. deformed fragments of the exopolymeric substances (EPS) have been recognized during SEM-EDX investigations of selected stromatolite samples.
3. Data obtained from stable isotope composition analysis show enrichment of the stromatolite samples in $^{13}C_{carb}$ up to 9.69‰ vs PDB. The same enrichment was

observed in the modern microbial mats from hypersaline environment of the Lagoa Vermelha in Brazil (Vasconcelos et al., 2006).

Preliminary results demonstrate environmental similarities between modern microbial mats growing in hypersaline coastal lagoons and Paleoproterozoic stromatolites from Eastern Fennoscandian Shield.

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PP-32

STRATIGRAPHIC AND GEOGRAPHICAL DISTRIBUTION OF CEPHALOPODS AT THE BAJOCIAN-BATHONIAN BOUNDARY (MIDDLE JURASSIC) IN EUROPEAN RUSSIA

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Until recently, the only known Bajocian-Bathonian boundary deposits on the Russian Platform were in the region of Don-Medveditsa dislocations of the Volgograd-Saratov-Povolzhye region. The cephalopod assemblages established are very similar in taxonomic composition to those of the northern (Northern Caucasus) and western (Sub-Mediterranean) margins of the Tethys Ocean. Deposits of this interval in the Boreal regions (Eastern Greenland, North Siberia) contain completely different ammonoid and belemnoid taxa. These differences led to the recognition of parallel biostratigraphic subdivisions (stages and zones) for the Boreal and Tethyan regions (Callomon, 1993; Meledina, 1994). This has significantly complicated the study of phylogenetic and ecological evolution and biogeographical distribution of the cephalopod communities of different basins. Data from the city of Saratov on the association and distribution of ammonites of Tethyan (Parkinsoniidae) and Boreal (Arctocephalitinae, Cardioceratidae) origin in the same section allow the Boreal and Tethyan scales to be correlated at the zonal level (Mitta & Seltzer, 2002; Mitta et al., 2004). The larger, lower portion of the Middle Jurassic series is dated as the local *Pseudocosmoceras michalskii* Zone, which is equivalent to the terminal Bajocian zone of the standard (Tethyan) scale and is characterized by exclusively Peri-Tethyan cephalopods. This zone is overlain by the *Oraniceras besnosovi* Zone, corresponding to the standard *Gonolkites convergens* and *Gonolkites macrescens* subzones of the lowermost Bathonian zone, which contains both Tethyan and Boreal taxa (belemnites and supposedly the first ammonites). The overlying *Arcticoceras ishmae* Zone is characterized exclusively by Arctic cephalopods. No indications of large gaps in sedimentation have been found in the section. The continuous sedimentary succession established (*Besnosovi* and *Ishmae* Zones) is part of the same cycle of sedimentation, and paleontological evidence allows the correlation of the *Ishmae* Zone with the upper half of the Lower Bathonian of the standard scale.

Studies in the basin of the Pechora River (at the Izma River), allowed the recognition in this region of European the earliest beds of the Boreal type (Upper Bajocian), characterized by the ammonite *Arctocephalites arcticus* (Newton). These sediments are overlain by the Bathonian *Arcticoceras ishmae* Zone, also containing cephalopods of Arctic origin. Thus, it has been established that the beginning of the first Boreal transgression onto the territory of Central Russia is dated as the bed of the Bajocian. At the beginning of the Bathonian, Boreal waters reached far south, reaching the latitude of Saratov. Importantly, migrations of various groups of molluscs, including cephalopods, were asynchronous. Paradoxically, the migration of belemnoids (and apparently bivalves), was more rapid than that of ammonoids. The new studies allow the geochronological correlation of the Boreal and Tethyan strata at the Bajocian-Bathonian boundary and recognition of the paleobiogeographical features of this interval of geological time.

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PP-33

BIOLOGICAL INPUT OF PROTEASE DIVERSITY

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Proteases are enzymes that are essential for all live organisms. They cut up biological polymers acting on peptide bonds (“biology’s version of Swiss army knives”, according to Seife, 1997). Proteases regulate the fate, localization, and activity of many proteins, modulate protein-protein interactions, create new bioactive molecules, contribute to the processing of cellular information, thus generating, transducing, and amplifying molecular signals. As a direct result of these multiple actions, different proteases are known to play key roles in multiple biological processes, including cell cycle progression, differentiation and migration, heat shock and unfolded protein responses, morphogenesis and tissue remodeling, neuronal outgrowth, angiogenesis, immunity, haemostasis, wound healing, ovulation, fertilization, autophagy, senescence, necrosis, and apoptosis (López-Otín, Bond, 2008). Proteases are also essential in viruses, bacteria and parasites promoting their replication and invasiveness, and on the other hand in hosts for the mediation and sustenance of diseases (Turk, 2006).

The biological significance of proteolysis has driven the evolutionary invention of multiple, extremely diverse types and families of proteases. Through evolution, proteases have adapted to the wide range of conditions found in complex organisms (variable pH, reductive environment and so on) (Nemova, Bondareva, 2008). Despite proteases share a common biochemical function, their catalytic domains exhibit sequence diversity. On the basis of the mechanism of catalysis, depending on critical amino acid residues in active site proteases are classified into seven distinct types: serine, cysteine, threonine (*N*-terminal nucleophile hydrolases), aspartic, metallo-, glutamic, and asparagine proteases (with the latter two being found only in fungi or viruses) (Rawlings et al., 2010). The diversity of proteases is further increased by the frequent attachment of auxiliary, non-proteolytic domains to the catalytic core (López-Otín, Overall, 2002; Puente et al., 2003) providing protease substrate specificity, guiding its cellular localization, modifying kinetic properties and sensitivity to endogenous inhibitors. According to evolutional protease classification – MEROPS (Rawlings, Barrett, 1993; Rawlings et al., 2010) – all proteases (192053 sequences, 3895 identifiers to date) can be further divided into 226 families on the basis of aminoacid sequence comparison, and these families can be assembled into 57 clans on the basis of similarities in their three-dimensional folding. Variability of known and putative proteases reflects the descent of modern proteins from a limited number of ancestral forms.

The recent availability of the genome sequence of different organisms has allowed the identification of their entire protease repertoire. The extensive biological and pathological implications of this large set of proteins with a common biochemical function led to the concept of proteases as a distinct subset of the proteome called degradome – the complete set of proteases present in an organism (López-Otín, Overall, 2002). For example, the human degradome consists of 569 active proteases, 175 putative proteases and pseudogenes, 410 inactive homologues, accounting for 2% of structural genes in humans (Quesada et al., 2009).

Many families of human proteases are also clearly recognizable in the genomes of *D. melanogaster*, *C. elegans* and *A. thaliana*. This indicates the existence of universal proteolytic routines in these organisms, although they are frequently expanded in vertebrates. It has become evident that, in addition to highly conserved protein turnover, proteases are also precise posttranslational modifiers of important signaling molecules, including ligands, receptors, adaptors, kinases and transcription factors. Moreover, proteases modify and influence each other forming the protease web. Biological meaningful of protease diversity (size, shape, specificity, optimal microenvironment, domain architecture, etc.) in the organisms of different taxa is on the centre of discussion with the special emphasis to protease family C2, or calpains.

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PP-34

EARLY STAGES OF MOLLUSCAN EVOLUTION

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The phylum Mollusca is one of the largest metazoan group, its taxonomical diversity is smaller only than that of the arthropods, and consists of approximately 130 000 nominal recent species and 70 000 nominal extinct species (Haszprunar et al., 2008). According to the recent estimations (Haszprunar et al., 2008; Ponder, Lindberg, 2008), the total biodiversity of modern malacofauna approaches the number of 200 000 species, so that about 70 000 unnamed recent forms await its formal description.

In addition to the high taxonomic diversity, molluscs are characterized by a number of different bauplans. The molluscs dwell in almost all types of habitats, occupying variable ecological niches in all range of marine and freshwater basins, and on the land. Such diversity and obvious ecological success were achieved during the long evolution of the phylum, lasting at least during the entire Phanerozoic.

The earliest finds of undoubted molluscs come from the terminal Precambrian (uppermost Nemakin-Daldynian) – basal Cambrian (lowermost Tommotian stage) strata (Parkhaev, 2005, 2008). The Vendian soft-bodied animals (*Kimberella*, etc.), recently declared as molluscan ancestors (Fedonkin, Waggoner, 1997), have principle ethologic and structural differences (Parkhaev, 2008), hence possibly represent other animals phyla but not molluscs.

Studies of ancient molluscs bring us closer to the problem of Mollusca origin, however, the pulling down of the molluscan stem to the Precambrian-Cambrian boundary, i.e. to the moment of appearance of skeletal fossils in the geological history, leaves us the very subtle hope, that the problem of molluscs origin can be solved on the base of paleontological finds of “transitional forms”, linking molluscs with their supposed ancestors, turbellarian flatworms (Salvini-Plawen, 1980), or annelids (Minichev, Starobogatov, 1975; Ivanov, 1990). Nevertheless, the study of Cambrian molluscs undoubtedly reveals interesting data for general and evolutionary malacology, shedding the light on the earliest diversification and evolution of major branches of the phylum. As a result, we can affirm the following peculiarities of the earliest molluscan evolution:

1) The oldest representatives of phylum appear just below the Precambrian-Cambrian boundary. The classes Monoplacophora, Polyplacophora, Gastropoda, and Bivalvia have

been formed already in the earliest Cambrian, i.e. from the beginning of paleontologically documented history of the phylum (Parkhaev, 2008). Other classes, Scaphopoda and Cephalopoda, have originated later, by the Late Cambrian – Early Ordovician.

2) Gastropods were the most morphologically variable and systematically diverse group of univalved Cambrian molluscs.

3) The major part of Cambrian gastropods was represented by the monophyletic subclass Archaeobranchia, composed of two orders Helcionelliformes (families Helcionellidae, Coreospiridae, Igarkiellidae, Rugaeconidae, Stenothecidae, and Yochelcionellidae) and Pelagielliformes (families Aldanellidae and Pelagiellidae) (Parkhaev, 2002, 2008).

4) The subclass Archaeobranchia was a “base” for further evolution of the class Gastropoda, being the ancestor of the larger gastropod branches, namely subclasses Cyclobranchia (=Patellogastropoda), Scutibranchia (=Vetigastropoda without Trochoidea, Turbinoidea and Seguenzioidea), Pectinibranchia (Trochoidea, Turbinoidea, and Seguenzioidea + Caenogastropoda), and the group Heterobranchia (subclasses Divasibranchia, Dextrobranchia, Sinistrobranchia, and Opistobranchia) (Parkhaev, 2007).

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PP-35

VARIATIONS IN MARINE ANIMAL DIVERSITY AND CARBON-HYDROGEN ACCUMULATION CYCLICITY IN THE PHANEROZOIC

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The relationship between biosphere evolution and oil accumulation changes in the Phanerozoic is studied. The stages of biosphere evolution are presented by the cyclic changes in diversity of marine animal genera. It is well known that the change in the content of atmospheric oxygen in the Phanerozoic was largely determined by the biospheric evolutionary processes, particularly, biodiversity evolution. As reported in [1], the cyclicity of oil accumulation in the sedimentary cover of the Earth is controlled by the formation of oxygen atmosphere and increase in the mass of carbon-hydrogen layer in the lithosphere. The data on actual petroleum reserves, which are representative of the changes in the intensity of oil accumulation processes, suggest that the periods of increase and decrease in oil reserves in the Phanerozoic coincide with those of transgression and regression of the World Ocean.

However, the interrelation between biodiversity and oil accumulation in the Phanerozoic have been investigated very insignificantly. So the prime objective of this work is study of the relationship between the cyclic changes in oil accumulation and the changes in marine animal biodiversity in the Phanerozoic. As the index of paleobiodiversity was used a number of marine animal genera, the most complete information on their changes throughout the Earth’s history given in the Sepkoski's global database [2]. The data source on the accumulated oil reserves used here is the global database on physico-chemical oil properties developed and compiled at the Institute of Petroleum Chemistry, SB RAS (Tomsk). The database on physico-chemical oil properties now includes [3] the information on 19000 oil samples from all main world oil-gas bearing basins.

Planetary climatogenic factors and stages of biosphere evolution were strongly affected by transgressions and regressions of the World Ocean changing the area of Earth’s water-surface and hence its reflectance. The epochs of maximal decrease in the World Ocean level correspond to the periods of climate cooling and glaciation. Cooling of the planet resulted in a decrease in vegetation productivity and in global extinction of animal genera, followed by a decrease in the mass of the carbon-hydrogen layer and intensity of oil formation processes.

The epochs of global cooling are referred to as “global geological winters” [1]. During the Earth’s history the global winters with poor vegetation and low increase in the mass of the carbon-hydrogen layer were followed by the epochs of global climate warming and luxuriant biosphere as “global geological summers”, which are characterized by an increased mass of the carbon-hydrogen layer and oil formation intensity.

It is shown that “the global summers” in the Ordovician, Carbonian and Cretaceous make the biggest contributions to the World Ocean level, which corresponds to the epochs of maximal breakdown of super continents [1]. The zones where the continents broke apart were well warmed up with the heat from the Earth’s bowels, and life was intensively developing there. Systematic changes in the geographical location of the continents exposed them to different climate conditions and promoted the evolution of living organisms. In this connection, an investigation of Phanerozoic biodiversity variations, cyclic mass variations of carbon-hydrogen layer as the main factor of oil formation, and explored oil reserves as a quantitative index of oil accumulation is appealing.

The foregoing shows that all phanerozoic time dependences of the number of existing and extinct genera of marine animals, mass of carbon-hydrogen layer, explored oil reserves, and the number of oil-bearing basins discussed above exhibit a cyclic character with periodic increases in the midpoints of geotectonic cycles and decreases at their boundaries**.** This close concordance of temporal changes in quantitative indicators of various geosphere-biosphere processes is validated by the high calculated values of pair correlation coefficients.

It should be noted that the results on cyclic oil formation-accumulation and global geospheric-biospheric processes in the Earth’s history obtained in this work not only explain the relationship between the cyclic changes in oil formation and accumulation and the variation of marine animal biodiversity in the Phanerozoic but could also be used to extend the theoretical view of the biosphere evolution over the Phanerozoic.

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PP-36

FORMATION OF NUCLEOBASES FROM FORMAMIDE IN THE PRESENCE OF IRON OXIDES

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Iron oxide hydroxide minerals, goethite and akaganeite were the probable constituents of the sediments present in the geothermal region of the primitive Earth. They might have adsorbed a variety of organics ontheir surface and catalyzed the condensation processes which led to the origin of life. The binding and reactions of nucleotides and polynucleotides on iron oxide hydroxide polymorphs has been studied (Holms etal., 1993). Formation of β-FeOOH in sterile sea water or brine, like in the deeps of the Red Sea, has beenobserved (Holms, 1984). Recently the role of hematite on Mars (Arora et al., 2007a) and the interaction ofzinc oxide with various nucleotides namely, 5' - AMP, 5'- GMP, 5'- CMP and 5'-UMP have beeninvestigated (Arora and Kamaluddin, 2007b). Formation of nucleic acid bases and their precursors fromformamide has been found in relatively higher yield by iron in lower oxidation state present in its sulfides(Saladino et al., 2008). Formamide, a hydrolysis product of HCN is a well known precursors of variousbiologically important compounds e.g., nucleobases (purines and pyrimidines and amino acids. We reportour results on the synthesis of nucleobases, adenine, cytosine, purine, 9-(hydroxyacetyl) purine and 4(3H)-pyrimidinone from formamide using iron oxide (hematite) and oxide hydroxides (goethite and akaganeite) ascatalyst. Goethite and hematite produced purine in higher yield as compared to akaganeite. The productsformed have been characterized by HPLC and ESI-MS techniques. Results of our study reveal that ironoxides might have worked as efficient prebiotic catalysts.

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PP-37

MULTIPLE PATHS TO ENCEPHALIZATION AND TECHNICAL CIVILIZATIONS

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We propose consideration of two possible evolutionary paths for the emergence of intelligent life with the potential for technical civilization. The first path to encephalization is exhibited by warm-blooded animals, the second is seen in the form of swarm intelligence in so-called superorganisms such as social insects. The path to each appears to be facilitated by environmental change: for warm blooded animals by decreased climatic temperature and swarm intelligence by increased oxygen levels. Beginning with a very warm early climate (Knauth 2005; Gaucher et al. 2008), the long-term cooling history of the Earth's biosphere correlates with the timing of major events in biotic evolution, e.g., the emergence of phototrophs, eucaryotes and Metazoa apparently occurred when temperatures reached their maximum tolerable values for these organisms, i.e., 70 °C (3.5 Ga), 60 °C (2.8 Ga) and 50 °C (1-1.5 Ga) respectively (Schwartzman 1999 2002). We proposed that the emergence of vertebrates and their correlative encephalization was similarly facilitated by decreased temperatures (Schwartzman and Middendorf 2000). Given an upper temperature limit for vertebrates of about 40 °C, the surface temperature history of the biosphere suggests only a narrow window exists for maximum encephalization, from roughly 500 MYA through the present. During this period not only was climatic cooling sufficient to allow efficient heat loss from a large energy-intensive brain, but encephalization is observed in hominin evolution--as well as for other warm-blooded animals including birds and toothed whales in the Cenozoic, and perhaps even for the mammal-like "reptiles" in the Permo-Carboniferous. We derived a first approximation estimate of the cooling required for hominin brain size increase from a simple model of heat loss, corresponding to temperature decrease of 1 to 2 °C, quite compatible with regional cooling during glacial episodes in the Pleistocene (Schwartzman et al. 2009). The second path, swarm intelligence, is apparently constrained by atmospheric oxygen levels which limit the size of insects and their brains. Remarkable structural, functional and developmental convergence between "mushroom" bodies in insect brains and the higher brain centers of vertebrates is noted (Farris and Roberts 2005). Is there is an atmospheric oxygen level for insect encephalization that is analogous to the climatic temperature constraint for warm-blooded animals? Did the insect giants of the Carboniferous show a burst of encephalization analogous to that of warm-blooded animals? Is the emergence of the collective superorganism intelligence of social insects (Hölldobler and Wilson 2008) linked to climatic changes? Is the attine ant and termite fungal agriculture and the functional architecture of the termite mound (Turner 2000) an analog of the human technosphere? Is the collective intelligence observed in social insects a second potential path to technical civilizations on Earth-like planets around Sun-like stars?

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FIRST MIKROIHNOFOSSILS FIND IN THE EARLY CAMBRIAN VOLCANO-HYDROTHERMAL FORMATION (KYZYL-TASHTYG PYRITE ORE FIELD, TUVA, RUSSIA)

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Kyzyl-Tashtyg pyrite deposits (Tyva) has attracted attention of researchers due to the fact that in its structural-geological features and the composition of ore, it has similarities with sulfide buildings hydrothermal fields at the bottom of modern marine basins. Of great interest is that the ore-bearing volcanic-sedimentary complexes of basalts and rhyolites of tumattayginskaya formation, synchronous with ore formation [1] are of Lower Cambrian age [2], that is field of Kyzyl-Tashtyg deposit is a unique well-preserved object, allowing to explore the ancient submarine volcanic hydrothermal system, similar properties to the modern black smokers (chimneys). Of particular interest in tumattayginskaya formation finds cause of microbial organisms (microihnofossils) in the amygdule of basalts at the base of the middle part of the upper strata above mentioned formation. These organisms are filamentous shape with a diameter of 5 to 25 microns, with a length of 500 microns. Filaments occur straight, curved, and branching. In rare cases, there contractions and cellular sructure of the filaments. Given the microscopic size, a simple morphology and similarity to modern analogues, these microorganisms can be roughly classified as *Cyanobacteria.* At the same time finding them in the amygdule of the rocks, in a confined space (the absence of light) suggests their likely chemotrophic nature. It should further be noted that microbial organisms are now known in ancient Archean pillow lavas [3, 4]. These microihnofossils are characteristic of Lower Cambrian deposits, where they have carbonate composition. In our case, which is extremely important microfossils are very different mineralogical composition. Studied in detail the samples is actually hydrothermal breccia. Fragments of basalt (up to 5 cm) with amygdule, with microfossils, cemented by hydrothermal material of carbonate composition with albite. In this predominantly carbonate matrix are also disintegrated (like melting, dissolving) relics (up to several mm) intensely chloritized and albitized basalts. Thus, according to these structural features and mineral composition, these breccias with fragments amygdule basalts were formed in the core crushing and penetration of hydrothermal fluids, which indicates a clear connection with the Kyzyl-Tashtyg hydrothermal ore field. Basaltic fragments from the hydrothermal breccia rich in rounded amygdule (up to 1 mm in diameter) filled microcrystalline gray mass, the crystallites of feldspar, epidote and clinozoisite. Usually in the central parts of the amygdule there are bright transparent crystals of feldspar, closely associated with light-green crystalline phases epidote. Sometimes albite located on the edges and the center amygdule - epidote with bright colors with crossed nicols. Analysis by scanning electron microscope showed that the gray microcrystalline mass that fills the volume of the amygdule, corresponds to the chemical composition of albite. Studies have shown that the material from which made tubular microihnofossils, in its chemical composition is most similar to epidote. Thus, the amygdales and microihnofossils are made of minerals, formation of which, according to the albite-epidote composition is clearly associated with hydrothermal processes that affected the basalts.

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THE ROLE OF ECHINOIDS IN SHAPING BENTHIC ENVIRONMENT

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Echinoids appeared in the Ordovician. During the Paleozoic, their diversity was low and their role in benthic communities was negligible. The only exception was probably the Early Carboniferous. During the Permian and Early to Middle Triassic echinoids were exceptionally rare. The genuine Mesozoic groups started to appear in the Late Triassic (regular echinoids); in the Jurassic their diversification was especially fast. The first irregular echinoids appeared in the Middle Jurassic. Since then, the class prospered, expanding into new habitats and playing an increasing role in shaping benthic environment.

Regular echinoids feed on sessile organisms, mainly macrophytes, transforming them into fecal pellets of specific size and shape, which can accumulate to form structured sediment. The latter provides favorable substrate for particular groups of animals, both epifaunal and infaunal (coprophagous). Fast population growth of some echinoids (e.g., *Strongylocentrotus droebachiensis* in the Barents sea) can result in catastrophic decline in algae density, so that large patches of the sea bottom may turn into ‘desert’. Among the regular echinoids, especially in the order Echinoida, there are many rock-boring species that change the microrelief of the hardground habitats. Traces of boring by echinoids are common trace fossils in the ancient beach rocks, starting from the Middle Jurassic (Palmer, 1982). One of the most important rock-boring echinoids is *Paracentrotus lividus*, distributed from Britain to Africa, including the Mediterranean. It forms large aggregations on rocky slopes and in dense seagrass from tidal zone to 30 m depth. Living in holes in the rock allows this species to withstand strong waves. *Strongylocentrotus purpuratus* produces numerous holes in steel supports of port facilities along the Pacific coast of California. This echinoid drills metal with its long spines and teeth.

Family Echinometridae appeared in the Paleocene. Echinometrids live in the tropics and represent an important component of reef communities. Virtually all echinometrid species are capable of drilling calcareous substrates. *Echinostrephus molaris* bores vertical holes up to 5-7 cm deep and up to 2-3 cm in diameter along the coasts of Papua New Guinea and some Pacific islands (Solovjev, 1980; personal observations). Each individual spends entire life in its hole. There are up to 80 individuals per 1 m^2. *Echinometra mathaei* inhabits hollows and winding passages and rarely can be found on the surface of the sea bottom. Each hollow appear to represent an integral result of boring by several individuals from several successive generations. Population density of this species can be up to 60 individuals per 1 m^2. *Heterocentrotus mammillatus* is a large echinoid that lives in niches in vertical or sloping walls of coral limestone in the tidal zone; sometimes it is found among the fragments of dead corals. These examples show an important geological role of echinometrids: they function as powerful destructors of reefs and tidal rocks.

Irregular echinoids inhabit loose sediments; most of them are infaunal and detritivorous (orders Holasteroida and Spatangoida; found from the Middle Jurassic to recent). By processing large quantities of sediment (bioturbation), they change the texture of its upper layers (e.g., extant species *Echinocardium cordatum* burrows up to 18 cm deep), and thus shape the environment of various benthic groups, including interstitial fauna.

Order Clypeasteroida ("sand dollars") appeared in the Paleocene and experienced extensive diversification since the Eocene. This group inhabits mostly shallow water habitats with coarse sandy, often oligotrophic, sediment. Their modes of feeding are highly unusual. They are either so-called sand sievers that sort particles by size with the help of the dense layer of small spines and use their tube feet and ciliary epithelium to transport food particles to the mouth along the grooves on the oral surface of the test; or they are typical suspension feeders that anchor the anterior portion of the test vertically in the sediment while positioning the oral surface against the current that supplies them with organic detritus. Population density of clypeasteroids can be quite high (e.g., tens of individuals of *Echinarachnius parma* per 1 m^2 can be found in the Sea of Okhotsk with total biomass up to 2-3 kg (Solovjev, Markov, 2006)).

Echinoids have numerous symbionts, such as bryozoans, bivalves, polychaetes, and barnacles. Symbionts often settle on the spines of cidarid echinoids. The coelom of many echinoids harbors numerous infusorians. The tests of the dead echinoids are used as substrate for settlement by various sessile and boring marine organisms: bryozoans, sponges, barnacles, algae, etc. The Late Cretaceous epoch, when fine calcareous sediments were widely distributed in the large epicontinental basins, is especially revealing in this respect. During the Late Cretaceous, the tests of large echinoids (e.g., Echinocorys) were convinient and sometimes the only available substrates for such organisms. Echinoids also affect pelagic communities. Their planctonic larvae, echinoplutei, along with the larvae of other bentic animals, provide trophic base for numerous pelagic planctivorous marine animals. Adult echinoids are fed on by starfish, gastropods, decapod crustaceans, octopuses, fish, birds, and sea otters. The gonads of echinoids is a favourite delicacy for people in several countries in Mediterranean and Far East regions.

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BIOMARKER HYDROCARBONS OF THE LOWER PROTEROZOIC OF THE KODAR-UDOKAN TROUGH (THE ALDAN SHIELD)

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Lower Proterozoic (1.86 Ga) organic matter (OM) in the Kodar-Udokan trough of the Aldan shield was found to be strongly metamorphosed, as evidenced by isotopically heavy carbon ($\delta^{13}C$ of insoluble OM ranging from —29.5 to —27.0‰), have the TOC values of 0.03-0.05% and a low chloroform-extractable bitumen content (0.0009-0.0015%), mostly resins (64.0-83.6%). The (fig. 1) results of biogeochemical studies suggest that this OM is aquatic, planktonic and bacteriogenic in origin, as indicated by the distributions of normal alkanes ($nC_{27}/nC_{17}<1$), acyclic isoprenoids (Pr/Ph<1), steranes (almost similar concentrations of C_{27} and C_{29} typical of aqueous deposits), and tricyclanes (tricyclane index $2C_{19-20}/C_{23-26}$ <1). Diasterane concentrations (Dia/Reg – 0.3-0.4) indicate that the initial OM was accumulated in the basin with prevailing carbonate-argillaceous sedimentation [1]. Diagenesis of OM in sediments occurred in a reducing environment without high content of hydrogen sulfide in bottom waters (C_{35}/C_{34} <1 [2]). Based on their biomarker distributions, Lower Proterozoic OM from the Kodar-

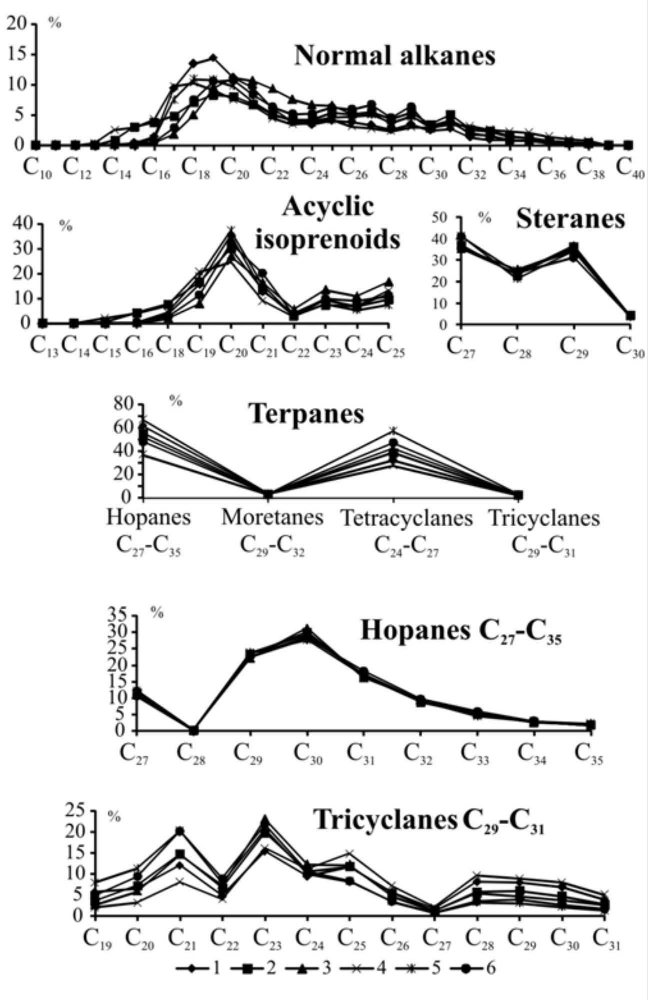

Fig. 1. Biomarker distribution in the chloroform-extractable bitumens of the Lower Proterozoic (1.86 Ga) rocks from the Kodar-Udokan trough of the Aldan shield (1, 2 - Sakukan Formation, 3-6 - Naminga Formation).

Udokan trough exhibits greater affinity to OM of the same age found in sediments from the Lower Khani graben-syncline and shungites from the Onega synclinorium [3], Upper Proterozoic OM from the Yenisey Ridge and Baykit anteclise [4], Vendian and Lower Cambrian oils from the Angara-Lena step and Bakhta mega-salient of the Siberian platform [5], as well as to some Precambrian oils and chloroform-extractable bitumens from the East European platform [6-8].

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THE STRUCTURE OF MICROBIAL COMMUNITY IN THE BOTTOM WATER LAYER OF LAKE BAIKAL AND POSSIBLE ROLE OF EUBACTERIA IN DESTRUCTION OF DIATOMS

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It is important to determine the possible role of bacteria in degradation of diatoms, as well as the role of factors and participants in the silicon cycle in aquatic ecosystems. The aim of this work was to study associations of bacteria and diatoms in natural objects before their burial in the sediments and under experimental conditions. The preservation of diatoms in the surface sediment layer and the amount of bacteria associated with diatom cells decreased with depth. The maximal abundance of bacteria associated with diatoms (112 thousand bacterial sequences of the 16S rRNA gene fragments) was recorded by means of pirosequencing in the bottom water layer. The microbial community was represented by the following dominant phylogenetic groups: *Proteobacteria, Acidobacteria, Actinobacteria, Cyanobacteria, Bacteroidetes, Verrucomicrobia, Firmicutes,* and *Nitrospira*. However, 32% of the sequences appeared to be non-classified because of the absence of analogues in the database. Seven strains of eubacteria were isolated during cultivation on a medium with diatom extract. According to the data of microbiological analysis and sequencing of 16S rRNA gene, these strains were identified as *Mycoplana bullata, Sphingomonas rhizogenes, Agrobacterium tumefaciens, Bacillus simplex, Acinetobacter johnsonii, Methylobacterium adhaesivum*, and *Deinococcus aquaticus*. Joint cultivation of these strains with a diatom *Synedra acus* subsp. *radians* (Kütz.) Skabitsch. caused inhibition of the diatom growth followed by cell destruction. Isolated strains revealed activity of hydrolytic enzymes: protease (*B.simplex, M. bullata,* and *D. aquaticus*) of β-xylosidase, β-glucosidase, β-galactosidase, chitobiase (*M. bullata, S. rhizogenes, A. tumefaciens,* and *B. simplex*), and amylase (*D. aquaticus*). The data obtained demonstrate that potential participants in silicon cycle that degrade siliceous valves of diatoms may be present among a great variety of microorganisms in the bottom layer of Lake Baikal.

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HOLLOW SPINES IN RADIOLARIAN SKELETONS AND SPONGE SPICULES

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The shape of main spines in radiolarian skeletons is very diversiform. In overwhelming majority the main spines are solid: rodlike, conical or faceted; rarer meet hollow spines. Spines frequently serve as a simple prop for axopodia; but in the inner channel of hollow spines or inside various microtubes can stretch axopodial filaments or bunches of axopods.

The texture of hollow main spines and other hollow skeletal structures is variant. Certain hollow spines and internal spicules represent the simple tubes (pl. 1, figs. 1-4, 6, 7, 8, 9). Other hollow spines and crossbeams are sectioned by horizontal lamellar septum (pl. 1, figs. 14, 15). Several hollow spines are complicated with development of special inner capsules (pl. 1, figs. 10, 13) which are supported precisely on the center of spine by radial lamellar septum (pl. 1, figs. 5, 10-13, 16, 17), quite often dual (pl. 1, figs. 5, 10). Capsules are hollow (pl. 1, figs. 10). If they are solid (pl. 1, figs. 13), it is most likely a secondary phenomenon. Wall thickness of capsule is comparable to wall thickness of hollow spine, or somewhat less (pl. 1, figs. 10). Internal surface of hollow spine smooth, but internal and external surfaces of capsules rough, with small tubercles and ledges (pl. 1, figs. 10, 13). Functional purpose of such capsules not clearly. Probably, they could be as a part of the hydrostatic apparatus.

The morphology of initial spicules and spiny radiolarians resemble sponge spicules. However, main difference between radiolarian skeleton and Porifera spicules consists is in peculiarities of skeleton formation: radiolarians spines grow spirally (pl. 1, figs. 18, 19), whereas spicules of sponges grow away from the center (pl. 1, figs. 20, 21).

Radiolarian hollow spines and other hollow skeletal structures, especially spines with hollow capsules, meet extremely rare in fossil state. Only twenty species with various hollow skeletal elements of all classes of radiolarians from Ordovician, Devonian, Carboniferous, Cretaceous and Paleogene are presented in our collection. Probably, subcylindrical spines with hollow internal channel are the initial, most ancient and primitive structures, which have originated in Cambrian. However, the further development of skeletons went on a way of formation of faceted solid spines. This was the optimal form, provides the greatest strength of spines in the least amount of a mineral material. Nevertheless, the morphogenesis of subcylindrical hollow spines repeated many times during all Phanerozoic up to the present.

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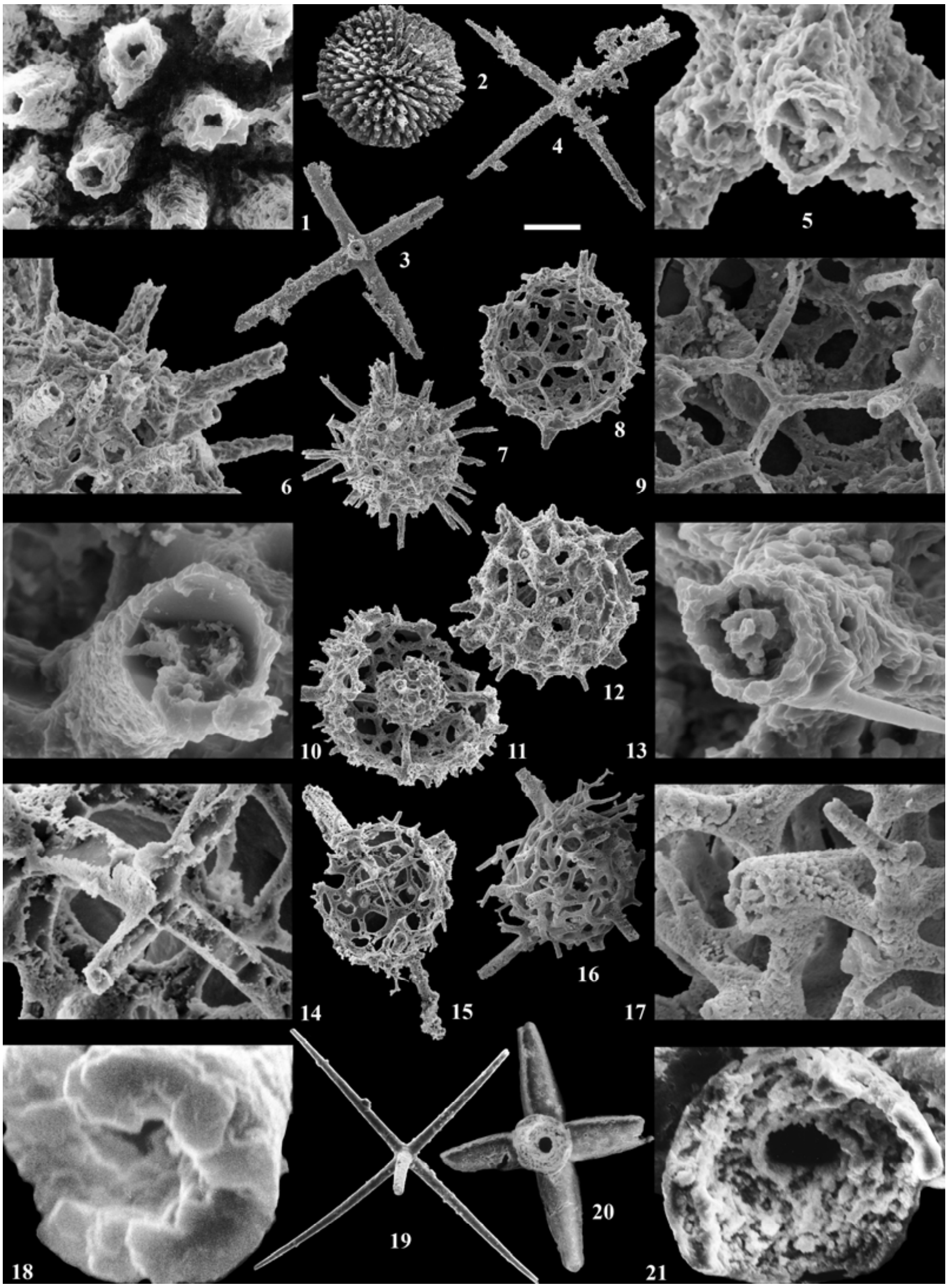

Plate 1. Middle Ordovician, Llandeilian, Kazakhstan, Chagan River (after Nazarov, 1988) – figs. 1, 2. Lower Carboniferous, Tournasian, South Urals, Orienburg Region – fig 2. Middle Devonian, Eifelian, Prague Basin, Czech Republic – figs. 3, 4. Upper Devonian, Lower Famennian: Polar Urals, Palnik-Yu River – figs. 8-13; Middle Urals, Perm Region, Vilva River – figs. 14-17; Middle Frasnian, Domanik Formation: Timan–Pechora Bassin, Lyajol River – figs. 18, 19, Domanik River – figs. 20, 21. Figs. 1, 2. *Anakrusa myriacantha*: 1 – (scale bar, 30 µm), 2 – (157 µm). Figs. 3-5. *Palacantholithus stellatus*: 3 – (126 µm), 4 – (110 µm), 5 – (13 µm). Figs. 6, 7. *Astroentactinia crassata*: 6 – (29 µm), 7 – (86 µm). Figs. 14, 15. *Polyentactinia rudihispida*: 17 – (18 µm), 18 – (59 µm). Figs. 10, 11. *Bientactinosphaera zuraevi*: 10 – (5 µm), 11 – (68 µm). Figs. 12, 13. *Entactinia bella*: 12 – (50 µm), 13 – (5 µm). Figs. 14-17. *Haplentactinia alekseevi*: 18 – (13 µm), 19 – (59 µm), 20 – (62 µm), 21 – (12 µm). Figs. 18, 19. *Palacantholithus stellatus*: 18 – (7 µm), 19 – (133 µm). Figs. 20, 21. *Triaxonida* sp.: 20 – (118 µm.), 21 – (29 µm).

PP-43

CAUSE-EFFECT RELATIONSHIP OF THE PALEOZOIC REEF-FORMATION EVOLUTION AND GEO-BIOLOGICAL EVENTS IN THE NORTH OF THE URALS

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The knowledge of processes leading to full transformation or ontogenic degradation of reef ecosystems is important for correlation of an initiation and disappearance of reef stages as display of large geo-biological events. The reef formation history in the North-uralian sea basin is subdivided into three stages each of which is characterised by different genetic types of biogenic frameworks.

The first longest Caradoc–Early Emsian stage is characterised by development of barrier ecological reefs from 100 to 1200 m in thickness in the conditions of various biospheric events. It was reflected in distribution of various metazoan-cyanobacterial (metazoa – rugose corals, bryozoans, sphinctozoan sponges, receptaculitids, hydroids) communities in reef ecosystems. Collision of Baltic and Laurentia paleocontinents has increased areas of erosion and, accordingly, mesotrophy of sea waters. Passive rifting and post-rifting immersing as result of an activization of the Pechora Plate basement blocks were shown in sharp differentiation of deposition settings within carbonate platforms. Global regressions as a result of a climate coolong at formation of glaciers on Gondwana caused an exposition of the carbonate platforms and accordingly of reef surfaces erosion. Climate warming generated global transgressions which were often accompanied in the beginning by occurrence of anoxic conditions sometimes fatally influencing on the reef ecosystems. At infringement of ocean circulation owing to global fluctuations of a sea level the anoxia phenomenon had global character and was accompanied by extinction events (the Hirnantian, Ireviken, Lau, Klonk, etc. events). However they did not occur an essential structural reorganisation of the reef ecosystems in the north of the Urals since pioneer communities accepted active participation in formation of the biogenic frameworks.

During the second Middle Frasnian-Tournaisian stage many benthic communities constantly tested hydrochemical and biological stresses in system of biospheric processes. Regeneration and active development of the Pechora-Kolva paleorift zone as a system of deeps at the shelf, frequent fluctuations of a sea level, a collling during the Famennian time, extinction events (the Kellwasser and Hangenberg) have led to development only the ecosystems of large (up to 600 m in thickness) microbial mounds. They were formed on slopes of shallow-water carbonate platforms surrounding of starved basins. Mass distribution of the pioneer cyanobacterial communities, non-skeletal calcimicrobial carbonates and oolitic sands are the stress indicators in the reef ecosystems. Global falling of a sea-level at the Frasnian-Famennian and Famennian-Tournaisian boundaries accompanied by as the biotic extinction and an ocean anoxia were not reflected catastrophically in the ecosystem structures of the microbial mounds since metazoan frame-builders played an insignificant role in them.

The final Late Visean-Early Permian stage is characterised by an abundance in the benthic ecosystems by fragile and small метазоа (fenestral bryozoans, sponges, palaeoaplysina, etc.), green phylloid algae. Biologically induced cement made a considerable part of biogenic frameworks. Prevailing pioneer communities in association with abundant cement formed skeletal, microbial-algal, and mud mounds from 5 to 330 m in thickness developing on slopes of deeps of the carbonate platform margin had been deformed because of a progradation of the Pre-Urals Foredeep on the one. During this stage, cardinal reorganisation of the reef ecosystem structures and accordingly of the biogenic frameworks was defined by mesotrophy of the sea waters in connection with sharp increase of the erosion areas as a result of closing of the Paleo-Uralian ocean, distribution mainly sessile metazoan organisms with the aragonite and high-Mg calcite skeletons, shallow-water seas and colling as a result of a glaciation of Gondwana in the Late Carboniferous-Early Permian time.

The allocated stages in evolutions of the Paleozoic reefs in the north of the Urals and an originality reef ecosystems ontogeny can be estimated as indicators of periodicity of the large biospheric reorganisations which can be used for global correlations of the Paleozoic reef formation.

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PP-44

DYNAMICS OF CARPINUS BETULUS L. AREA ON A LATE GLACIER PERIOD AND HOLOCENE IN EAST EUROPE

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The traditional problem of ecology and geography is researching of influence of paleoclimate variability on a plant migration. The paleogeography aspect is the most developed. It includes reconstruction of plant area for different time interval (Post, 1926; Huntley, Birks, 1983; Grichuk, 1989 et al.) and paleoclimat conditions through the plant structure (Bruks, 1952; Webb, 1971; Velichko, 1973 et al.). The less developed direction is reconstruction of plant dynamics according to self-development and variable environmental conditions.

Paleopalinology databases weren’t developed for East Europe before. We developed database “PALEO” based on published information (most of paleopalinology literature after 1940) (Kozharinov, 1993).

Area of *Carpinus betulus L.* occupies Europe part of Russia, the Baltic states, Belarus, Ukraine. Researches of climate determination of area *Carpinus betulus L.* show dependence between hornbeam expansion and climatic factors (Kozharinov, 1989).

According to maps of *Carpinus betulus L.* paleoareas, his becoming dated 12000 – 12500 y.a. and connected with Volynskaya highland (up to our time).

Volynskiy center was clear registered up to 10000 y.a., then near by 9500 y.a. Kaliningradskiy, Polskiy, Karpatskiy and Kodry centres were activated. Area’s configuration has saved stable through 1000 years up to 8500 y.a., when pollen of *Carpinus betulus L.* is detected near Vidzemskaya and Podolskaya highlands. *Carpinus betulus L.* becoming is registered near Sudomskaya and Bezhanitskaya highlands up to 8000 y.a. In Meschera’s peat profiles *Carpinus betulus L.* becoming near by 7500 y.a. The north board of *Carpinus betulus L.* expansion goes through 57 °N. By the time hornbeam occupied the territory of Ukraine forming forests.

Through 5000 y.a. *Carpinus betulus L.* was registered near by coast of Baltic Sea. We suggest “baltic” migration passage was the main for the most of broadleaf species expanse to the north-west. Single pollen of *Carpinus betulus L.* were registered at North-East of Europe. The “zero” zone (where hornbeam wasn’t registered) is wide and divided the main area (where pollen was detected in every alternative peat profiles). *Carpinus betulus L.*

expansion goes through 40 ° E at the east, and *Carpinus betulus L.* was detected in Meschera and Donetskiy ridge. Hornbeam grows in that conditions up to resent time.

According to our data, the north-east board of area was stable through out last 3000 – 4000 years, but “central” exclave disappeared recently.

According to starting time of detection of pollen, we suggest *Carpinus betulus L.* conservation was in high-relief regions with fat carbon soils – Volyn, Karpaty, Kodry.

The local maximums – Kaliningradsko-Polskiy, Volynskiy et all. – we determine as “climatic refugiums”. The processes of hornbeam’s introduction and elimination into association were registered here according to climate changes. In the “absolut refugiums” hornbeam was registered constantly during late glacier period and Holocene. They less depend on climate changes. There are Karpaty, the south of Pridneprovskaya highland and Kodry.

Statistically average configuration of *Carpinus betulus L.* area reminds modern area, and we suggest *Carpinus betulus L.* area mainly “inherent” from the past. The general developing trend of *Carpinus betulus L.* area and Tilia and Quercus the same. The main difference connects with later *Carpinus betulus L.* becoming in East Europe. This period is dated 10500 – 10000 y.a. when area structure of other broadleaf species have gotten features of latitudinal zonality. The zones of most variable part *Carpinus betulus L.* into association situate at North-West (Karelia, coast of White Sea), within the bounds of Predpolesye – Minskaya highland and along by modern north-east board of area.

Fluctuation of *Carpinus betulus L.* area boards usually have 500-year period or close. Inside pattern of area is more clear, but its period of fluctuation expresses weakly.

PARTITION OF MICROELEMENTS IN CARBONACEOUS-PHOSPHATIC DEPOSITS IN SOME ANCIENT AND RECENT BASINS

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According to geological data, the carbonaceous and phosphatic deposits are often co-existing in geological sequences beginning from early Pre-Cambrian time owing to their common biogeochemical origin related to C-P coupling in organic matter. The similar phenomenon is observed in the Recent ocean in its most biologically productive shelf areas. Besides, the both types of deposits are more or less enriched in several microelements which might be helpful for paleo-environmental reconstructions and for practical use. In last years the geochemistry of microelements in such deposits has been studied rather thoroughly, but the comparative geochemistry of these bodies is less developed.

This work presents some analytical results based on materials collected by the author and many colleagues from associated carbonaceous and phosphatic deposits on land and on sea bottom, namely Karatau (Kazakhstan, Cambrian), Maardu (Esthonia, Ordovician), Maikop Basin (Kazakhstan, Oligocene) and from Namibian and Peruvian shelves (Recent and Late-Quaternary organic-rich and phosphatic sediments, described by Baturin, 1982).

The Karatau deposit consists of interbanded microsphorite and black shale layers, the Maardu deposit comprises the lower shelly phosphorite layer covered by black shale, the Maikop ore body has a form of extended breccia bed consisting of fish bone debris intermixed with clay material impregnated by finely dispersed iron sulfides, with rarer inclusions of pyrite and phosphatic nodules.

The samples have been analyzed by ICP-MS method in the Institute of Mineral Resources and Institute of Microelectronic Problems and Ultra-Pure Materials, RAS (Moscow).

The group of elements choosed for consideration includes Ag, As, Ba, Bi, Cd, Cu, Hg, La, Mo, Ni, Pb, Sb, Se, Sr, Tl, U and Y.

The range of element concentrations

In each type of deposits the range of elements concentration is usually rather large, so it is reasonable to deal with average values which might be compared with the averages offered for clayey sediments (Turekian and Wedepohl, 1960; Vinogradov, 1962), black shales

(Ketris and Judovich, 2009), and phosphorite (Altshuler, 1960). The range of some element concentrations in analyzed samples (in ppm) is shown in the table.

The comparing of these values with average concentration of elements in black shale shows that Karatau shale is enriched only in Sr and Y, being depleted in all other elements.

The Maardu shale is enriched in Mo, U, Pb, V, and according to preliminary determination, also in Hg, which is unusial in ordinary sedimentary deposits.

The concentration of microelements in Maikop clays underlying the ore breccia is relatively near to values typical for black shales and even higher for Mo.

The Recent organic-rich oozes with phosphatic inclusions from both Peruvian and Namibian shelves are enriched relative to black shales in Cd and Mo, but equal in Ni, Sr, U, slightly depleted in Ag, As, Ba, Cu, Pb, V, Zn, and essentially depleted in La, Sb, as well as in Bi and Re.

The data concerning average concentrations of microelements in phosphorite are not complete and need some reconsideration but still valid in the present case.

When compared with average values offered by Altschuler (1960) the Karatau phosphorite is enriched in As and Sr and depleted in other minor elements. The Maardu phosphorite is highly enriched in Hg and Mo, to lesser extent in Sr and Pb, along with negligible fluctuation of other elements. The Maikop breccia is exceedingly rich in Mo and enriched in U, Ni, Se, Cu, Zn, Sr, La, Y, and Sc. The Recent and Late-Quaternary phosphorites are enriched in Sr and Mo.

Average concentration of elements (ppm) in carbonaceous-phosphatic deposits

Element	Karatau		Maardu		Maikop		Peru shelf		Namibian shelf	
	Shale	Phos.	Shale	Phos.	Shale	Phos.	Sedim.	Phos.	Sedim.	Phos.
Ag	0.13	0.28	2.7	0.27	0.40	0.75	0.50	0.35	0.60	0.19
As	14	62	35	49	43	72	21	10	19	14
Ba	264	240	380	170	336	215	365	190	235	115
Cd	0.13	0.10	1.9	0.17	1.4	5.7	31	8.4	40	13.5
Cu	12	10	65	30	78	300	43	25	49	19
La	23	150	32	200	40	600	17	10	10	85
Mo	5.5	10.7	200	19	122	214	37	6.5	85	36
Ni	12	70	85	18	110	470	63	43	98	48
Pb	23	29	94	180	30	64	18	9.5	6	8
Sb	0.9	4.0	8.8	30	11	30	2.8	1.4	0.65	3.55
Tl	0.06	0.05	6.6	1.4	1.5	13	1.5	2.3	1.3	11.0
U	18	21	98	50	34	1480	10	46	23	84
V	35	50	680	25	185	75	120	97	130	33
Zn	19	50	57	14	152	786	97	50	93	38

According to these data, the average concentrations of several microelements in coupled carbonaceous and phosphatic deposits reveal positive correlation which might prove that both ancient and Recent deposits formed in comparable marine environments owing to similar biogeochemical processes (Baturin, 1982). The partial correlation of some metal contents (Pb, Ni, Cu, Zn) with average world shale abundances might be related to their terrigenous origin. Besides, the exotic Hg enrichment of Maardu shale and phosphorite (our data) might be interpreted as postdepositional hydrothermal input induced by tectonic activity.

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SURVIVAL OF HALOPHILES AT DIFFERENT SALT CONCENTRATIONS AND FREEZING CYCLES

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Earth's microorganisms can be delivered to Mars by impacts of meteoroids of Earth's origin and modern mission to Mars. To study of the possibility of survival of Earth's microorganisms on Mars, we need to select the most suitable types of them. Halophiles are one of the most interesting types of microorganisms, because salt solutions on Mars could be more widely distributed through subsurface martian soil in comparison with pure liquid water. The existence of salt solutions that could serve as media for organisms analogous to halophilic archea at -23 °C and high salt concentrations on Mars has been widely discussed [1]. Study of the elemental composition of the Martian soils shows high concentrations of Cl [2], perchlorates, and solubable sulfates [3].

The aim of this study was to select bacterial and archeal strains most adapted to Martian conditions for the next step of our experiment about the possibility of the active growth of these microorganisms at dryness, low atmospheric pressure and other extreme conditions.

Methods. Bacterial (*Halomonas* sp. H-8, *Halomonas* sp. H-12, *Salicola* sp. H-9) and archeal (*Halorubrum* sp. H-2, *Halorubrum* sp. H-3, *Halorubrum* sp. H-4, *Halorubrum* sp. H-7, *Halorubrum* sp. H-11, *Halorubrum* sp. H-13) strains were isolated from different salt lakes of Altay region. Strains were grown in medium, which contained per liter 0-300 g NaCl, 5 g $MgCl_2$, 1 g KCl, 1 g $CaCl_2$, 4 g tryptone, 2 g yeast extract, and 10 ml of a trace metal solution, at 37^oC. For exposure experiments cells were suspended in a medium with the same NaCl concentration. Following treatments, cells were plated on solidified growth medium and incubated at 37^oC for several days. Cell numbers were estimated from CFU. Treatments were as follows: aliquots of cell suspensions were kept both at – 70 ^oC and - 18 ^oC for up to seven days. At least three exposure experiments were performed.

Results. *Halomonas* sp. H12 strain had the widest growth range (50-300 g L^{-1}) and optimum at 100 g L^{-1} NaCl. Other strains grew at 100-300 g L^{-1} and had the growth optimum at 100 and 200 g L^{-1} (*Halomonas* sp. H8, *Salicola* sp. H9); and *Halorubrum* strains H2, H3, H4, H7, H11, H13, at 200 and 300 g L^{-1}. Freezing of cultures at -70 °C и -18 °C for 168 hours usually resulted in reduction of CFU. At 100 g L^{-1} NaCl and after freezing at -70 °C and -18 °C, bacterial cultures, except *Halomonas* sp. H8 at -70 °C had high CFU number; in only a single case of *Halomonas* sp. H8 at -70 °C, CFU number decreased for 27%. At 200 g L^{-1} NaCl, freezing at -70 °C decreased CFU number for 8% to 97% in all cases, but complete extinction was not observed. The most dramatic growth depression was observed for *Halorubrum* strains H4 and H7. The H8, H9, H12, and H13 strains had a high survival rate. The majority of cultures successfully survived freezing at –18 °C: 0 to 40% decrease of CFU number was detected. Freezing at -70 °C at 300 g L^{-1} NaCl resulted in complete extinction of all cultures, while freezing at -18 °C led to extinction in six cases; CFU number decreased significantly in H3 and H7 strains, and the *Salicola* sp. H9 quantity didn't change.

Discussion. Halotolerant bacteria belonging to the *Halomonas* genus had the widest growth ranges. Growth optimums of bacterial strains were shifted towards smaller NaCl concentrations (100, 200 g L^{-1}). Obligatory halophilic archeal strains had smaller growth ranges and had growth optimum at 200-300 g L^{-1} NaCl. Bacterial strains were more tolerant to different incubation temperatures. Archeal strains were less tolerant to freezing; the most significant mortality was detected at -70 °C, which was earlier demonstrated for the halophilic archeobacterium *Natronorubrum* sp. [4]. Judging from the results of our experiments, we can suggest that these are not halophilic archea but halotolerant bacteria that could be the analogs of Martian organisms, since they can survive wide mineralization ranges and low temperatures with the lowest decline of viability. In earlier studies, the effects of different stress conditions have been tested on several microorganisms from the bacterial domain with various ecological properties [3]; in this study we demonstrated a high survival potential of halotolerant bacteria, which makes them likely candidates for life on early Mars. We are planning to present an additional experiments with lower organic content in the solution and adding of perchlorates and sulfates. Also the impact of low atmospheric pressure and ionizing radiation on survival of halotolerant bacteria will be studied by simulation experiments.

The financial support by Integration Project 10 of the Siberian Branch of RAS, RFBR 11-05-00717 is gratefully acknowledged.

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PP-47

ISOPRENOID BIOMARKERS AND MICROBIAL TRANSFORMATION OF DEEP HYDROCARBON FLUID FLOWS

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A hydrocarbon-water fluid moving from higher pressure and temperature conditions to lower ones is chemically nonequilibrium with decomposing and rebuilding molecules. These features of oils cannot persist for a long time and they disappear under the effects of either abiogenic processes or microorganisms. The energy contained in such chemically nonequilibrium fluids is sufficient for anaerobic feeding of microorganisms. Isolated media having neither income nor outcome of matter are justly considered to be lifeless. The evident regularities in the chemical composition variation of oils with change of the depth have been revealed. The deepest seated oils and gas condensates contain only negligible quantities of isoprenoid biomarkers taken from the particulate organic matter. The original set of their pseudobiomarkers is similar to those discovered in the carbonaceous meteorites. The main components of this kind of oils are n-alkanes and the optical activity of such oils has not been revealed. Up-seated oils with a significant amount (up to 1% and more) of the chain isoprenoids of the phytane, pristine and their homolog types are generated during the deposit processes with the participation of archaea consuming geofluids as a substratum. In this case the temperature in which they exist may be as much as 100° C and even more. As a result, chain isoprenoids of the membranes of those microorganisms find themselves in the oils. It is essential that the formation of the above-mentioned biomarkers is simultaneous with the formation of oil deposits but not in their further secondary transformation.

PP-48

BACTERIAL MINERALOFORMATION IN WATER ECOSYSTEMS OF MUD-VOLCANIC ORIGIN (THE BAIKAL REGION)

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Geologic setting and hydrogeological peculiarities of water ecosystems formation (salty lakes, thermal sources) situated in mud-volcanic structures of Cainizoic age of the Baikal region have been studied. Salty lakes and thermal sources are the microorganisms and their community environment and participate in lythogenesis, petrogenesis and mineraloformation processes.

The objects of study are sandy-silt formations of salty lakes, silts, travertines and geyserites of thermal sources of Torey, Undino-Dainskaya, Ivolginskaya, Tsipikanskaya, Eravninskaya, Barguzinskaya and Tunkinskaya depressures, some cutting of hollow sides and bottoms in the latter ones.

It is revealed that some salty lakes (Kulinye, Alginskie bogs of Baunt resort) are formed nowadays due to pouring out of alkaline waters of thermal sources of gryphon type. All types of salty lakes and alkaline thermal sources are characterized by extreme conditions of vital activity of haloalcalophile communities microorganisms.

Taking into account the travertine sediments of Garga mineral source of the Baikal zone it was established by us that thermophile cianobacteria are able to form actually monomineral calcite rocks and a number of accessory ore minerals including native gold in them.

A great diversity of microorganisms has been revealed in microbe mats and silts of carbonate waters of Zhoigon source in Vostochno-Sayanskaya province depositing calcite travertine with numerous lytiphics biofilms of bacterial mats. Microscope study of mucous ochric sediment formed in this source waters pouring out place revealed the presence of noticeable number of filiform ferrobacteria close to *Leptothrix* sp. and Gallionella sp. associating with cianobacterial mats.

SOME PECULIARITIES IN THE DISTRIBUTION OF Ra, U, Th AND SPECIES OF FORAMINIFER IN THE DERUGIN BASIN (SEA OF OKHOTSK)

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As a result of influence of the increased radioactivity on biocenosis is a reorganization of the structure of community, in which the dominants are the most resistant species.

Thus, the zones of the increased natural radioactivity are of interest for research of evolutionary transformations in the history of biosphere of the Earth.

Real consequences of long influence of the increased natural radioactivity on a biodiversity and abundance in the biocenosis may be detected in these zones.

The benthic organisms living directly in the bottom sediments or on sediment surface are the most subjected to the influence of radiation from radionuclides, which are concentrated in sediments. One of such regions is the Derugin Basin characterized by the increased radioactive background. The study of Th, U and Ra distribution in sediment and the analysis of some peculiarities in the structure of benthic foraminifer community has been made. Comparison of percentage Saccorhiza ramosa in community of benthic foraminifers and concentration of radionuclides in sediments showed that the quantity of shells Saccorhiza ramosa correlate with concentration of Th, U and Ra in the sediment. Thus domination of Saccorhiza ramose in community increases with the increase of concentration of Th, U and Ra in sediments. Coefficients of correlation with Th, U and Ra concentration make 0.75, 0.84 and 0.85, accordingly.

As for limy shells, Th, U and Ra may have suppressing effect. Anyway, the part of these shells decreases with growth of radionuclide concentration. Factors of correlation with Th, U and Ra concentration are equal -0.58, -0.61 and -0.74, accordingly.

The revealed changes in the structure benthic foraminifers may be also caused by another factors. Thus it is necessary to examine if the radioactivity is the dominating factor or these changes are the result of a number of reasons making a multiplied effect.

PP-50

STATISTICAL EVALUATION OF THE HOLOCENE TEMPERATURE PARAMETERS IN THE NE OF EUROPEAN RUSSIA (BY PALINOLOGICAL DATA)

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In the given work present paleoclimatic investigation included palynological and statistical analyses, radiocarbon dating of the Holocene lake, alluvial (oxbow lake) and swamp sediments in middle and northern taiga subzones of the Komi Republic. On the basis of cores of four boreholes and fourteen outcrops, synchronous spectra correlation and Holocene separation were accomplished [1].

Mean annual and July temperatures were estimated by zonal method of the Holocene paleoclimates reconstruction [2], based on palynological assemblages for characteristics of environmental changes during the interval. It has been established that the sediments accumulated during the Preboreal–Subatlantic interval, when repeated climatic changes occurred.

To determine the main trends of paleoclimate changes climatic curves have been drawn. The curves show deviations of the mean annual and July temperatures during the Holocene from their current values. For this purpose, the statistical weight of mean temperature values are taken into account in paleoclimatic curves approximating, as the temperature ranges in certain intervals of the Holocene vary considerably.

According to the palynological data and statistical analyses three periods with warmer climatic conditions (Early Boreal, Middle Subboreal and Late Atlantic) were estimated. It is established, that climatic optimum have developed at the end of the Atlantic period to what distribution of the most thermophilic tree species (oak, elm, hazel and maple) and the highest temperatures testifies. The Atlantic period is characterized by mean July temperature on 2.5–3.5 °C and mean annual temperature on 2–3 °C warmer, than at the present time. The Boreal and Subboreal temperature maxima had the subordinated value. Thus, from the Preboreal period the increase tendency of temperatures up to the maximal values at the end of the Atlantic period is observed. Then reduction of temperatures to the present has followed.

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EVOLUTION OF INFAUNAL SCAVENGERS AND CLOSURE OF THE VENDIAN TAPHONOMIC WINDOW

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Fossil record of Ediacaran soft-bodied organisms discontinues at the lower Tommotian boundary. Were these organisms members of extinct groups or was it the termination of unique taphonomic circumstances (closure of the Vendian taphonomic window) that led to disappearance of the fossils? Was it vanishing of sediment-sealing microbial mats, an increase in degree of bioturbation, or an advent of scavenging that led to the ultimate closure of the taphonomic window? The answer is probably found in Arctic Siberia in a package (26 m) of wavy-, hummocky-, and convolute-bedded sandstones interstratified with shales, siltstones, and calcitic mudstones constituting the Syharghalakh Formation of the Kessyusa Group. The package contains trace fossils (Treptichnus pedum), small skeletal fossils (Purella antiqua Zone) and macrofossils (Sabellidites cambriensis) of pre-Tommotian (Fortunian) age. Upward the section is succeeded by a unit (80 m) of alternating shale and siltstone, with laterally discontinuous sandstone and ooid grainstone beds, marked by the first appearance of arthropod trace fossils Rusophycus avalonensis, macrofossils Platysolenites antiquissimus, and small skeletal fossils of the Tommotian Nochoroicyathus sunnaginicus Zone. Sandstones of the Syhargalakh Formation are bioturbated, except for the lowermost part containing a fossil assemblage of soft-bodied organisms of frondomorphs (fronds and holdfasts) and corrugated tubular sheaths. The fossils are preserved in exquisite detail, with considerable relief, which is typically found in the Vendian taphonimic window; however, lithified microbial substrates and associated fossil soft-bodied organisms of the extinct kingdom Vendobionta are not present in the assemblage. The pre-Tommotian increase in bioturbation could have been responsible for disappearance of sediment-sealing microbial mats, but it did not alter sediment properties to a degree that would facilitate disintegration of soft tissues prior to the onset of diagenesis. The absence of vendobionts, therefore, most likely reflects the destruction of microbial substrates, their principal biotope in the wave- and current-agitated zone, by sediment-mixing animals. The soft-bodied frondomorphs are preserved as Ediacaran death masks in bioturbated, biomat-free sediment. This occurrence suggests that neither bioturbation nor destruction of microbial substrates, but scavenging of smothered dead organisms by infaunal macrophages, was responsible for the ultimate closure of the taphonomic window.

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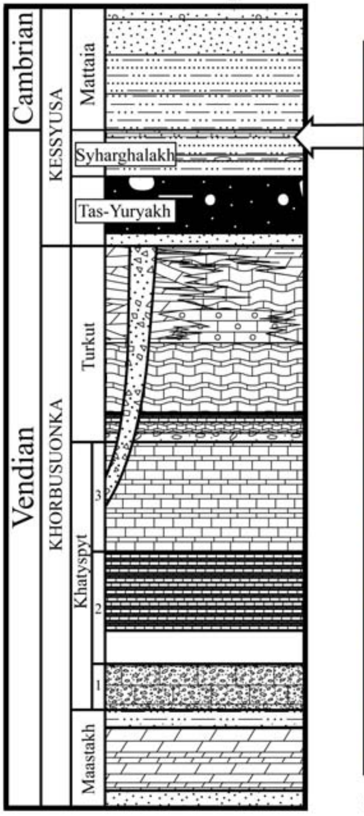
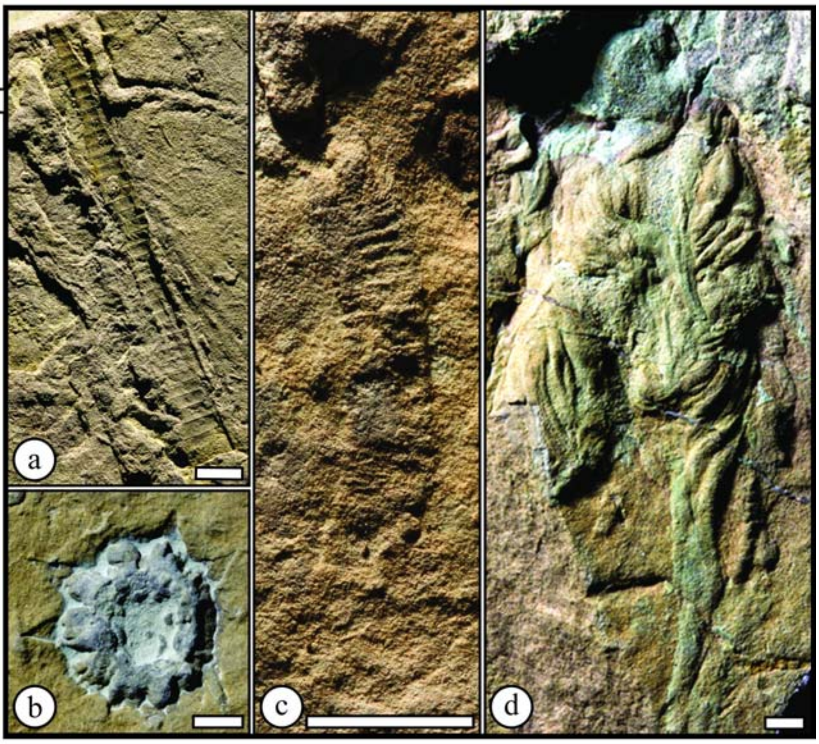
Composite section of Vendian and lowermost Cambrian of the Olenek Uplift



Fossil assemblage of soft-bodied organisms from the Syharghalakh Fm



scale: 5 mm

- ▨ - sandstone
- ▨ - dolomitolite
- ▨ - siltstone
- ▨ - intraclast limestone
- ▨ - finely laminated bituminous limestone
- ▨ - coarsely-stratified limestone
- ▨ - thinly laminated limestone
- ▨ - calcareous sandstone
- ▨ - alternating shale and sandstone
- ■ - diamictite
- ▨ - cross-bedded limestone
- ▨ - oolitic limestone
- ▨ - microbial limestone
- ▨ - medium bedded limestone

ⓐ - corrugated tubular sheat

ⓑ - holdfast of a frondomorph organism

ⓒ - mold of a compresed sheath *Sabellidites cambriensis*

ⓓ - frond of a frondomorph organism

EARLY PROTEROZOIC BIOMORPHIC STRUCTURES IN SIBERIA AND PROBLEMS IN SEARCHING EXTRATERRESTRIAL LIFE

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Microtectonically deformed metacrysts in the Lower Proterozoic Butun Formation of the Udokan Group (Transbaikalia, Siberia) are remarkably biomorphic in their appearance. Hollow column, or sheath-like metacrysts, in particular if there are less resistant secondary minerals in the core, often weather out as **tubular structures**. Metasomatic mono- and polymineral fridges in the weathered out metacrysts are often misinterpreted as **external walls**. Microtectonic deformation transforms abutting metacrysts and druses of metacrysts into variously **curved and branching objects**, whereas the deformed metacrysts themselves have rounded faces and cylindrical shapes. Prolonged metamorphism leads to fragmentation of the metacrysts by transversal microcracks that become filled with secondary mineral resembling **septa** and **monoseriate arrangement** of tubular structures. Growth-related corrugated morphology of the metacrysts can be taken for growth-lines of tubular objects. Petrographic and SEM study of metacrysts from the Butun Formation confirmed the presence of two types of biomorphic structures. (1) Metacrystalline aggregates of lawsonite (occurs at low-T, medium to high-P conditions) and associated secondary minerals have columnar shape and square cross-section, sometimes with rounded corners as a result of microtectonic deformation. Lawsonite. These aggregates were described as metazoan fossils *Udokania problematica*. (2) Metacrystalline aggregates of olivine (high-T and high-P) and accessory minerals heavily deformed by microtectonics. These aggregates were described as metazoan fossils *Udokania leitesi*. Despite the mineralogy and relying solely on the shape, *Udokania* is currently regarded as the oldest metazoan fossils. These biomorphic structures pose problems in terms of pattern recognition: in brief, when do shapes become significant? The example with *Udokania* is especially relevant for atrobiology because just such images might be returned from the unmanned vehicular exploration of other planets. It is worth recalling therefore that in the future exobiologists may be faced with a similar set of conundrums that even today face us with certain terrestrial fossils. This study was supported by the RAS Program “Biosphere origin and evolution”.

PP-52

FROM OFFSHORE TO ONSHORE: A NEW RANGEOMORPH SPECIES FROM CENTRAL URAL

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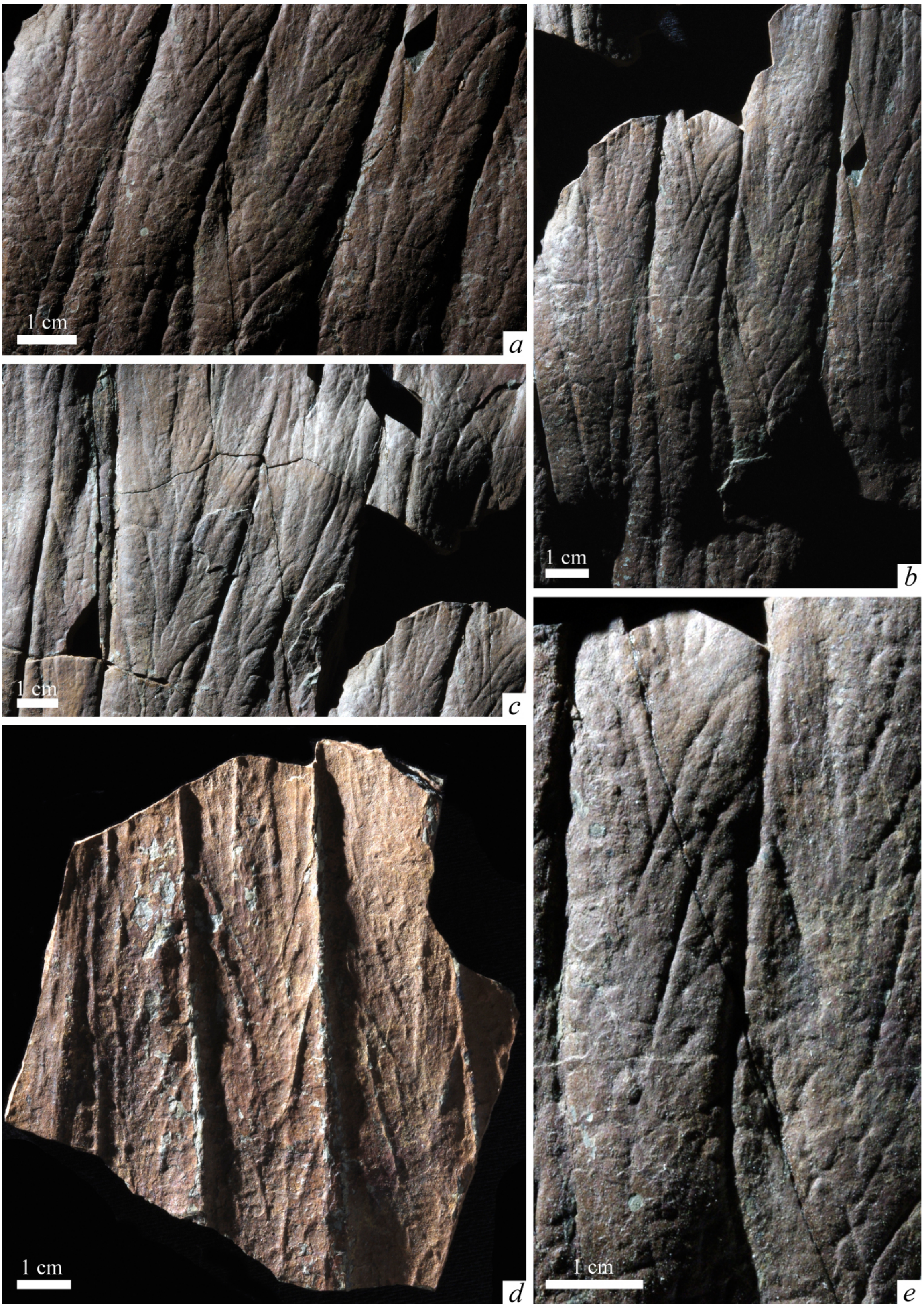
An onshore to offshore evolutionary pattern is evident in benthic marine invertebrate clades of the Paleozoic and post-Paleozoic age. Ordinal rank taxa are observed to originate onshore, diversify offshore, and eventually relinquish nearshore habitat (Jablonski et al., 1983). An important exception to this pattern is found in rangeomorphs, a group of Late Proterozoic foliate organisms that have a body divided by numerous commissures into chambers resembling ramified tubules. It is the oldest group of Vendian macroorganisms, as suggested by the fossils found in the Drook Formation of the Conception Group of Newfoundland with U–Pb-zircon age 578.8 ± 0.5 Ma (Van Kranendonk et al., 2008). Theoretical growth modeling of rangeomorph structural elements has demonstrated that the growth strategies used by these organisms allowed them to maintain high surface area to volume ratios despite their macroscopic size, which is consistent with morphological expectations for osmotrophs (Laflamme et al., 2009). Rangeomorphs originated offshore in distal low-energy shelf where they dominated sessile macrocommunities until their sudden mysterious disappearance 560 My ago (with a notable exception of *Charnia masoni*). There is growing evidence, however, that 560 My ago rangeomorphs migrated from distal low-energy shelf to higher energy proximal habitats. For example, the rangeomorphs *Rangea schneiderhoehni* and *Bomakellia kelleri* from the time interval of 560–545 Ma are confined to distributary channels of prodelta. In 2003 fossils of a new rangeomorph species (see figure) was found in the Krutikha Member of the Chernokamen Formation cropping out along the banks of the Usva River in the Central Urals. Preliminary study allows the following conclusions to be drawn: (1) The new rangeomorph species is characterized by unusually large chambers and relatively simple arrangement of commissures; hence, it would be incapable of attaining the surface area to volume ratios necessary for strict osmotrophy. (2) The Krutikha Member is correlated on the basis of sequence stratigraphy with the Zigan Formation of the South Urals; volcanic tuffs within Zigan Formation in a section near Ust-Katav gave a U–Pb-zircon age of 548.2 ± 7.6 Ma which makes the new species one of the youngest members of the group. (3) The Krutikha Member is characterized by chanellized sandstones with multistory cross-bedding, casts of desiccation cracks, salt crystal pseudomorphs, and weathered surface paleohorizons; the new species, therefore, was adapted to extremely shallow water habitats with variable salinity and periodic exposure. Discovery of the new rangeomorph species in the Central Urals is the first demonstration of invasion of terrestrial environments or at most extremely shallow-water environments by a major group of benthic marine macroorganisms previously restricted to offshore, relatively deep-water environments. This work was supported by the RAS Program “Biosphere Origin and Evolution” and RFBR grant no. 09-05-00279.



PRODUCTS FROM BIRCH BARK FOR TREATING AND AS PROBIOTICS

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Micro-organisms is not only defining link of appearance and evolution of biosphere, the most important factor for maintaining biological variety of life on our planet, but also applied to humans and animals are the major biogenic factor of in determining health or development disease. Permanent influence antimicrobial, antitumor and other drugs, food additives technological, industrial toxins, pesticides, radiation, stressors agents other nature of living organisms leads to breach of the symbiotic microbiological systems and become the reason of changes important parameters of the functioning living systems.

The purpose of of this work was to study products produced from birch bark for treatment of human organisms and animals.

The outer layer of birch bark is a unique source of valuable biologically active substances. Betulin is the main of them. Betulin (3β, 28-dihydroxy-20 (29) Lupeni) - pentacyclic triterpene alcohol, derived from birch bark, extensively studied at recent times due to anti-inflammatory, antiviral, hepatoprotective and others biologically activity. The inner birch bark treatment with dilute NaOH solution allows to obtain enterosorbent, which is characterized by the ability to absorb toxins of different nature and their properties are similar with industrial enterosorbent brand «Polyphepan» obtained from the hydrolysis lignin.

Betulin was obtained and recrystallized from the birch barkПрослушать. Identification of the betulin was confirmed using physicochemical methods (IR, NMR spectroscopy, gas chromatography and mass spectrometry). Antiulcer activity was studied on 30 male white mongrel rats. The experimental model of ulcer formation was carried out by introducing via metal tube into the stomach by 0.1 HCL 4.5 ml. The test substances were introduced one hour before the introduction of HCL for the implementation protector models or one hour after the introduction of HCL for correction model in experiment. It was established that betulin have the antiulcer and gastroprotective activity 2,52 units, taking into account index Pauls.

The rise of cancer, atherosclerosis, diabetes, rheumatoid arthritis, coronary heart disease and other diseases are growing due to the deteriorating environmental situation, particularly in industrialized areas. Large role in these pathologies become free radical processes, whose intensity depends on the environment. Targeted correction of changes in antioxidant status of the organism may be the introduction of synthetic and natural antioxidants. In this regard, it is necessary to search and study of drugs with antioxidant activity. Much interest in extractive substances isolated from the bark of birch.

About the antioxidant activity of betulin and extract from outer birch bark, was concludid by its ability to influence the activity of enzymes of protective system of cells, as well as the accumulation of free radical oxidation products under oxidative stress. As the initiators of oxidative stress using a system of «ascorbate + Fe» at concentrations 0.1 mM and 1.0 mM, respectively. To determine enzyme activity and the number of products of free radical oxidation from aliquots of samples were taken through the thirty-minute intervals for two hours. In the experimental samples compared to controls, was found to decrease the concentration of diene conjugates and the activity of superoxide dismutase, catalase, glutathione, glutathione-S-transferase. These results indicate that betulin and extract from outer birch bark exhibits antioxidant activity.

It was found that betulin and birch bark extract have the antioxidant, antiulcer and others properties and prevents the harmful influence of antibiotics with the manifestation of a direct dose-effect "and" time-effect. "The use of betulin and birch bark extracts against the impact of xenobiotics normalizes the structure of biological membranes, restores the synthetic function of the liver, improves blood forming organs and prevents the development of destructive changes in the liver and kidneys.

Experiments were conducted on mice shows that betulin has more pronounced anti-tumour effects to ascites adenocarcinoma Ehrlich than ethanol birch bark extracts. It was shown that betulin and birch bark extract may be used for the prevention and treatment of tumors.

Comparison of sorption activity industrial enterosorbents sorbent and enterosorbents from the birch bark bast show the competitiveness of the latter to remove the toxin protein nature. Established that enterosorbent birch bark is an effective and nontoxic drug for the treatment and prevention of gastrointestinal infections and has a positive effect on the qualitative and quantitative composition of intestinal microflora.

This work was supported by a grant program of RAS «Fundamental sciences – medicine».

THE STRUCTURE OF MICROBIAL COMMUNITY IN THE BOTTOM WATER LAYER OF LAKE BAIKAL AND POSSIBLE ROLE OF EUBACTERIA IN DESTRIBUTION OF DIATOMS

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EVOLUTION OF ORGANISM–SEDIMENT INTERACTION IN TRANSITION TO PHANEROZOIC BIOSPHERE

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That infaunal habit evolved concurrent with origin of Bilateria has long been appreciated, but the triggering mechanism remained unclear. J. Dzik (2005) argues that trace fossils from the Vendian–Cambrian transition represent shelters of infaunal animals feeding from the sediment surface, and that infaunal habit evolved as a protective measure against predators. We studied trace fossil record through Vendian–Cambrian transition in the Khorbusuonka and Kessyusa Groups in the Olenek Uplift of Arctic Siberia and came to the following conclusions. 1. The world's oldest bioturbation is in the Khatyspyt Fm of Khorbusuonka Gr and represented by meniscate backfilled burrows Nenoxites. Several features of the Nenoxites ichnofabric (absence of fecal material, avoidance of earlier self-made trails) suggest that the organism actively burrowed by peristalsis without processing sediment through the gut. The most likely purpose of borrowing was search for food. 2. Lower Cambrian is characterized by a diversity of meniscate burrow systems that represent sediment processing behavior in search for food. These are U-shaped burrows with spreite-structures formed as a result of intensive horizontal or vertical sediment reworking (trace fossils Rhizocorallium and Diplocraterion), meniscate backfilled burrows radiating from a central vertical mine (Zoophycos), J-shaped burrows with protrusive or retrusive spreite-structures (Syringomorpha). 3. Trace fossil Treptichnus is generally regarded as permanently open burrows used as shelters by a surface detritus feeders (Jensen, 1977). Importantly, ichnofabric in the uppermost Vendian Syharghalakh Fm of the Kessyusa Gr consists of compact descending spirals typical for sediment-processing behavior. These trace fossils were discovered and described by M.A. Fedonkin (1985), albeit as two separate ichnospecies Planispiralichnus grandis and Protospiralichnus circularis; however, the spirals consist of series of sediment-probing elements that are diagnostic of treptichnid trace fossils and are therefore reinterpreted as ichnospecies Treptichnus circularis (see figure). Trace fossil record of the Khorbusuonka and Kessyusa groups reveals the true meaning of the Vendian–Cambrian Agronomic Revolution: organism-sediment interaction started as exploration of new food resources, and not as sheltering from evolved predators. This study was supported by RFBR grants no. 09-05-00520 and 10-05-00953, RAS Program "Biosphere Origin and Evolution" and National Geographic Society.

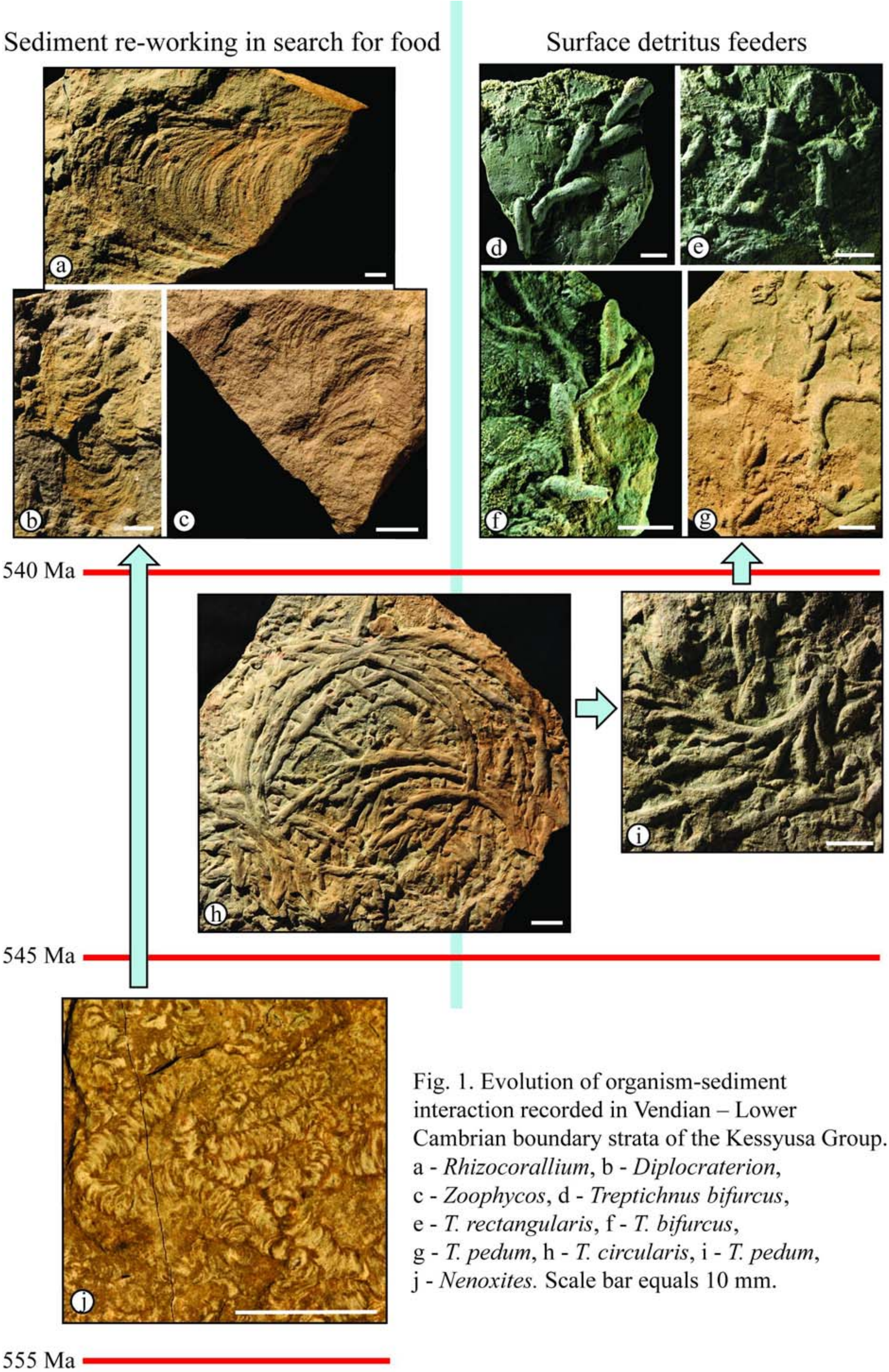

Fig. 1. Evolution of organism-sediment interaction recorded in Vendian – Lower Cambrian boundary strata of the Kessyusa Group. a - *Rhizocorallium*, b - *Diplocraterion*, c - *Zoophycos*, d - *Treptichnus bifurcus*, e - *T. rectangularis*, f - *T. bifurcus*, g - *T. pedum*, h - *T. circularis*, i - *T. pedum*, j - *Nenoxites*. Scale bar equals 10 mm.

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THE GENETIC RELATIONSHIP OF THE FINNISH-UGRIC, SLAVIC AND GERMANIC POPULATIONS ACCORDING TO GENETICAL AND ANTHROPOLOGICAL DATA

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Summary

The calculation of genetic distances of 55 human populations belonging to four great human races considering loci of proteins, enzymes and blood groups, and construction the dendrogram of this populations distinguished some relationship of German, Slavic and Finnish-Ugric populations. So, Russians are in one subcluster with Poles, Iranians, Komi, Chuvashes, Udmurtians, Nentses and Ossetians. Germans are in one subcluster with Serbs, Moldavians, Hungarians, Croatians and Czechs. Greecs are in closeness with Slavic populations on this dendrogram, too.The calculation of genetic distances of 35 Slavic, Finnish and Germanic populations, and constructing the dendrogram confirmed this results. There were common migrations of this populations from places of first differentiation in Asia. In Europe German populations were migrated by another way than ancestors of Russians, which were migrated in Europe across North of Siberia. The ancestors of Germans probably migrated by the same way as Hunnu. Now are investigated settlements of ancient Caucasoids in Central Asia. The studing of mt DNA of rural Russian population in Yaroslavsky region discovered all haplogroups of Russians and even Caucasoids (H, W, I, U, X, T1). The last decoding of petrogliphs in Baical region discovered the presence of ancestors of Caucasoids in Siberia in paleolithic.

Key Words: Human Populations, Genetic Relationship, Finnish-Ugric, Slavic, Germanic Populations, Genetic Distances, Anthropological Data

PP-58

EARLY CAMBRIAN EVOLUTION OF SMALL SHELLY FOSSILS

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The appearance and evolution of animal organisms capable to a biomineralization on Precambrian - Cambrian boundary – the major stage in the biosphere development, characterized by "explosive" occurrence the most of types and classes of the animals existing till now. The special place occupies small shelly fossils (SSF) – are a group of problematic organisms containing chancelloriids, protoconodonts, molluscs, hyoliths, paleoscolecids, sponges and others, most are short-lived and have no modern analogues. The complexes of SSF assemblages Siberia, Mongolia, China and Australia are the most numerous and diverse. Question of the origin of mineralized skeletons is still debatable.

The beginning of Lower Cambrian the Siberian platform as well as around the world related to the onset of regressive cycle. Notes outbreak of speciation in most groups of SSF (Chancelloriids, Sachitids, Siphonoguchitids, Halkieriids, mollusks, et al.), but have appeared previously observed complication of morphological elements. Phosphatic structures are discovered in the tube interior of the hyolithelminth species *Hyolithellus vitricus* from the Lower Cambrian of the Siberian Platform. Anatomic interpretation of these structures suggests that these small sized shelly fossils represent the earliest worm shaped organisms probably closely related to modern Nemathelminthes (Novozhilova, 2010). Most workers considered these organisms as the order Hyolithelminthes Fisher, 1962 of uncertain systematic position, or assigned it to the phylum Annelida. Hyolitelmintes find out rather low rates of evolution, but the fact of their mass occurrence and blossoming in bottom of Cambrian on a global scale does this group by reliable enough marker of the Lower Cambrian boundary. At the beginning of Atdabanian stage starts declining species and quantification of SSF biodiversity. By the end of stage their number is significantly reduced, in addition, to this moment end their existence Angutiochreida, Sahitida, and most species of Tommotiida. Since this time the same peak in the development of Cambrian organogenic constructions in the world. Complex skeletal problematic organisms is not representative in the Botomian stage, the majority of species - the transit of the more ancient deposits.

Thus the small shelly fauna, presented benthic organisms, predominated in the Early Cambrian (Tommotian - Atdabanian stages) ecosystems and gradually loses its value to the end (Botomian, Toyonian stages). Further studies require a more detailed examination and reconsideration of the systematics of all problematic organisms.

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PP-59

BLACK SHALE BIOMARKERS FROM THE KUONAMKA COMPLEX OF THE EASTERN SIBERIAN PLATFORM AND ESTIMATION OF CAMBRIAN MARINE BIOCOMMUNITY DIVERSITY

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In the Botomian, Toyonian, and Amgian ages of the Lower and Middle Cambrian, anomalously organic-rich sediments accumulated in the north and east of the Siberian Platform [Kontorovich, Savitsky, 1970 and others]. They formed carbonaceous rocks of the Kuonamka complex (Shumnaya, Kuonamka, Inikan, Sekten, and Sinyaya Formations). It is suggested that the most of lipid matter of Cambrian black shales has been derived from remains of lower plants and bacteria, while the contribution of microfauna is much less. The first attempt to estimate the microbiotic diversity in the Kuonamka time seas from variation in composition and distribution of biomarkers has shown that three communities of microorganisms could be established [Parfenova, 2007]. The known research results have been taken as a basis of diagnostics of biocoenoses: steranes and tricyclanes are biomarkers of eukaryotes, and hopanes are biomarkers of prokaryotes [Ourisson et al., 1984; Peters, Moldowan, 1993; Revill et al., 1994]. Based on steranes/terpanes and tricyclenes/hopanes ratios, the communities have been divided into predominance of planktonic-algal microbiocenosis, community with predominance of bacterial organisms, and planktonic-bacterial microbiocenosis. Recently, sterane, lanostane, and hopane hydrocarbons (HCs) of the Lower Cambrian Sinyaya Formation have been studied in detail [Parfenova et al., 2010; Parfenova, 2011 and others]. The results of investigation of the composition, distributions, and ratios of terpane HC from bitumen extracts of the Kuonamka, Inikan, and Sinyaya Formations are shown in this work. Saturated HCs have been identified using gas chromatography-mass spectrometry system Agilent 5973N. Comparative molecular analysis made it possible to propose for discussing the biomarker parameters of four biocommunities.

The first biological community is characterized by the following parameters: steranes/terpanes ratio is higher or equal to 0.3; tricyclanes/hopanes ratio is higher than 1; steranes are generally dominated by cholestane and ethylcholestane; lanostanes and 28,30-bisnorhopane (C_{28}) are absent; C_{29}/C_{30} hopane ratio is less than 1. The C_{35}/C_{34} homohopane ratio is lower than 1. This suggests [Peters, Moldowan, 1993 and others] that there was no anomalous hydrogen sulfide contamination of bottom water and sediments, from which the examined carbonaceous rocks formed. These characteristics are peculiar to the organic matter (OM) of the Kuonamka Formation (collections of the Molodo R., Kyulenke R.). The molecular parameters of the **second biocommunity** are as follows: steranes/terpanes ratio is lower or equal to 0.1-0.2; tricyclanes/hopanes ratio is lower than 1; steranes are dominated by ethylcholestane; lanostanes and 28,30-bisnorhopane are absent; C_{29}/C_{30} hopane ratio is higher than 1. The C_{35}/C_{34} homohopane ratio is higher than 1, which is indicative of hydrogen sulfide contamination of sediments and, possibly, bottom waters. These characteristics are peculiar to the OM of the Inikan Formation (collection of well Khotochu-7). **The third biocommunity**: steranes/terpanes are at the level of 0.3; tricyclanes/hopanes are at the level of 1; steranes are dominated by ethylcholestane; lanostanes and 28,30-bisnorhopane are absent; C_{29}/C_{30} hopane ratio is lower than 1. The C_{35}/C_{34} homohopane ratio is lower than 1. These parameters are typical of the OM of the Kuonamka and Inikan Formations (collections of the Molodo R., Kyulenke R., well Khotochu -7). **The fourth biocommunity**: generally, steranes/terpanes ratio is equal to 0.1-0.2, and tricyclanes/hopanes ratio is lower than 0.1; steranes are generally dominated by ethylcholestane; lanostanes and 28,30-bisnorhopane have been identified; C_{29}/C_{30} hopane ratio is less than 1. The C_{35}/C_{34} homohopane ratio is greater than 1. These characteristics are typical of the OM of the Sinyaya Formation (collection of the Sinyaya R.).

Conclusion. The study of HCs from the rocks of the Kuonamka complex in the east of the Siberian Platform has made it possible to distinguish four ecological niches in the Lower and Middle Cambrian seas. It has been established that biological communities and their habitat conditions either alternated in time, or changed, or remained stationary. The preliminary estimation of the distribution of ecosystems in area extent has been performed from the results of OM examination in four sections.

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HOPANES IN LOWER AND MIDDLE CAMBRIAN CARBONACEOUS ROCKS IN THE EASTERN SIBERIAN PLATFORM

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Highly carbonaceous sediments of the Lower and Middle Cambrian Kuonamka complex deposits were accumulated in a pericontinental open shelf separated from the epicontinental salt-bearing system by barrier reefs [Kontorovich, Savitsky, 1970]. The Kuonamka complex deposits include the Kuonamka, Inikan, Shumnaya, Sekten and Sinyaya Formations. These formations are distributed in the northern and eastern Siberian platform. The biomarkers of the Kuonamka and Sinyaya Formations were studied [Kashirtsev, 2004; Kontorovich et al., 2005; Parfenova et al., 2004; Parfenova et al., 2010 and others].

This investigation deals with the three collections of carbonaceous rocks from three sections of the Kuonamka, Inikan, and Sinyaya Formations. Saturate hydrocarbons (HCs) of bitumen have been examined by gas chromatography-mass spectrometry methods. The goal of study is to analyze homologs of hopane series. These hydrocarbons are biomarkers of bacterial and cyanobacterial organisms [Peters, Moldowan, 1993 and others].

Bisnorhopanes (C_{27} (Ts, Tm)), norhopanes (C_{29}), C_{30} hopane (C_{30}) and homohopanes (C_{31}-C_{35}) have been identified in the fractions of hydrocarbons in all samples (Fig. 1). Usually, the C_{29}/C_{30} ratio is less than 1 in bitumens of Cambrian OM in the Siberian platform. However, the concentration of C_{29} norhopane is higher than that of C_{30} hopane in organic matter (OM) of the Inikan Formation (Fig. 1b). Relatively high amounts of 28,30–bisnorhopane (C_{28}) were detected in samples of the Sinyaya Formation (Fig. 1c). Thus, three types of distributions of homologs of hopanes occur in the examined collections. Perhaps, the diversity of hopane distributions is connected with the biochemistry of initial prokaryotes of the Kuonamka, Inikan, and Sinyaya marine basins. This information may be used to reconstruct the Cambrian microbiocoenosis and the evaluation of prokaryote by biochemical parameters (by variations of the content and distribution of biomarkers).

The C_{35}/C_{34} ratio is less than 1 in HCs fractions of the Kuonamka and Inikan Formations. The concentration of C_{35} homohopanes is higher than that of C_{34} homohopanes in HCs of the Inikan and Sinyaya Formations. These results suggest that the redox conditions varied in the marine basin of the Lower and Middle Cambrian.

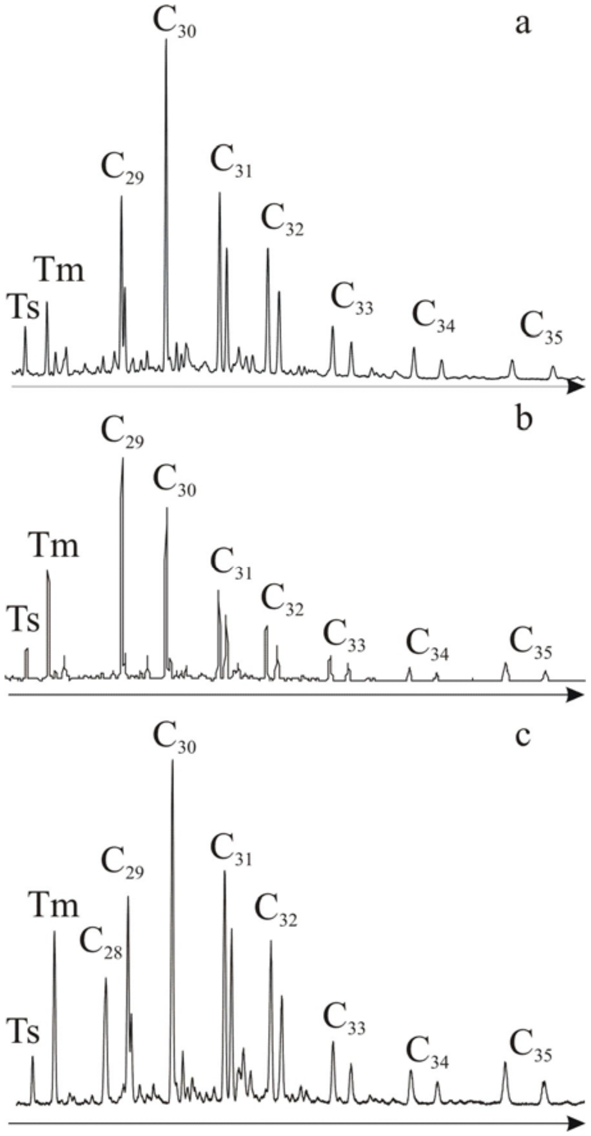

Fig. 1. Masschromatograms for *m/z* 191 fraction of saturated HCs of bitumen:
a – Kuonamka and Inikan Formations;
b – Inikan Formation;
c – Sinyaya Formation.

This study was supported by the Russian Foundation for Basic Research (project no. 10-05-00705), by the Leading Scientific Schools Grant of the President of the Russian Federation (grant no. NSh-6244.2010.5), as well as by the Biosphere Origin and the Evolution of Geobiological Systems Program no. 15 of the Presidium of the Russian Academy of Sciences, and the ONZ-1 Program of the Russian Academy of Sciences, by Multidisciplinary Integrative Project no. 36 of the Siberian Branch of the Russian Academy of Sciences.

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PP-61

MOTIVE FORCES AND STAGES OF FORMATION AND EVOLUTION OF PRE-BIOLOGICAL SYSTEMS

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Usually, at studying, a problem of the life origin concerns with five separate points (stages): 1) formation of a planet with atmosphere and hydrosphere where there are "raw materials" for life occurrence; 2) synthesis of biological monomers, life bricks, for example amino acids, sugars and the organic bases; 3) synthesis of biological polymers; 4) formation of separate particles of type of drops of a broth on Choldane, microspheres on Fox, coacervates on Oparin, their transformation in pro-bionts with their own primitive methabolism; 5) occurrence of the reproductive systems transferring to daughter cells chemical and metabolic potentialities of parents. In short, it is formulated as a problem of initial raw materials, formation of monomers, polymers, isolation and a reproduction. Within the limits of the work we'll have short consideration of points 1) and 2), having paid separate attention to point 4). We directly correlate point 3) to point 4), believing, that the accelerated synthesis of active polymers and, in particular, their natural selection are possible only in connection with their finding in the dynamical phase-isolated structures capable to growth and to exchange with environment. The primary substance on a surface of our planet, taking into account motive forces - continuous flows of energy (mainly from the Sun), was transformed and changed. These primary physical and chemical transformations should have cyclic character as energy flows first of all cause mechanical cycles of moving of gases and liquids. Well-known, that in any limited system cyclic transformations and streams, various in the sizes and duration are formed.

Let's note once again very important property of phase isolation or presence of borders in the closed system. The polymers arising in solutions, cannot reach high concentration, in particular, because of the course of back reactions. And polymerization in the limited, allocated volume reduces the concentration of monomers in it and, accordingly, lowers osmotic pressure. Such decrease leads to swapping monomers from environment. And thus pro-bionts are capable to "exhaust" organic chemistry from a primary broth to grow and multiply. According to prof. Mednikov: «not the life has generated a cell, but the cell has arisen before the life».

The term - «natural selection» - is applicable to evolution of drops- probionts as any specific differences between populations of pro-bionts and real microorganisms are not important from the point of view of selection action. In both cases, selection leads to increase in fitness of population that is expressed through change of operating growth rates. And character and a selection direction are defined by conditions of environment. In this sense application of methods of continuous cultivation of the microbial populations is rather perspective for studying of action of selection in populations pro-bionts and finally for the modeling of the early stages of evolution consisting in occurrence and development of a metabolism.

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THE EXTREME LIFE OF A WATER BEAR (*HYPSIBIUS KLEBELSBERGI*) IN A HOSTILE HABITAT

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The term „extremophile” is usually applied to certain bacteria that show extraordinary tolerance to conditions which seem to be unpleasant for anthropogenic standards like high or low temperatures, desiccation and radiation, but it is frequently used for multicellular eukaryotic organisms. Among metazoans, only tardigrades, rotifers, and nematodes include taxa that are extremophiles during their whole life cycle. *Hypsibius klebelsbergi Mihelčič,* 1959, a tardigrade, has the ability to occupy a particular ecological niche on the glaciers. Only this species occurs in a large number in so called cryoconite holes, microcaverns on the ice surface in the glacier`s abalation zone. These unique freshwater environments can cover 0,1-10 % of the abalation zone of a glacier and occur globally in glaciated environments. The holes are caused by absorbtions of solar radiation by dark particles in the ice surface; they are predominantly water filled and frozen throughout the winter or even during a day-night cycle. The living conditions in this extreme habitat are characterized by a high light intensity (UV-radiation), a low water conductivity (1.9 to 6.0 µS), low temperatures (0,1-0,2°C), little dissolved oxygen and a lack of nutrients. It is settled by mainly microbial communities (viruses, bacteria, microalgae and protozoa). Depending on the geographic region also metazoa such as tardigrades, rotifers, nematodes, copepods and insect larvae can be found. Both the microflora and -fauna are probably decomposed by fungi and bacteria. 12 tardigrade species are known from cryoconite holes (all over the world), excluding questionable identifications. *H. klebelsbergi* and *H. janetscheki* (a Himalayan species), two very highly pigmented species, have only been reported from the glacier surface. Until now the glacier-dweller *Hypsibius klebelsbergi* is the only species known from the Alps. Due to this harsh living conditions this species needs certain adaptation abilities. Tardigrades (except marine Arthrotardigrada), have the ability to form a tun, caused by dehydration. In this ametabolic dry stage these animals show no visible sign of life, but become active again if rehydrated. While in anhydrobiosis, tardigrades can be tolerant to a variety of extreme enviromental conditions. The importance of tardigrades and their food preference within the food web of cryoconite holes are still unknown. The objectives of this research are the investigation of dietary patterns and trophic relationships of tardigrades with stable isotopes (δ^{15} N; δ^{13} C). It is important to know, if the food web concept works on this harsh environment as well. Also the ability to form a tun is investigated. Tardigrades are well known as model organisms for astrobiology due to their high ability to adapt to most hostile conditions which could be prevailing on other exoplanets.

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MORPHOGENETIC (?) TRENDS IN ADAPTATION TO SESSILITY THROUGH THE LATE PRECAMBRIAN: VENDIAN DISCS

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Ediacaran (Vendian) sessile benthic organisms seem to be the first complex macroscopic colonizers of the substrate whose role in the bioaccumulation and “landscape design” has yet to be recognized as such. "Cyclic" imprints many of which identified now as the attachment discs of problematic organisms (e.g., Gehling, 2000) are the most abundant macrofossils found in the Upper Precambrian strata. Such discs may often be the only evidence of luxuriant benthic communities after their destruction. Nevertheless the systematic position and relationship within the groups of Petalonama's fronds whose members appeared to have the attachments discs of different types is not properly understood. So the questions of possible development of the groups and of their importance for biostratigraphy are still under discussion (e.g., Fedonkin, 1985; Waggoner, 2003; Grazhdankin, 2004; Narbonne, 2005).

As is known morphogenetic studies make it possible to identify some trends in the modification of morphological structures and to discuss the probable adaptive significance of the variation. It should be admitted that consideration of many species of diverse attachment discs as a single aggregation is not always adequate because of we don't always know anything about the structure of the upper parts. On the other hand the morphological diversity of known upper parts is very low whereas the diversity of attachments structures is much higher. Also, if we try to reconstruct the scheme of an organ's development, e.g. an organ of attachment, our arguments shouldn't be so ambiguous. Such a development may be considered as a result of general morphogenetic processes in the Precambrian settings. The case study includes the identification of structural elements, their combinations, and then recognition of some morphotypes and arrangement of the morphotypes in possible series in order of rank. B.V. Preobrazhensky (1982) has demonstrated a great potential of the method for the study of tabulate corals. We can start by detecting elements and the principle of their combination for the analysis of structures. The most obvious structural units of Vendian attachments seem to be concentric and radial elements which are common for almost all discs. Radial units look like fine straight bands along the fossils; they are sometimes combined and spread out to form root-like appendages. Concentric units resemble thin or wide strips bounded by fine circular bands; elastic membranes which separated the adjacent areas of different pressure seem to be the structural element in this case. It is clear that a configuration of the attachment disc depends on the disposition of structural units and on the type of the growth. For example, if the concentric membranes dominate the construction the attachment becomes similar to disc more or less flattened; the prevailing radial units, on the other hand, look like root-like outgrowths (A. Seilacher (2001) described the two similar morphospaces of concretions such as Liesegang rings and dendrites). Besides of the two morphospaces, quite a number of intermediate forms may be expected. What can we see in fossils? There are common and easily diagnosed morphotypes of Vendian attachment structures: discoidal cyclic forms; flattened forms (e.g. *Ediacaria*); conical forms with radial outgrowths arranged both in chaotic (e.g. *Hiemalora* from Siberia) and in regular cyclic (e.g. *Eoporpita*) patterns; composite forms exhibiting a combination of some features of the above three morphotypes (e.g. *Palaeophragmodictya* and others) (Serezhnikova, 2007, 2010). These morphotypes are not restricted to certain systematic groups, but rather ethological and ecological categories — that is, they reflect different manners of attachment to or within the substrate. Let's place some morphotypes of attachments in the matrix with the discoidal forms along the horizontal axis and radial forms along the vertical one. It is two lines of "pure" forms. The arrangement of the objects should be in hierarchical order, for example, an object of the lower level can be transformed into the higher level etc. So the following pattern is expected in the line of radial forms: small discs with outgrowths lying in the plane, with outgrowths going through the sediment and spreading out and eventually branching out. The line of discoidal begins from irregular concentric forms and then ascends to regular zonal ones. Such a pattern for cyclic forms is suggested by M.A. Fedonkin (1985) and Yu.A. Gureev (1987). The members of mean matrix points can be selected according to basic features of some attachment discs.

As a result of these simple operations, we have a table (matrix) with a number of cells arranged hierarchically. According to the data table, the most simple and uniform discs occur in the late Neoproterozoic sediments of Newfoundland, Canada, the "middle" forms are from the Yudomian of Arctic Siberia and the most complex attachment discs occur in the fossil assemblages from the Ediacaran of Australia and from the Vendian of the White Sea.

Thus there are some morphogenetic (?) trends which can be detected in the development of attachment discs of Ediacaran (Vendian) sessile benthic organisms. In general terms they are similar to those of root system in plants although the disc-bearing Petalonama are often thought to be of cnidarian grade (e.g. Jenkins & Gehling, 1978). Further research on the basis of the above model could improve the use of attachment discs for biostratigraphy.

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BIOMARKERS IN PRECAMBRIAN KARELIAN SHUNGITES

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The results of elemental analysis, composition of normal and iso-alkanes, polycyclic hydrocarbon biomarkers in Karelian shungite rocks with various content of organic carbon and PT-conditions of organic substance formation are presented. Earlier similar researches were carried out basically for low-carbon shungite rocks (Corg < 35 %) [1-3]. Thus, bitumoid's from high-carbon shungites (Corg > 60 %), owing to their low concentrations, were studied only by magnetic resonance and infrared spectrometry [4].

It was established, that distribution of n-alkanes differs for various types of deposits. For example bimodal distribution of n-alkanes with C_{17}-C_{19} and C_{21}-C_{23} maximum was fixed for the higher anthraxolite from Shunga deposit. Similar distribution was established in lidite, shungite rock with lower organic carbon content (3 %) where dominated C_{17} and C_{21} n-alkanes. Obtained data confirm a similarity source of organic substance in various types of shungite rocks within the Shunga deposit [4, 5].

In samples from Zazhogino and Chebolaksha deposits domination of C_{21}-C_{23} n-alkanes was not established. It is connected with accumulation of small molecular weight n-alkanes during thermal destruction of their high-molecular homologs, since the temperatures influenced on organic substance of Zazhogino and Chebolaksha deposits, were considerably greater, than in Shunga deposit.

The low contents of iso-alkanes in the higher anthraxolites were observed. The $(Pr+Ph)/(n\text{-}C_{17}+n\text{-}C_{18})$ coefficient is about 0.5 in the higher anthraxolites, and in III-type of shungite it increased up to 1. The iso-alkanes content increase in comparison with normal alkanes also confirm to a high thermal degree of shungite carbon from Zazhogino and Chebolaksha deposits and/or theirs bacterial oxidation.

The results of alkanes researches indicate a significant change of initial hydrocarbon composition under heating. It does not allow using their distribution for determine of shungite substance source.

Among polycyclic biomarkers steranes and hopanes were identified [5]. It was established, that biomarkers composition of organic substance in various types of shungite is characteristic for marine organic matter (phytoplankton and cyanobacteriae) accumulated under shallow conditions mainly in reducing facial environment.

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MICROFOSSILS OF BACTERIAL, MUSHROOM AND ALGAL NATURE IN EARLY PROTEROZOIC OF AROUND THE BAIKAL SIBERIA (UDOKAN RIDGE AND PRISAYAN'E)

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Finds of eucaryotic nature fossils are rare in Early Proterozoic. The nature of microfossils this time is often ambiguous. It is connected with replacement of organisms by authigenic or diagenetic minerals and coalification under influence of a heat at metamorphism. Microfossils, received by us, show a different degree of safety and a variety of sea organisms 2 billion years ago. All samples are processed by acids for extraction organogenic fractions. Sterility of a material was provided with preliminary dissolution and the subsequent washing. Naminga formation of Udokan complex of Udokan ridge consists of grey sandstones and dark grey aleurolites. Radiochronological data from granites and diabases which are breaking through Udokan complex, show an age interval 1,8-2,0 billion years. Carbonaceous microfossils have been received at dissolution of aleurolites. Fine forms (3-20 μm) have been define, how the remains of chemolithotrophic bacteria and their colonies. Existence of eucaryotic algae has been assumed because of a find acritarch *Leiosphaeridia cf. L. crassa* (Naum.). 50 thin sections are studied. Arkose aleurolites and aleuro-argillites have been certain. Ilmenomagnetite, neogenic hematite-goethite and leucoxene clots contain in cement of rock. Similar trichomes microfossils are present at the majority studied thin sections. More than 30 "filaments" have been found. Their width is 15-20 μm, less often 10-15 and 25-30 μm. Their length changes from 50 up to 500 μm, on the average 120 μm. Trichomes were kept in the form of silhouettes. Their contours are executed by hydrooxides of iron and sustained enough on length. Internal parts of "filaments" are filled of leucoxene. They are sometimes deformed and bended by clasts of quartz and feldspar. Taxonomic definition of trichomes is based on the sizes of forms. Their part corresponds to diagnosis *Botuobia* Pjat. because of the sizes 10-30 μm and 50-500 μm. More thin "filaments" have been certain as *Leiotrichoides* Herm. and *Eomycetopsis* Schopf. It is supposed, that these remains have been taken down from coastal sites of development of stromatolites.

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Sections of Daldarma formation are in Urik-Iya graben of Prisayan’e zone of the south of Siberian craton. The composition of formation includes dark rocks from gravelites up to aleuro-argillites, limestones, tuffstones and volcanic rocks of the basic and acid compositions. Rocks were generated in basin of an island arch. Carbonaceous deposit with sulfides, most likely, have been formed in the bent zones of paleobasin with a stagnant environment. Granites, breaking through Daldarma formation, have age 1,86 billion years (Levitskii et al., 2002). 8 samples of dark aleuro-argillites and 1 sample of dark limestone have been dissolved. The material was studied also in thin sections. *Bavlinella (?)* Schep., *Eosynechococcus (?) sp., E. cf. giganteus* Gol. et Bel., *Germinosphaera (?)* Mikh., *Leiosphaeridia cf. crassa* (Naum.) em. Jank., *L. cf. minutissima* (Naum.), em. Jank., *Majasphaeridium (?)* Herm., *Octoedrixium (?) sp.*, *Polysphaeroides (?) sp.*, *Protosphaeridium div. sp*. and fragments of carbonaceous films have been certain. Numerous (up to 1000 in one preparation) fragments of carbonaceous "filaments" in the length from 10 up to 800 μm are prominent feature of a material. It is supposed, that algae had a benthic way of life on shoaliness and have been taken down in rather fondo and stagnant zone of paleobasin. Fine spherical forms (*Bavlinella (?)* Schep., *Protosphaeridium div. sp.*) are preliminary compared with benthos of chemolithotrophic bacteria, usual for stagnant zones of basins. Dark forms, round or the pear-shaped form with growths, or some forms in accretions are met in different samples. They can be compared to association of forms from phosphate black slates of the Early Proterozoic Zhdanov formation on the Kola peninsula (Ahmedov et al., 2000) through conformity of morphotypes, preservation of volume and sizes.

Forms of the Zhdanov formation have been compared to reproductive and vegetative organs of the lowest mushrooms lived in deposits of a stagnant zone of marginal paleobasin.

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BIOSTRUCTURE OF ASSEMBLAGES OF FILAMENTOUS FUNGI ASSOCIATED WITH BIVALVES IN THE RUSSIAN WATERS OF THE SEA OF JAPAN

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Filamentous fungi associated with bivalve mollusks *Mytilus trossulus, Mizuhopecten yessoensis, Crenomytilus grayanus, Modiolus modiolus,* and others have been investigated. About 700 strains of filamentous fungi have been isolated, 55 species have been identified, including 7 ascomycetes, 43 anamorphous fungi and 5 zygomycetes (Zvereva, Vysotskaya, 2005; Zvereva, Borzykh, 2010). Fungi were found in mollusks internal organs: mantle, gills, kidneys, digestive gland, male and female gonads. The patterns of filamentous fungi distribution on the shell surface and in the internal organs of mollusks were found.

Diversity of mycobiota from *Mytilus trossulus* and *Mizuhopecten yessoensis* bivalves has been studied in natural populations and in mariculture (Zvereva, Vysotskaya, 2007).

Taxonomic composition of filamentous fungi, associated with *Mytilus trossulus* bivalve, has been established. Sixteen filamentous fungi species have been isolated from mollusks of natural population in Vostok Bay, including 14 anamorphic micromycete species from *Penicillium* (7 species), *Cladosporium* (3), *Aspergillus* (3), *Trichoderma* (1) genera, 1 ascomycete from *Chaetomium* genus, and 1 Zygomycete from *Rhizopus* genus. Fifteen filamentous fungi species have been isolated from mollusks farmed in suspended culture in Vostok Bay, including 12 anamorphic fungi from *Penicillium* (5 species), *Cladosporium* (3), *Aspergillus* (3), *Trichoderma* (1) genera, 1 ascomycete from *Chaetomium* genus, and 2 Zygomycetes from *Rhizopus* and *Mucor* genera. Comparative analysis of biodiversity of filamentous fungi, associated with *Mytilus trossulus* from natural population and mariculture (Vostok Bay), using coefficient of likeness (or difference) of Serensen, has not revealed evident differences.

Taxonomic composition of mycelial fungi, associated with *Myzuhopecten yessoensis* bivalve, has been established. Eighteen filamentous fungi species have been isolated from mollusks of natural population in Vostok Bay, including 17 anamorphic micromycete species from *Penicillium* (5 species), *Cladosporium* (5), *Aspergillus* (3), *Trichoderma* (1), *Alternaria* (2), *Aureobasidium* (1) genera, and 1 zygomycete from *Rhizopus* genus. Fifteen filamentous fungi species have been isolated from mollusks farmed in suspended culture in Possyet Bay, including 14 anamorphic fungi from *Penicillium* (5 species), *Cladosporium* (2), *Aspergillus* (2), *Trichoderma* (1), *Alternaria* (2), *Acremonium* (1) genera, and 1 ascomycete from

Chaetomium genus. Comparative analysis of biodiversity of filamentous fungi, associated with *Myzuhopecten yessoensis* from natural population (Vostok Bay) and mariculture (Possyet Bay), has revealed differences in taxonomic composition of associated fungi, at that likeness coefficient of Serensen was 0.39.

Thus, taxonomic structure of mycobiota of bivalves from natural populations and mariculture on the whole is similar for both examined mollusk species on the level of genus, and on the level of species it is similar for mycobiota of *Mytilus trossulus,* inhabiting the same area (Vostok Bay). For mycobiota of *Myzuhopecten yessoensis* distinctions have been revealed on the level of species, which is connected with different ecological conditions in Vostok Bay and Possyet Bay, including different anthropogenic stress on the investigated water areas.

Microbiological monitoring of mollusks from different parts of Peter the Great Bay (Sea of Japan) demonstrated that the biodiversity of opportunistic and toxin-producing filamentous fungi, primarily from the genus *Aspergillus*, found in the internal organs of bivalve mollusks increases with the increase of pollution in the coastal waters (Zvereva, 2008; Zvereva, Vysotskaya, 2005, 2007; Zvereva, Borzykh, 2010). The species of the genera *Aspergillus, Penicillium, Cladosporium, Chaetomium*, and some others found in the studied bivalve mollusks are opportunistic and toxic fungi capable of causing mycoses and mycotoxicoses in marine organisms. The immune-enzyme analysis of the Primorsky scallop *Mizuhopecten yessoensis* showed that the internal organs of these bivalves accumulated mycotoxins, particularly aflatoxin produced by the filamentous fungus *Aspergillus flavus* Link (Zvereva et al., 2009).

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