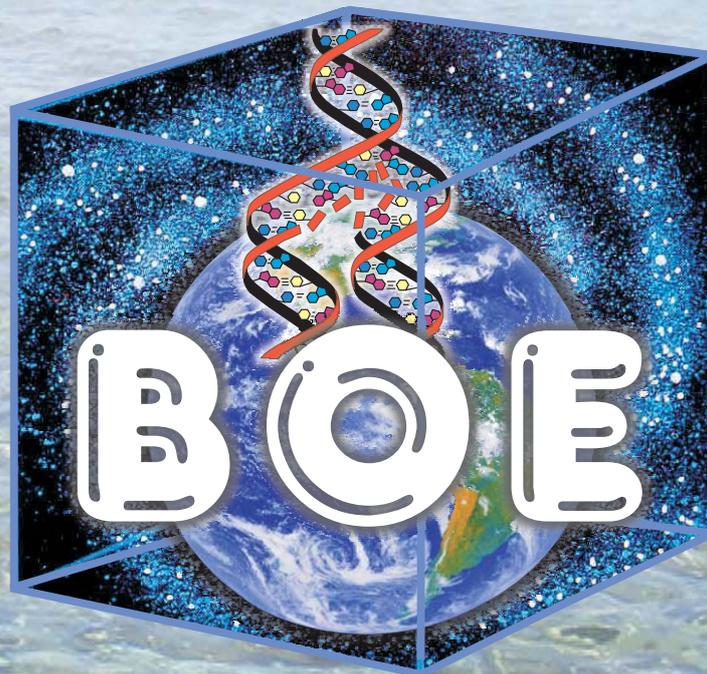


II International Conference
BIOSPHERE ORIGIN AND EVOLUTION

OCTOBER 28 - NOVEMBER 2, 2007

LOUTRAKI, GREECE



ABSTRACTS

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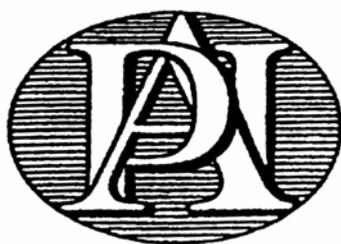
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ABSTRACTS

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PLENARY LECTURES

**THE ORIGIN AND EVOLUTION OF THE BIOSPHERE:
AN INTERDISCIPLINARY VIEW**

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The results obtained during the execution of Subprogram II *Biosphere Origin and Evolution* (2004-2006) of the Scientific Program of the Presidium of the Russian Academy of Sciences that put together geologists, paleontologists, chemists, molecular geneticists, ecologists and archeologists in 20 institutes of the Russian Academy of Sciences are presented. The project included a comprehensive study of pre-biological chemical evolution, the RNA world, biomineral formation, a comparative study of fossil Precambrian ecosystems and their modern counterparts, a study of biosphere-geosphere co-evolution, evolution at the ecosystem, genome and molecular biological level and a study of issues in anthropogenesis. Gravitational instability in accretional stellar discs can have triggered the emergence of gas-and-dust cocoons, with pressures and temperatures quite suitable for the synthesis of primitive organic matter to start. Darwinian selection was on the scene as early as when the abiogenic synthesis of the most primitive “bricks of life”, sugars, was underway. The RNA world endows recombination-based variability: template-based RNA complementarity enables restriction/ligation reactions and the self-assembly of primitive ribozymes and enzymes riboproteins. Cells may have originated from RNA molecules that were associated with lipid microspheres, could change conformation and therefore membrane permeability. The bioinitiating role of montmorillonite in the emergence of self-reproducing RNA colonies and the evolution of the siliceous skeleton in the biosphere have been investigated. The initiation process, the condensation of silicic acid on polyamines, accounts for the observed similarity in the respective biochemical machineries of cyanobacteria, algae and sponges. An unexpectedly high level of biodiversity was revealed in Late Archaean microfossils. A fairly high level of biodiversity is revealed in shallow-water hydrotherms and soda lakes. A comparative study of the modern and fossil bacterial mats reveals a striking similarity between them. This similarity suggests that their function in the ecosystems (part of which they form) is identical and that the evolution of the prokaryotic biota is additive in nature.

A comparison of how the time intervals change between mantle convection cycles and how biodiversity change suggests that mantle convection and associated volcanism promoted Permian-Triassic extinction. A comprehensive study of terrestrial tetrapods at

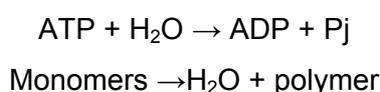
Vyazniki, which is associated with the terminal Permian, suggests that at the end of the Permian their communities were destroyed and at the beginning of the Triassic they were on the scene only as pioneer communities again. A reconstruction of Pleistocene ecosystems in Altai suggests that, of what the accessible biocoenoses had to give in as early as the Late Pleistocene, man took away much more than massive predators like cave lion or cave hyena. Thus, humankind has been an important factor of biotic evolution ever since humans set up large communities. Studies of the genes for embryogenesis in Metazoa revealed that the primary target for molecular evolution are the genes that encode regulatory proteins (morphogens, their receptors and modulators), the adaptive evolution whereof shows a good correlation with the most important aromorphoses on the phylogenetic tree (the Vendian-Cambrian boundary, the Cambrian explosion). The mathematical modeling of gene networks for embryogenesis demonstrated that their functioning is very sensitive to mutation in such genes. Comparative studies of the evolution of various taxa using molecular phylogeny, computer genomic and cytogenetic approaches and classic evolutionary morphological and paleontological approaches revealed that evolution neither always runs at identical rates nor is it always the same at different levels of biological organization (gene, chromosome, genome, morphological). Thus, evolution is a many-parameter process, with a complex interplay of those parameters, and the more complex the associations among them, the larger the number of levels in the evolving system. It is possible that the variation in evolutionary rates is due to that interplay. The evolution of taxa cannot rely upon any of molecular, chromosomal or morphological phylogeny alone. To reliably reconstruct evolution, the all the available data that reciprocally add to one another should be recruited. In particular, archeological excavations in Altai and western Tian Shan suggest that there is a continuity in Paleolithic culture traditions and that crosses between the aboriginal (neanderthaloid?) dwellers and later comers-ins were possible there. To be sure, molecular phylogenetic data are required.

**THE CONCEPT OF ORDERING AND ORIGIN OF LIFE
(RAS PROGRAM "BOE-I")**

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The concept of ordering is suggested. It is shown that a system of conjugated irreversible reactions, dwelling near a steady state, is charged to produce ordering. In chemistry conjugation occurs when product of one reaction is an immediate reagent of another reaction. Then order may emerge next to the disorder. The events of ordering conjugated with disordering are ubiquitous in nature, both in organic and mineral world. In inorganic world the evolution of ordering cannot proceed too far. It stops after a few consecutive steps. In contrast, in a world of organic compounds the ordering may evolve through billions steps for billions years. This is due to unique properties of some organic compounds. The model has been proposed, in which molecule of adenosine triphosphate (ATP) played a key role in prebiotic evolution (Galimov, 2004). More precisely, this is the reaction of ATP hydrolysis conjugated with the polymer synthesis reaction:



Among the polymers different peptides from individual amino acids, as well as RNA like chains from individual nucleotides, might be synthesized.

The ordering is determined as a restriction of freedom. Chemical ordering begins when the freedom of interaction is restrained, when a compound or a system can react with a certain partner and only via a limited number of mechanisms and ways. There are no other natural organic compounds comparable with peptides on the efficiency of ordering through selective catalysis. A catalyst plays this role. The best organic catalyst is peptides. All biochemical processes in organisms are controlled by enzymes, consisting of folded peptide chains. Modern enzymes are products of prolonged evolution, but even short amino acid chains show an amazingly high catalytic activity.

However, amino acid chains cannot self-replicate. Therefore, ordering based on the synthesis of peptides alone would have had no long evolutionary prospects. In contrast to peptides, nucleotide chains can self-replicate. Owing to the complementary structures of purines and pyrimidines, the self-replication capacity of nucleotides chains like RNA is unrivaled in the world of organic compounds. I argue that the genetic code emerged not as a miraculous information transfer system, as is qualified by some authors, but as the only possible mechanism of autocatalytic coping of peptides along the evolutionary path of

ordering consistent with the given properties of organic compounds. The emergence of the genetic code marked the completion of the stage of prebiotic evolution and the beginning of the stage of life evolution.

Among countless organic compounds only peptides can provide ordering, and only nucleotides have reproductive ability. Therefore it is very probable that the molecular appearance of life is significantly uniform throughout the universe. The individual amino acids and nucleotides involved into evolving ordering may be different in different worlds but the principle is common.

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PREBIOTIC EVOLUTION AND THE ORIGIN OF LIFE: A STATUS REPORT

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The origin of life is, by its very nature, a multidisciplinary issue that needs to be approached as a historical problem within an evolutionary perspective. However, there is no geological evidence of the environmental conditions on the Earth at the time of the origin of life, nor any fossil register of the evolutionary processes that preceded the appearance of the first cells. Direct information is lacking not only on the composition of the terrestrial atmosphere during the period of the origin of life, but also on the temperature, ocean pH values, and other general and local environmental conditions which may or may not have been important for the emergence of living systems.

The lack of an all-embracing, generally agreed definition of life sometimes gives the impression that what is meant by its origin is defined in somewhat imprecise terms, and that several entirely different questions are often confused. For instance, until a few years ago the origin of the genetic code and of protein synthesis were considered synonymous with the appearance of life itself. This is no longer a dominant point of view; the discovery and development of the catalytic activity of RNA molecules has given considerable support to the idea of the 'RNA world' --a hypothetical stage before the development of proteins and DNA genomes during which alternative life forms based on ribozymes existed. This has led many to argue that the starting point for the history of life on Earth was the de novo emergence of the RNA world from a nucleotide-rich prebiotic soup. Others with a more skeptical view believe that it lies in the origin of cryptic and largely unknown pre-RNA worlds. There is even a third group that favours the possibility that life began with the appearance of chemoautotrophic autocatalytic metabolic networks, lacking genetic material.

Despite the seemingly insurmountable obstacles surrounding the understanding of the origin of life (or perhaps because of them), there has been no shortage of discussion about how it took place. Not surprisingly, several alternative and even opposing suggestions have been made regarding how life emerged and what were the defining characteristics of the first organisms. However, it will be argued that while it is true that the classical version of the hypothesis of chemical evolution and primordial heterotrophy needs to be updated, it still provides the most useful framework for addressing the issue of emergence of life.

SODA CONTINENT AND ITS MICROBIOTA

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Conventional idea that "life comes from the sea" might be opposed by the studies of microbes from soda lakes. Genesis of the ancient biosphere depends on the composition of the atmosphere. One of the main processes was scavenging of CO₂ by its subaerial reaction with silicates. CO₂ is bound into Ca and Mg carbonates producing neutral environment for calciphilic microbiota. After Ca pool is exhausted excessive Na produces soda environment in endorheic regions. Soda lakes represent an extreme pockets of typically terrestrial environment as opposed to the NaCl ocean. Microbial communities of soda lakes might be analogous to the microbiota of the inner parts of the ancient terrestrial territories. Soda lakes are characterized by high pH up to 10.2 and salt content up to saturation. Microbiota of this environment should be alkaliphilic and halophilic. Alkaliphilic microorganisms are represented by two groups: those developing in NH₃-rich patches produced by ammonifying alkaligenes during mortmass decomposition as e.g. urobacteria, and those developing in natron depositing environment produced by geochemical processes. Aerobic organotrophic alkaliphilic species of *Bacillus* were used since late 1980-th by Horikoshi and by Krulvich as the models for the extensive studies of enzymology. Phototrophs are the main biogeochemically significant alkaligenes, which develop local pH>10 during photosynthesis. However biogeochemical role of alkaliphiles on the global scale remained out of scope. In our studies (Trudy of the Winogradsky Institute of microbiology, v.14, 2007) soda lakes from Africa and Central Asia were used as some kind of natural enrichment cultures. From 99 validated species of haloalkaliphiles 50 were described during these studies, mainly anaerobes, lithotrophs, anoxygenic phototrophs. Microbial community of soda lakes is selfsufficient. High productivity results here from non-limited mineral nutrition. Prime producers are represented by extremely haloalkaliphilic phototrophs as cyanobacteria *Eubalthece*, *Rhabdoderma* and occasionally by green alga *Dunaliella viridis*. Cyanobacterial mats dominated by *Microcoleus* are similar in architecture to the halophilic mats. Anaerobic decomposition proceeds via saccharolytic and proteolytic pathways performed by highly specialized *Tindallia*, *Natroniella*, *Natronincola*, *Halonatronum*, *Anoxynatronum*, *Alkaliflexus* etc. The final step of conjoined decomposition is performed by the sulfur trophic loop with hydrogenotrophic sulfate reducers *Desulphonatronovibrio* and *Desulfonatronum*. They interact with decomposers via acetate decomposing syntroph *Contubernalis* with excessive production of H₂S as e.g. in combined culture with cellulolytic *Clostridium*

PL-1

alkalicellulosi. Regeneration of sulfate is performed by purple anoxygenic phototrophs, among which in addition to the known *Ectothiorhodospira* are new genera *Heliorestis*, *Thioalkalicoccus*, *Thiorhodospira*. Aerobic oxidation is performed by the full range of lithotrophs, including alkaliphilic species of the known genera and of new genera *Thioalkalivibrio*, *Thioalkalimicrobium*, or of facultative *Roseinatronobacter*, *Alkalispirillum* and *Alkalilimnicola*. Unsuspected was discovery of acetate utilizing iron-reducing alkaliphile *Geoalkalibacter* in asian and african soda lakes. Alkaliphiles from soda lakes represent main phylogenetic phyla including Cyanobacteria, Proteobacteria, Firmicutes, Spirochaetes, Bacteroidetes, Euryarchaeota. Microbial community of soda environment is functionally complete and autonomous. There seems now to be no limitations for development of such communities on Proterozoic platforms in subaerial environment of the ancient atmosphere. That means that for the ancient pioneering prokaryotic community limnetic pathway from the subaerial terrestrial environment into the sea is not forbidden.

WHEN, WHERE AND IN WHICH CONDITIONS COULD RNA WORLD ARISE AND EVOLVE?

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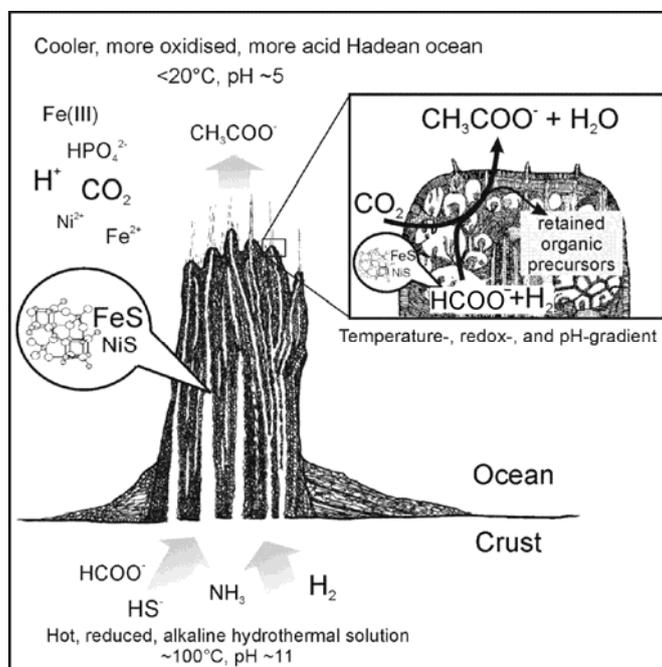
Environmental conditions required for existence, amplification and evolution of the hypothetical ancient RNA World, as well as the difficulties with abio-genous RNA synthesis and the paradoxical situations with stability of RNA, its functional conformations and the place of the RNA World in geological history of the Earth are considered. Three evident paradoxes are mentioned. First, the so-called “water paradox” consists in the incompatibility of the well-known chemical instability of the covalent RNA structure in aqueous solutions with the necessity of water for the formation of functionally active conformations of RNA. Second, the stable double-helical conformation of RNA required for RNA replication is not compatible with stable compact conformations of single-stranded RNA necessary for catalytic functions (“conformational paradox”). Third, in the geological history of the Earth the window between the end of the massive meteorite bombardment (3.9 billion years ago) and the first evidence in favour of the existence of life in the form of single-cell organisms (bacteria) (3.8–3.85 billion years ago or even earlier) is too short or absent (“geological paradox”). The conclusion is made that the appearance, existence and evolution of the ancient RNA World into cellular forms of life was unlikely on the Earth. The alternative possibility of the cosmic origin of the RNA World, its extraterrestrial evolution and the subsequent cosmic distribution of life (panspermia), predominantly in the cellular form as much more resistant to harsh environments as compared with free RNA, is briefly discussed.

THE ALKALINE SOLUTION TO THE EMERGENCE OF LIFE

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Hydrogen dissolved in ~100 °C alkaline submarine springs was unstable with respect to the CO₂ dissolved from the ancient atmosphere in the 4.3 Ga ocean. But reaction between the two volatiles was strongly inhibited by kinetic barriers. One of these barriers was overcome during serpentinization of the crust in off-ridge alkaline hydrothermal convection cells as H₂ reacted with bicarbonate to produce formate. On exhalation and mixing of this hot solution, now containing H₂, NH₃, HCOO⁻ and HS⁻ with the cool Fe²⁺-bearing carbonic ocean, metastable acetate was synthesized in a co-precipitating hydrothermal mound—a natural hydrothermal reactor comprising freshly precipitated metal sulfides (e.g. Fe₅NiS₈) that catalyzed the reductions [1]. Such sulfides were later sequestered by heterochiral peptides to form the first enzymes [2]. Thus the acetyl co-A pathway emerged, a pathway generating both organic carbon and energy. CH₄ generation faced higher kinetic barriers which may have been surmounted by an electro-geochemical input. These two variants of the pathway became genetically stabilized in the acetogens and the methanogens while still within the mound. The bacteria and archaea, the two prokaryotic domains, may have emerged from this early metabolic differentiation.



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ASTROCATALYSIS

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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 autocatalysis, 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.

The catalytic processes formed the planets. The primary organic compounds were most likely formed by the abiogenic synthesis in the "space catalytic reactor" with the following features. This is a fluidized, or boiling, solid-phase reactor. In it the reducing hydrogen-helium atmosphere with the gas pressure up to or above 10 atm. The size of the granules of the solid phase is about 1-10 m. The solid phase represents compounds, mainly composed of SiO₂-MgO-Fe. The solid phase has a huge catalytic surface, on which water and other compounds are condensed at certain distances from the protostar. The size of the reactor at different times varied from hundreds to tens of times the diameter of the Sun. The input of energy into the zone of reactor was performed by the radiation from the protostar heating the surface of the protoplanetary disk. Hydrogen and helium cooled the zone of synthesis during exothermal reactions. The reactor synthesizing chemical compounds existed for about ten years. At the final stage of this synthesis, organic compounds of high molecular weight, H₂O, and other hydrides of elements, and possibly the "RNA world," were formed.

Physically the final stage represented bodies of many kilometres in size in a reducing atmosphere. The number of such birthplaces of life like the reactor of chemical synthesis and of the "RNA world" is determined by the details of the development of gravitational instability in the two-phased medium of the disk. At the initial stage of the development of instability, a "zone of life" may contain a few or even more such birthplaces of life.

Thus, astrocatalysis, i.e., the abiogenic synthesis of prebiotic compounds, the "RNA world," and the origin of life in the solar system are placed onto the temporal astrophysical and paleontological scales.

VOLCANIC GLASS A HABITAT FOR THE ORIGINS AND EVOLUTION OF MICROBIAL LIFE

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Bioalteration of basaltic glass in pillow lava rims and volcanic breccias (hyaloclastites) produces conspicuous petrographic and chemical signatures. These include granular and tubular morphologies that are formed by the microbial dissolution of volcanic glass [1]. Numerous examples have been described from the upper 300 m of in situ oceanic crust spanning the youngest to the oldest oceanic basins (0 to 170 Ma). These microbial trace fossils contain nuclei-acids localized at the interface between fresh and altered glass and it is thought that Fe and Mn oxidizing bacteria are principally involved [2]. Comparable, mineralized structures have also been found in meta-volcanic glasses from Phanerozoic to Proterozoic ophiolites and Archean greenstone belts [3]. The latter include pillow lavas and hyaloclastites from the Archean Barberton Greenstone Belt of South Africa (BGB) and the East Pilbara Terrane of the Pilbara Craton, Western Australia (PWA).

Multiple lines of evidence suggest that these Archean textures were also formed by the microbial etching of formerly glassy lavas [4]. Firstly, there are striking morphological similarities between Archean tubular structures from both the PWA and BGB and bioalteration textures in modern glasses. Secondly, X-ray mapping indicates carbon enriched along the margins of the Archean tubular structures. Thirdly, disseminated carbonates in the BGB pillow rims have C-isotopes depleted by as much as -16‰ which is consistent with microbial oxidation of organic matter. Furthermore, direct in-situ U-Pb dating of titanite (CaTiSiO_4) which infills the PWA textures confirms a late Archean age [5]. This represents the first direct radiometric age determination upon an Archean biosignature and suggests that seafloor volcanic glasses were important habitats for the origins and evolution of life.

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EVOLUTIONARY INSIGHTS FROM STUDIES ON VIRUSES OF HYPERTHERMOPHILIC ARCHAEA

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Double-stranded (ds) DNA viruses of hyperthermophilic members of the domain Archaea represent a collection of diverse unique morphotypes, not encountered among ds DNA viruses of the two other domains of life, the Bacteria and Eukarya [1]. Their genomes are also unique, with more than 90% of putative genes without recognisable functions and detectable homologs in other viruses or cellular life forms [2]. Moreover, unusual properties of many of these viruses challenge our ideas on virus structure and functions [3]. The results allowed concluding that the viruses form a unique group in the viral world, with a single or, more probably, multiple origin, evolutionarily unrelated to viruses of Bacteria and Eukarya [4].

By revealing a unique group of archaeal viruses we are faced with the intriguing perspective that each of the three domains of life was originally characterized by a unique set of associated dsDNA viruses. A plausible cause for the existence of these three “viropheres” is that they were selected when the domains first arose. Thus, the first evolving organisms of each separate domain could have already been infected by different subsets of viruses from the ancestral virosphere which predated the Last Universal Common Ancestor, LUCA.

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ENVIROMENTS AT THE EARLY EARTH

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1. Current literature contains numerous contradictory suppositions about natural environments at the early stages of Earth evolution. Among them an idea of reducing conditions is most stable.

2. According to this idea, in the Archean time there existed only anaerobic organisms.

3. Studies of sedimentation that was documented by the earliest geological records lead many authors to conclude that both sedimentational processes and their set are not significantly different in the Archean, Proterozoic, and Phanerozoic.

4. A large portion of sedimentary rocks in Archean sections and absence of any rocks older than 3.9 Ga (beside zircon grains) are perplexing.

5. Available isotopic data do not provide unambiguous evidence for anaerobic situation in the Archean either.

6. Data on rounded uraninites and pyrites, which are commonly used for substantiation of Archean anaerobic environments on the Earth, appeared to be less reliable than supposed for a long time.

7. A set of discovered Archean organisms does not indicate anaerobic atmosphere as early as 3.5 Ga.

8. The RNA-world must have existed at least at 4.9 Ga and, likely, close to the beginning of degasification and appearance of water on the Earth surface.

9. The earliest cellular organisms (membranes) also appeared before 4.0 Ga.

MIGRATION AS AN INTRINSIC ATTRIBUTE OF LIFE

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Wherever and whenever life has established itself, it has shown a natural instinct to expand ultimately the area from which its resources are drawn. The driving forces for migration to new settlements can be endogenous (e.g., hormones) or exogenous (e.g., deprivation of food or space, overcrowding by other species, unfavorable environmental conditions, light stimulus). Migration has certainly played a role in the evolution of our biosphere.

Prokaryotes dominated the Earth's biosphere during the first two billion years of life's history before the unicellular mitotic eukaryotes appeared. Since then, microorganisms have developed sophisticated strategies to conquer the whole surface of the Earth as well as subsurface regions and to adapt to "extreme" niches that would not sustain eukaryotic life. Examples are hot vents, permafrost areas, "eternal" ice, subsurface regions down to several kilometers, the high atmosphere, rocks, and salt crystals. Hence microbial life has stretched its limits to invade nearly all regions of the Earth spreading down below the surface to several kilometers. Traces of microbial activities have been left everywhere on our planet, especially in the soils, in rocks, and in the atmosphere. Plants, although most of them are of sessile nature, have developed several mechanisms for increasing their habitat. Most of their spores or seeds can be easily transported over long distances through air or water; other seeds use animals for passive movement. Phytoplankton uses the circadian light cycle for its vertical migration in the ocean to optimize photosynthesis. Most animals are capable of active movements. Food depletion, limited space or unfavorable climate can cause mass migrations, several without return to the starting site. Examples are given by insects, birds, lemmings and horses; migrating birds change their habitat following the seasonal rhythms.

Concerning the origin of humans and their subsequent distribution over the globe, the fossil records date the evolution of a distinct hominid line at 5 million years ago. The early evolution is exclusively African. Between two and one million years ago, hominids moved north and colonized large parts of Asia and Europe. As early as 150,000 years ago in Eastern Africa, we find fossil skulls of essentially modern type. Successive migrations out of Africa replaced the regional populations, such as the Neanderthals, in all parts of the inhabited Old World. One of the novelties associated with the modern humans is their drive for global colonization. In the last 50,000 years these people colonized Australia, the Pacific islands, the northern parts of Asia, the American continents, and the Arctic. This great prehistoric migration was achieved by people with a hunting and gathering lifestyle, and drew

the demographic and geographical map for the later development of ethnic and regional populations of *homo sapiens sapiens*. Massive migrations of peoples have occurred in Europe since the third millennium B.C. Best investigated are the wanderings of Germanic tribes. Migrations of peoples have continued until today. Escaping natural and anthropogenic deprivations or disasters are certainly dominating reasons in many instances. However, human curiosity, the spirit of research, and the zest for discovery and exploration are other powerful forces driving migration. Humans have crossed the seas, climbed the highest mountains, visited the poles, studied the abysses of the ocean. Hence, humans have identified and reached the outer limits of habitability on our planet.

With the advent of space technology, migration is not anymore constrained to the planetary realm: Experimental evidence has been obtained that microbial life forms can be transported by meteorites between the planets of our solar system. Humans have developed the technology to leave their home planet and to explore the other bodies of our solar system. Besides political reasons, aspects in science, technology, culture, and economy may also inspire humankind to explore the neighborhood of the Earth. This evolutionary step is still in its infancy, with the Moon being the only celestial body visited so far, yet the technology exists for more ambitious projects, such as a visit to the neighbor planet Mars. Hence, our "Weltbild" slowly transforms from a geocentric to a more universe-oriented one. However, human spaceflight to other planets should never serve as an "exit option" for terrestrial mismanagement.

GENETIC RECOMBINATION IN THE LIGHT OF EVOLUTION

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Recombination is a process that promotes gene shuffling in the progeny and insures genetic uniqueness of each individual. This process has been discovered in the beginning of XX century, but it still poses a lot of difficult problems. What are the advantages of sexual reproduction and genetic recombination? Why meiotic recombination is organized in a wasteful, cumbersome and illogical way? How the hot and cold spots of recombination are distributed along the genomes and what is the biological sense of such distribution? In this report I try to answer some of these questions looking at the genetic recombination in the light of evolution.

First, I evaluate several hypotheses explaining the advantages of sexual reproduction and genetic recombination: (1) an increase of genotypic/phenotypic variability favorable in variable environments and as an adaptation to resist parasites (2) elimination of slightly deleterious mutations due to generation of mutationally overloaded gametes, (3) repair of DNA damages due to gene conversion.

Then I demonstrate that molecular mechanisms of meiotic recombination have evolved from ancestral prokaryote and somatic cell functions of DNA replication and repair. They retained some of these functions, although in much modified form. They also adopted new functions, becoming the mechanisms of homologous chromosome recognition, alignment, pairing and disjunction. Occurrence of these new functions put stringent constraints on the frequency and distribution of recombination evens along the chromosomes.

Finally, I show how a complex interplay between new and old meiotic functions led to formation of species-specific recombination patterns in several species of mammals, studied in our laboratory, and how these patterns were modified due to accumulation of various chromosomes rearrangements and genetic divergence accompanying speciation, local adaptations and directed selection.

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**MODERN HUMAN ORIGIN
AND APPEARANCE OF MODERN HUMAN BEHAVIOR:
LOOK FROM CENTRAL ASIA**

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In process of an intensification of Paleolithic researches outside the Europe, dominated over last quarter of the last century in prehistoric archeology the harmonious scheme of dependence of change of type of material culture from evolution of physical characteristics and mental abilities of ancient humans has lost the universality. New data force a scientific world to bring remarkable corrective amendments in the developed concepts. So, if earlier appearance of anatomically modern humans directly connected with an epoch of transition from Middle to Upper Paleolithic, now available data confidently specify that, on the one hand, the modern human anatomy has appeared much earlier, and on the other hand, a number of the main cultural attributes of Upper Paleolithic is fixed in archeological complexes of a much greater antiquity. As the transition from Middle to Upper Paleolithic in territory of Eurasia is characterized by significant structural change of culture of ancient humans, in last researches the term «modern human behavior» is entered. This concept combines such elements, as transition to prevalence of the seasonally-focused purposely-planned hunting activity (unlike domination of scavenging human activity in Middle Paleolithic), settling of regions with harsh environments (high mountains, deserts and tundra landscapes); expansion of an exchange between different populations; regular manufacture of tools from not stone raw material; prevalence economically more effective blade technology; expansion of artefactual repertoire in connection with its standardization and strengthening of functional specialization; the expressed display of spatially-structural perception of habitable space (including allocation of functional zones within settlements, complication of hearths, etc.); increase of mobility level of the groups, connected, probably, with the advent of more complex social hierarchies; mass occurrence of symbolical and ritual activity.

The purpose of the given presentation is an attempt of revealing of conformity of the Paleolithic industry of Obi-Rakhmat rockshelter with the attributes of "modern behavioral complex" for definition of competency of reference Obi-Rakhmat industry to "Transitional" or "Initial Upper Paleolithic" complexes of Eurasia, and also the analysis of recovered in 2003 paleoanthropological material which is throwing light on the physical nature of manufacturers of the Transitional industries and appearance of modern humans in Eurasia.

TITAN: A PLANETARY-SCALE LABORATORY FOR ASTROBIOLOGY STUDIES IN THE SOLAR SYSTEM

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After less than three years of close observation by remote sensing and in situ instrumentations from the Cassini-Huygens mission, Titan looks more and more as one of the key planetary bodies in the solar system for astrobiological studies. Titan does not look anymore like a frozen primitive Earth, but it looks now like an evolving planet, geologically active, with cryovolcanism, eolian erosion, clouds and precipitations, and a methane cycle very similar to the water cycle on Earth. But the new data also show that a very complex organic chemistry is taking place in the very high atmospheric zones of the satellite, with the formation in the ionosphere of high molecular weight (up to several 1000 Daltons) organics feeding the lower zones with these compounds, down to the surface. In spite of the low surface temperature, these organics are probably evolving once in contact with water ice and form organic molecules of biological interest. This evolution may explain the reflectance spectrum of Titan's surface observed by the DIRS instrument on Huygens, although, the lack of spectroscopic data in the near IR makes difficult the retrieving of these data. Thus, contrary to what was expected, the organic chemistry on Titan seems mainly concentrated in the ionosphere, on the surface and in the aerosols. These aspects will be examined, some of the associated questions will be answered on the basis of the already available Cassini-Huygens data. The needed post Cassini exploration and the associated future instrumentation will be also discussed.

EARLIEST TRACES OF LIFE ON EARTH

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The highly metamorphosed 3.8 Ga old Isua Supracrustal Belt (ISB) in southern West Greenland contains the most widely studied example of ancient Archaean water-lain sediments that may carry traces of ancient life. Ferrous carbonate deposits in the ISB were originally interpreted as primary platform sediments in a shallow marine environment. Isotopically light graphite occurring in relatively high concentrations in these rocks has been interpreted as a remnant of ancient biogenic matter, pointing to the existence of a vast microbial ecosystem in the early Archaean (1,2). Recent discoveries, however, suggest that these carbonates are secondary deposits, resulting from extensive metasomatism at elevated temperature in the interior of the crust (3,4). The isotopically strongly fractionating disproportionation of siderite; $6 \text{FeCO}_3 \rightarrow 2\text{Fe}_3\text{O}_4 + 5\text{CO}_2 + \text{C}$, is the process seemingly responsible for the graphite formation (5,6). Equilibrium isotope fractionation between siderite and graphite in these rocks indicates a temperature of metasomatism between 500 and 600°C, which coincides with other estimates of metamorphic temperature for the ISB. This graphite, forming the basis for earlier biogenic interpretation, is entirely restricted to the metasomatic carbonate deposits, while previously investigated sediments like BIF's and metacherts contain virtually no elemental carbon. The siderite-graphite-apatite association in the ISB consequently appears to be an entirely abiogenic metasomatic feature, which does not point to traces of an ancient Early Archaean ecosystem.

In contrast a locality has been found in the western part of the ISB, where isotopically light graphite occurs in sequences of graded beds, seemingly representing true sediments in the form of cyclic turbidites (7). The absence of siderite and/or magnetite makes it clear that inorganic formation of graphite by siderite disproportionation can not be the source of carbon in these metasediments. This particular formation is thus likely to contain the only currently suggestive remnants of Archaean life in the ISB with an age of 3.8 Ga and thus possibly representing the oldest known remnants of life on Earth. The highly altered (metamorphic) state of the ISB rocks and the discovery that isotopic fractionation, as earlier believed, is not a unique indicator of a biogenic origin of elemental carbon has made it necessary to rely on other features indicative of its origin. Techniques that have proven particularly useful are

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order-disorder studies of crystal structure by X-ray diffraction (8), and high resolution transmission electron microscopy and electron diffraction, revealing defect structures, characteristic of carbon residues from graphitizing organic matter (9) with results shown in the present investigation.

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KEY-NOTE LECTURES

CATALYSIS IN THE RNA WORLD

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RNA world was the first step to development of living systems. In the RNA world, RNA molecules were the only biopolymers, and they had to manage all processes needed for functioning of primitive cells- ribocytes.

Due to poor stability of RNA polymers, these primitive cells could survive in a narrow window of physico-chemical conditions. Therefore efficient catalysts were of primary importance for manipulating different reactions under ambient temperatures.

Apparently, metal ions played important roles in different reactions of RNA molecules. Small primitive ribozymes harnessed the metal catalysts for manipulating large RNA molecules. The primitive ribozymes could be represented by supramolecular complexes composed of small oligonucleotides assembled by complementary interactions of their substituents. Primitive peptide-like organic molecules could be involved in processes of cleaving and ligation of RNA.

EXTREME ACCUMULATION OF NUCLEOTIDES IN HYDROTHERMAL PORE SYSTEMS: A SOLUTION FOR THE CONCENTRATION PROBLEM OF THE ORIGIN OF LIFE?

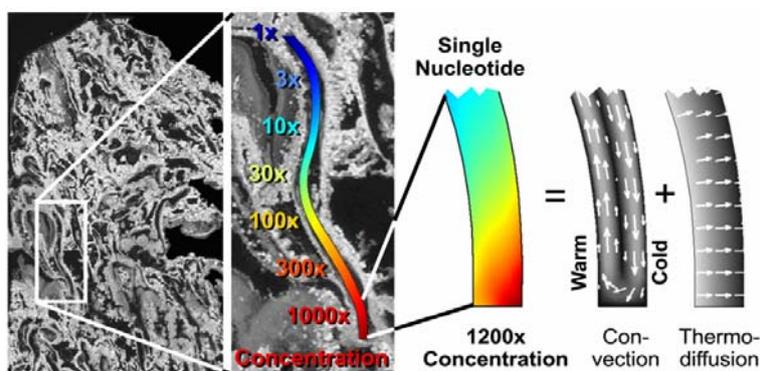
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We simulate molecular transport in elongated hydrothermal pore systems influenced by a thermal gradient. We find extreme accumulation of molecules in a wide variety of plugged pores [1]. The mechanism is able to provide highly concentrated single nucleotides, suitable for operations of an RNA world at the origin of life. Accumulation is driven solely by the thermal gradient across a pore. On the one hand the fluid is shuttled by thermal convection along the pore, whereas on the other hand, the molecules drift across the pore, driven by thermodiffusion. As a result, millimeter-sized pores accumulate even single nucleotides more than 10^8 -fold into micrometer-sized regions. The enhanced concentration of molecules is found in the bulk water near the closed bottom end of the pore. Since the accumulation depends exponentially on the pore length and temperature difference, it is considerably robust with respect to changes in the cleft geometry and the molecular dimensions. While thin pores can concentrate only long polynucleotides, thicker pores accumulate short and long polynucleotides equally well and allow various molecular compositions. This setting also provides a temperature oscillation, shown previously to exponentially replicate DNA in the protein-assisted Polymerase Chain Reaction (PCR) [2]. Our results indicate that for life to evolve, complicated active membrane transport is not required for the initial steps. We find that interlinked mineral pores in a thermal gradient provide a compelling high-concentration starting point for the molecular evolution of life.



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**ORIGIN AND EVOLUTION OF BACTERIAL AEROBIC RESPIRATION:
IMPLICATIONS FOR EARLY EARTH ATMOSPHERE**

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Based on geological data it is generally thought that, prior to a great oxidation event at circa 2.4 billion years ago (Ga), linked to the accumulation of oxygen (O₂) produced by Cyanobacteria through oxygenic photosynthesis, O₂ was either absent or present only in trace amounts in the atmosphere and oceans during the Archaean (3.8 -2.5 Ga)^{1, 2}. Following this logic, aerobic respiration is generally assumed to be more recent than oxygenic photosynthesis³. Here, we have performed an exhaustive phylogenetic analysis of type-M cytochrome oxidases, the terminal enzyme of most aerobic respiratory chains. Our results strongly suggest that this type of cytochrome oxidase was present in the ancestors of a number of major bacterial phyla- and most likely in the ancestor of all Bacteria-, thus prior to the emergence of Cyanobacteria. This indicates that aerobic respiration arose before the onset of oxygenic photosynthesis and was a common feature throughout the early evolution of present-day bacterial lineages. These results should be taken into account in models and discussions on early Earth atmosphere and early bacterial evolution.

VOLATILES AND BIOGENIC MATTER DELIVERY BY SMALL BODIES AND DUST PARTICLES

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Migration of small bodies and dust particles from the outer regions of the solar system is an important mechanism of the inner planets evolution, and specifically of the formation and evolution of atmosphere and hydrosphere of the terrestrial planets. It is assumed that these bodies and particles could be responsible for the delivery of the original matter (mainly volatiles) and thus could give rise to the life origin.

Our studies of volatiles delivery is based on the results of numerical integration of the migration of small bodies and dust particles in the Solar System [1]. Basically, our modeling involving 30,000 Jupiter-crossing objects favors the idea that in early epoch soon after solar system formation millions of comets which migrated inward the solar system and collided with the terrestrial planets could be responsible for delivering a great amount of volatiles including water to Earth. Mars acquired even more water (per unit of mass of a planet) than Earth, and the total amount of water delivered to Venus was about the same as that for Earth. As a result, the ancient ocean on Mars could be relatively large. The model also concurs with the scenario that some former comets moving for a long time inside Jupiter's orbit could be disintegrated while other become Sun-grazers and disappear.

It was therefore shown that both the exogenous mechanism of heterogeneous accretion and the endogenous mechanism of the interior degassing may contribute to the formation of planetary atmosphere and hydrosphere at least comparably. Assuming the total mass of planetesimals beyond Jupiter's orbit was about a hundred of Earth masses, then the total mass of volatiles delivered to the Earth could exceed the water storage in the Earth's oceans.

Contribution of dust particles produced mainly by comet showers and asteroid collisions to the volatiles delivery is much less than that related to small bodies. The results of our study of the migration of dust particles of various genesis lead to the conclusion that a fraction of trans-Neptunian particles highly enriched by volatiles can be significant compared to particles from other regions. It is believed that some matter transported inward the solar system could be pristine particles of interstellar origin, which embedded protosolar nebula and preserved for a long time at the outskirts of the solar system. Although it is difficult to obtain exact estimates of the dust influx to the Earth and neighboring planets, the dust contribution was derived 3-4 orders of magnitude smaller compared to asteroids/comets.

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However, dust particles could have been most efficient in the delivery of organic prebiogenic and likely, biogenic matter, because they experience substantially weaker heating when entry the atmosphere. An excess heat is radiated effectively due to high total surface-to-mass ratio for a dust particle than for a larger body. This conclusion is confirmed by the lab investigations of of bacteria and phages heated up to 200 °C survival [3] and it allows one to consider dust as a potential carrier of biogenic material from outer space. This is why one may assume that life forms drastically different from their terrestrial analogs are unlikely to be found elsewhere in the solar system (if any), for example, either extinct or extant life on Mars.

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MICROFOSSILS IN CARBONACEOUS METEORITES: IMPLICATIONS TO THE ORIGIN AND EXTENT OF THE BIOSPHERE

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Field Emission Scanning Electron Microscopy (FESEM) studies of CI1 and CM2 carbonaceous meteorites have revealed an extensive indigenous suite of well-preserved permineralized microfossils embedded in the meteorite rock matrix. All of the filamentous microfossils found in the meteorites have morphologies and sizes consistent with known modern morphotypes of cyanobacteria and the associated filamentous trichomic prokaryotes typically found in the anoxic regime of cyano-bacterial mats. Many of the meteorite filaments have complex differentiated cellular configurations such as apical, basal, and intercalary heterocysts, akinetes, hormogonia, calyptra, terminal hairs and lophotrichous tufts of fimbriae. These highly distinctive microstructures and nanostructures establish that these microfossils are unambiguously biological and can reliably be interpreted as morphotypes of *Cyanobacteriaceae*. Many others are isodiametric (uniseriate or multiseriate) mineralized filaments enclosed within carbonaceous sheaths. Although the morphological convergence of cyanobacteria with trichomic filamentous sulphur bacteria (e.g. *Thioploca*, *Beggiatoa*, etc.) does not permit definitive identification of these morphotypes, they are undeniably biological in nature. Energy Dispersive X-ray Spectroscopic spot data, 2-D X-ray maps and comparison of the ratios of life critical biogenic elements (C/N; C/S; and C/O) in the meteorite microfossils with living and herbarium cyanobacteria, hair and tissue from Egyptian Mummies and *Mammuthus primigenius* establish that the meteorite microfossils are indigenous and modern biological contamination can be positively ruled out. Visible light and FESEM images, EDS data and C/N and C/S ratio plots will be presented for the meteoritic microfossils and for modern morphotypes and Pleistocene, Cambrian and Archaean analogs will be shown. Implications of the discovery of valid microfossils in meteorites to the Origin of Life and the extent of the Biosphere will be briefly considered.

METAL CATALYSTS AND HYDROGEN IN THE INITIATION OF LIFE**M.A. Fedonkin**

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Most of known enzymes contain the transition metal ions as a cofactor of their active sites. These metalloenzymes lose their catalytic activity when the metal ions are being removed from the protein molecule. These facts indicate the primary role of the metals in the origin of biocatalysis. Taxonomic distribution of the metalloenzymes gives a hint on the biogenesis as well. For example, the tungsten enzymes are discovered so far in prokaryotes only. However, obligatory dependence on tungsten is documented merely for hyperthermophilic Archea. Their basal position on the molecular tree of life points to the W-rich hydrothermal systems as a cradle of life. But the major catalysts on the earliest stages of the biogenesis were iron and nickel. The fact that nickel makes 5-20% of the iron meteorites indicates that both metals were abundant on young Earth. At present iron and nickel are actively involved in hydrogen metabolism which plays a key role in the prokaryotic and even eukaryotic organisms: virtually all hydrogenases contain Fe and/or Ni cofactor. This should turn our attention to the role of hydrogen in biogenesis.

Hydrogen, the most abundant element in the Universe, well could be the primary fuel for early life. The availability of hydrogen on early Earth was much higher than at present. Two major sources of hydrogen were (1) the degassing of the mantle that released the neutral or slightly acidic fluids saturated with H₂, CH₄ и H₂S, and (2) the serpentinization, reaction of the rocks, rich with olivine and pyroxene, with water. Two additional processes, such as photolysis of water by UV light and radiation-induced dissociation of H₂O could contribute to the hydrogen budget as well. Abundance of hydrogen on early Earth gave easy access to the protons and electrons, the very motor of the life's energy machine. The subsequent evolution of life was in a great extent driven by the competition for access to hydrogen. Decline of the primary sources of hydrogen mentioned above made life to switch for the hydrogen compounds such as H₂S, CH₄, NH₃, and at last, H₂O in the oxygenic photosynthesis. The succession and degree of involvement of these simple molecules into early metabolic evolution could correlate to the energy required for breaking their chemical bonds in the conditions of early Earth. This concept helps to understand the historical causes of the atmosphere chemistry, in particular, the high content of nitrogen and oxygen as the by-products of hydrogen metabolism. Early kinds of biochemistry, once established, have been saved throughout of the later history of life via addition of complementary metabolic modules in response to the irreversible changes of the environment. This was the major driving factor of evolution towards the higher biological complexity.

LATE PROTEROZOIC EVOLUTION OF MACROBENTHOS

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The biosphere's earliest known macrobenthic communities are represented by the extinct late Proterozoic Khatyspyt-, Avalon-, Ediacaran- and Nama-type biotas, each with its known evolutionary pathway. The Khatyspyt-type biotas were restricted to transgressive low-energy shelf environments and combined multicellular or coenocytic, eukaryotic macroalgae and possible metazoans, all preserved as carbonaceous compressions. The Avalon-type biotas were distributed in regressive low-energy shelf habitats and consisted of rangeomorphs (closely related problematic fusiform, frondose and plumose organisms characterized by their diagnostic fractal quilting) and various stalked organisms with holdfast structures. The Ediacaran-type biotas inhabited microbial substrates in wave- and current-agitated marine settings and represented the most diverse communities of segmented and non-segmented fossils with bilateral and trilateral symmetry, some of them being demonstrably motile. The Nama-type biotas were found in channelized sandy shoals and comprised infaunal forms, the most exotic to mainstream biology, dominated by serially quilted body plans.

The available U-Pb zircon age constraints and the inferred paleoecology of late Proterozoic biotas suggest a rather complex evolutionary history, in which three major sequential diversification events occurred. Insofar as the Khatyspyt-, Avalon-, Ediacaran- and Nama-type fossil assemblages correspond to in-life ecological associations of benthic organisms preserved in situ, the evolutionary history of late Proterozoic macrobenthic communities and the quantitative proportion of taxa within these communities provide the basis for establishing a succession of Upper Vendian biostratigraphic zones:

Biozone I (580–560 Ma) – Ancestral diversification of the Avalon-type biotas in low-energy shelf environments. Microbial mats and discoidal microbial colonies dominate in shallow marine settings. **Biozone II (560–550 Ma)** – Diversification of the Ediacaran- and Nama-type biotas in shallow marine outer prodelta fans and sandy channelized shoals, accompanied by a notable decline in morphological disparity of the Avalon-type biotas and a diversification of the Khatyspyt-type biotas. Global distribution of the Khatyspyt-, Avalon-, Ediacaran- and Nama-type biotas and their coexistence in different environments. **Biozone III (550–540 Ma)** – Sudden disappearance of the Avalon- and Ediacaran-type biotas, concurrent with increase in behavioral complexity of burrowing organisms and the first appearance of bioturbation; diversification of the Nama-type biotas in channelized sandy bars; several morphological innovations in the Khatyspyt-type biotas (appearance of vendotaenids). Importantly, the disappearance of the Avalon- and Ediacaran-type biotas and the diversification of trace fossils were coeval with the appearance and evolution of metazoans with biologically controlled mineralization, which were restricted to stromatolitic and thrombolitic bioherms in normal marine settings.

**MORPHOGENESIS AND ADAPTATIONS: CHANGES
IN CONSUMERS COMPOSITION OF MARINE COMMUNITIES
IN THE EARLY PALEOZOIC**

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In the Early Paleozoic, the consumers composition changed in two stages. The first stage was connected with the appearance of plankton filter-feeders in the Early Cambrian (Cambrian evolutionary explosion), while the second stage was provided by the appearance of benthic organisms capable of feeding on living plankton (Ordovician evolutionary radiation). The Cambrian and Ordovician evolutionary radiations initiated the formation of the modern pattern of the biosphere. Each stage in the development of the consumers composition of the marine biota corresponded to pronounced morphological and taxonomic changes. At the first stage (beginning of the Cambrian), the archetypes of all phyla of Metazoan animals developed, and the Cambrian evolutionary fauna was formed. At the second stage, in the Ordovician, the formation of archetypes of all classes of primary marine animals was accomplished. This is reflected in the replacement of the Cambrian evolutionary fauna by the Paleozoic one. The diversity of archetypes was limited by intrinsic causes, which restricted developmental directions of the morphogenesis. As new classes appeared, new archetypes could have been realized successfully, unsuccessfully, or intermediately. The successful archetypes of classes gave rise to wide and diverse adaptations in a large number of new taxa of lower rank (large classes). The intermediately successful archetypes restricted adaptations, morphological and taxonomic diversity (moderately large and small classes). The unsuccessful archetypes are only represented by small monotypic taxa and aberrant forms. The same archetype could have provided the basis for different adaptations and, vice versa, different archetypes could have been the basis for similar adaptations. Communities that appeared at the beginning of Ordovician radiation were dominated in number and biomass by small and intermediate short-lived classes and in generic diversity, by large classes characteristic of the Paleozoic fauna. After the Late Ordovician fall in temperature and regression of the sea, which resulted in extinction of many Ordovician lineages, large classes, with their labile morphology, became the sole dominants.

LAKE BAIKAL: A NATURAL LABORATORY FOR STUDIES OF BIOLOGICAL SPECIATION

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Studies of the sedimentary infill of Lake Baikal revealed characteristics of the climate of East Siberia of the last 8 million years. The major signal of changing paleoclimates in this section is the content of diatom algae frustules. Diatoms became extinct during global glaciations and were highly numerous in the pelagial of the lake during the interglacials, responding to all the known details of the global climate change. Studies of the content of the isotopes of uranium in the sedimentary record yielded a geochemical model which suggested that during the glaciations the major tributary of the lake, the Selenga River, dried out, and the level of the lake decreased by 30-50 meters, compared to the present level. Extinction and well-being of diatoms, the first member of the food chain of Lake Baikal, was the major driving force which gave more than 3 thousand endemic animals. The method of molecular clock applied to all animal kingdoms gave the dates of speciation. Some animals such as crustaceans and oligochaets have very ancient roots spanning the age of Lake Baikal (Miocene, 25 MY). Other animals such as mollusks gave flocks in the Pliocene, at the time of the first global glaciations. Endemic cottoid fishes of Lake Baikal appeared in the Pleistocene, when climate change was the most abrupt. Endemic sponges of Lake Baikal, in spite of the unusual morphology, are close relatives to ubiquitous cosmopolitan freshwater spongillid species.

**APPLICATION OF MOLECULAR MARKERS IN THE STUDIES OF
PHYLOGENY AND PHYLOGEOGRAPHY: ADVANCES, PITFALLS
AND PERSPECTIVES OF DEVELOPMENT**

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Application of molecular markers, particular analysis of DNA sequences obtained from mitochondrial and nuclear genomes, became the most popular in the studies of phylogenetic relationships at various taxonomic levels. Advances of molecular phylogenetics and systematics are evident, the number of publications devoted to individual taxa in different groups of animals and plants increase from year to year in a geometric progression. Today it is already impossible to imagine the further development of zoology and botany without the application of molecular markers. Advances both in molecular phylogenetics and phylogeography related not only to dramatic progress of DNA-technologies (PCR, automatic sequencing) but also to explicit research program, easy formalization of data obtained and developed algorithms of their analysis. It is worth to note one more advantage of molecular data – reproducibility and comparability and a great achievement here is an International database both in nucleotide and protein sequences. Undoubting contribution of molecular phylogenetics is a wide distribution and popularization of phylogenetic thinking and a new powerful spur to the discussions on the species problem and species boundaries.

However, despite significant advances a whole number of serious unresolved problems related to the application of molecular markers became now evident. These pitfalls influence the topology of obtained gene trees and correspondingly the inferred evolutionary scenario and taxonomic conclusions. One of the less studied but very serious issues here is a question of applicability of molecular marker to the recovery of phylogeny at a particular taxonomic level. Inappropriate molecular markers with a high level of homoplasy are more often the true reason of observed polytomies on the gene trees than a rapid diversification of the group. Within the scope of this communication we on the experience of our study of molecular phylogenies of various groups of animals show that it is impossible to use one and the same marker to the study of phylogeny at different taxonomic levels and set forward important guidelines for the choice of molecular markers for the study of phylogeny and phylogeography.

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THE CONTRIBUTIONS OF COMETS TO THE EARLY EARTH

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The idea that comets could have brought their constituents to the Earth began with Edmund Halley circa 1700. He was trying to explain the Biblical flood and needed a source for all that water. Numerous scientists since Halley's time have endeavored to assess the magnitude and the significance of this delivery system, not only for water, but also for carbon, nitrogen, and organic compounds that might have contributed to pre-biological chemical evolution on Earth and Mars. This talk will review contemporary views of these possibilities and discuss a rigorous test of them that includes the use of spacecraft.

CHEMOFOSSILS IN ORGANIC MATTER AND NAPHTHIDES OF THE SIBERIAN PLATFORM AT THE PRECAMBRIAN/PANEROZOIC BOUNDARY

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Advances in organic geochemistry in the field of fossil biomarker molecules, allowing reconstruction of evolutionary succession of paleobiochemical processes, enable us to speak of its new trend, the chemical paleontology or chemical paleogenetics. The present report considers one of the turns of evolutionary development of the organic world on the Earth, which coincides by the geochronologic scale with the boundary of the Late Proterozoic/Phanerozoic (545 Ma) by the example of investigation of molecular structures of the fossil organic matter and its derived naphthides of the Siberian Platform.

The features of distribution of molecular structures (based on GC-MS data) in Precambrian organic matter and naphthides do not show essential differences from that in Early Paleozoic deposits, as the composition of the bulk of the biomass in the sediments (planktonic-algal-bacterial) has not undergone pronounced alterations in spite of appearance of skeletal organisms, benthos, etc. However, it should be noted that there are some specific biomarker molecules which have not “overstepped” the Precambrian boundary. First of all, these are the branched alkanes with methyl group in the middle of the chain (C₁₈-C₂₈ 12-, and 13-monomethylalkanes). Similar structures suggest the existence in the Precambrian of C₂₅ 12, 13-methylene-tetracosanic acid, although these acids are not known now. There are similar acids (lactobacillic acid, etc.), extracted from lipids of bacteria, but they could be only the precursors of 7, 8-monomethylalkanes. Essential predominance of ethylcholestanes over other steranes, which is characteristic of Precambrian aquagene organic matter, as well as relatively light carbone isotope composition ($\delta^{13}\text{C}$ – minus 32-35‰), is inherited by Precambrian organic matter and, correspondingly, naphthides. The essential reorganization of the Earth's organic world at the Precambrian/Phanerozoic boundary has been reflected in the composition of chemofossils only in terms of equalization of the balance of terpanes and steranes, and in the latter – in terms of some increase in cholestane and diasterane concentrations. The precursor of appearance of higher plants was insignificant synthesis by algae of mono-, and diterpanes, reduced in Cambrian deposits prior to sesquiterpanes and their aromatic derivatives, 1,6-dimethylnaphthalene and cadilene.

Thus, at the Precambrian / Phanerozoic boundary, the composition and distribution of chemofossils have not undergone so significant changes (increase in the aromatic component) as have occurred later with the appearance and expansion of higher plants on the continents.

NEOARCHAEAN CARBONATES AND VANISHED EVAPORITES – THE MICROBIAL CONNECTION

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Field and petrographic evidence from bedded strata and thin sections of the Neoproterozoic Kogelbeen and lower to middle Gamohaan formations of South Africa argue for the former existence of evaporites, and suggest deposition in mainly shallow subtidal and sabkha environments. Large tepee-like fold structures, intrastratal karst, pseudomorphs after evaporites, solution collapse breccias, autobrecciation, corrosion surfaces, nucleation cones, irregular bedding contacts and flowage structures are all indicative of evaporites, their dissolution and their replacement by carbonate. Replacement was largely fabric destructive, leaving few obvious clues at the microscale to the former presence of vanished evaporites. However, fold shapes indicative of enterolithic gypsum, picked out by trails of degraded organic matter preserved within replacive calcite, are evident in thin sections of some microbialites formerly interpreted as fenestrae. Rippled dolomitic sandstones, abundant microbialites and organic matter with rare, well-preserved cyanobacterial fossils, indicate a microbially-dominated, shallow water ecosystem in the photic zone. By analogy with modern microbial mats, anoxic conditions would develop beneath the living cyanobacterial surface, providing an ideal environment for sulphate reducing bacteria. Sulphur isotopes of pyrite samples from the Cambellrand carbonates show a wide range of values indicating biogenic fractionation of sulphate. Mass microbial colonization of extensive shallow-water platforms in the Neoproterozoic set the scene for the microbiogeochemical transformation of the Earth's hydrosphere, atmosphere and biosphere. Photosynthetic oxidation of the surface ocean converted reduced sulphur to sulphate – allowing extensive evaporites to form in restricted epeiric seas. The vanished evaporites may represent a series of events of global significance - the desulphurisation of the ocean brought about through extensive shallow-water photosynthetic oxygenation coupled with bacterial sulphate reduction, leading to the widespread precipitation of marine carbonates on a massive scale, and the beginning of a new Era – the Proterozoic.

ORAL PRESENTATIONS

LIFE STARTING UP: THE QUEST FOR A MECHANISM

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Current models of biogenesis do not suggest a mechanism for how an initial chemical metabolism could have started up, nor how a flux of energy was generated, keeping this metabolism running. Sooner or later, metabolic pathways for generating amino acids, proteins, or other polymers, for example, should replace the supposed lightning flashes or shock waves. The same applies to compounds like adenine or lipids supposedly being supplied by outer space or by the general environment, respectively. And this also applies, again, to the flux of energy going through the present cells: at some point, a mechanism should have evolved for generating it; a supposed energy-richness of the primary environment has to be replaced by an energy-generating mechanism as part of the system.

We suggest an evolutionary bootstrapping process for describing subsequent stages in the early development of life (Hengeveld and Fedonkin, 2007). The first stage was dominated by heavy non-metals. Their reaction with hydrogen, the primary fuel of life, was catalysed by some transition metals forming the porous mineral precipitates. This hydrogenation-dehydrogenation reaction dependant on the exchange of electrons is known as a redox reaction. The metals and the operation concerned are still found in metal co-factors of many proteins. The second stage would have added reactions of another type, the exchange of protons, which are basic to condensation-hydrolysis cycles and are known as acid-base reactions. These cycles result in condensations – polymerisations, as well as in the hydrolysis still found throughout the biochemistry of the present cell. These acid-base reactions particularly concern nucleotide coenzymes. Proteins include either these coenzymes or the initial transition metals as their active site. In this stage, lipids could have been inserted into that mineral crust that surrounded the developing system. The third stage would have built on this already highly complex and integrated system, applying external solar energy for the photolysis, first of H₂S and then of H₂O. Initially, this supplied the system with an over-abundance of energy for which an extensive biochemical storage and release system was later installed with respect to carbohydrates.

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THRESHOLD OF LIFE: BIFURCATION OF A PREBIOTIC MICROSYSTEM UNDER NONEQUILIBRIUM CONDITIONS

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Some kinds of prebiotic models were experimentally based: RNA World macromolecules, liposomes, proteinoide microspheres, aromatic hydrocarbons, etc. In accordance with the elaborated conception¹, further evolution of still indefinite kind of prebiotic models to the living state is possible through the intermediate stage. This stage consists in bifurcation of an organic microsystem at the critical point of transition from the initial into advanced states occurring under conditions far from equilibrium. Relative stability of such a system is maintained by means of balanced oscillations around the critical (bifurcation) point. The balanced swing to the forward (advanced) and reverse (initial) states allow such chemical system to acquire the paradoxical way of organization - "stabilized instability". The remarkable characteristic of such organization is that the principally unstable point of bifurcation is "incorporated" between two opposite but equal forces. The organized in this way prebiotic microsystem maintains the following properties, which are at the foundation of life: self-maintaining heterogeneity, incessant inner fluctuations and re-arrangement of molecules; integrity through cooperative events; exchange by matter and energy with the environment (open system); latent biforked structure consisting of two co-structures. Through the existence of such called "bistate" type of chemical systems some important characteristics of living organisms can be easily explained: natural dichotomy of a cell at the end of its cycle of existence, evidences of biforked structure of advanced multicellular organisms (pair limbs, eyes, ears, cerebral hemispheres etc.), variable oscillating processes in living systems (for instance, oscillations of flagellums in independent eucariotic cells or hierarchical biophysical rhythms in complex forms of life). The original program of experimental research is suggested. It is aimed to getting of the bistate prebiotic microsystems, which are able to evolve to life. During future experiments various prebiotic models should be explored at the state of bifurcate transition and under oscillating conditions in the experimental chamber.

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THE HETEROGENEITY OF SPATIAL DISTRIBUTION OF PRIMORDIAL ORGANIC SUBSTANCE AS AN INITIAL STAGE OF THE BIOLOGICAL EVOLUTION: MODELLING AND COMPUTER SIMULATION

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An approach to describe the emergence of the primordial evolving system was presented. Dynamics of polymerization/depolymerization of some spatially distributed pre-biological structures was analyzed and two phases of system development were supposed. The external factors induce polymerization of organic monomers in the first phase and depolymerization in the second one, whereas both processes are accompanied with diffuse mixing of products of reactions. During the mixing, the aggregation of polymers and disintegration of aggregates are considered to be a result of specific interconnections between polymers. Dynamic equations of system are presented.

Numerical examination of model equations has shown that, under initial conditions of almost uniform distribution (slightly periodically disturbed), a typical non-uniform solution is represented by a number of discrete peaks of non-zero density which are isolated from each other by free space. Such non-uniform distributions are stable when being close to the bifurcation point, yet, in other conditions, they can lose their stability that entails more pronounced non-uniformity of space dynamics.

Thus, the interaction of polymerization/depolymerization and aggregation/disintegration processes results in the chaotic self-organization and leads to arising of complex and non-homogeneous (patchy) spatial structures. Dynamics of these structures can reflect the emergency of the spatial non-uniformity in primordial prebiotic realm, in physical space, and in the distributive space of characters; as well as can correspond to the initial steps of individualization of the first discrete domains fixed later in the biological evolution.

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ON ARISING MATRIX SYNTHESIS OF LINEAR POLYMERS IN PHASE-SEPARATED AUTOCATALYTIC SYSTEMS

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Molecular chemical evolution leading to the arising living cells is unconditionally associated with arising and evolution of linear polymers inside phase separated autocatalytic systems (PSAS).

Usually the beginning of chemical evolution is considered to be the arising of linear polymers capable of matrix synthesis. However matrix copying requires complex machinery, which also has to exist in the beginning of matrix synthesis.

In addition monomers of determined chirality which are unavoidable component of linear polymers in living cells are required. Since in the course of natural chemical processes racemic mixtures of substances are produced it is not clear how essentially prevailing amount of optically pure monomers has appeared.

These and other difficulties discussed in many publications lead to suggestion that modern matrix mechanism of inheritance itself has aroused as a result of sufficiently long chemical evolution inside initial PSAS. Analyses of known difficulties of concepts on life origin results in the following order of key steps of matrix inheritance arising.

1. Initial PSAS are particles capable of self-assembling from amphiphiles presenting in the environment.

2. Arising and evolution of simplest multivariant autocatalytic system inside PSAS^{1,2}. This autocatalytic system produces the set of different oligomeric catalysts including “oligomerases” and “ligases”. The system is capable of non-genomic inheritance “stitch in” kinetic properties of oligomers of the kind. This system can provide PSAS by the number of different substances including amphiphiles, monomers of different types. Monomers of determined chirality are synthesized due to the presence of phase boundary. This system provides relatively stable pre-biotic metabolism, and PSAS including this system can be denoted as pre-biotic cells.

3. Further evolution of PSAS is associated with arising more effective autocatalytic systems on the base of monomers of new chemical classes which are produced by collateral catalytic activity of existing multivariant autocatalytic system.

4. Arising in PSAS and further evolution of multivariant autocatalytic system with matrix copying.

5. Embryo of genetic machinery arising of on the base of linear oligomers with matrix copying and its evolution.

Theoretical models and computer simulation of possible mechanisms of PSAS evolution leading to matrix synthesis of polymers are considered in the paper.

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CHEMICAL EVOLUTION IN OPEN SPACE: A LINK WITH THE ORIGIN OF LIFE ON EARTH

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The chemical evolution of complex biological compounds would take place on early stage of the star system evolution, inside the protoplanetary nebula and reached the stage of polymerization before the end of planet accretion. All young solar 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 over time significantly. Energetic processing of organic compounds into more complex species can be driven by UV field in star-forming regions, high energy particle bombardment and UV-radiation from the T-Tauri phase in stellar birth, and UV-radiation of different wavelengths, protons of Solar wind and flares at early stage of evolution and at present days. The surviving remnants of the population of planetesimals which filled the inner early solar system during the late stages of collapsing solar nebula had a tremendous total surface and the reactions of complex organic compounds could take place on the solid surface of those bodies. It was important to test experimentally how far the process of chemical evolution could take place on the surface of space bodies under action of energy sources available at that period.

In our experiments the solid mixtures of biologically significant compounds (nucleosides, nucleotides and amino acids) were exposed to either vacuum UV photons or ionizing radiation. Investigation dealt with further reaction of nucleic acid components to nucleotides and oligonucleotides – main components of RNA and DNA, and single amino acids to oligopeptides.

The compound synthesized in these conditions could have survived inside comets, the last witnesses of the formation of our Solar system. Meteorites and comets may have imported prebiotic elements to early Earth, which, when mixed with liquid water, have allowed the synthesis of all molecules thought to be necessary for the origin of life.

BIOSPHERIC SELF-ORGANIZATION

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The Earth's biosphere has evolved quasi-deterministically as a self-organized system since it emerged some 4 billion years ago [1, 2]. Major physical and geochemical constraints on biotic evolution have included: temperature constraining the emergence of major organismal groups; atmospheric pO_2 constraining the emergence of macroeucaryotes; and atmospheric pCO_2 constraining cyanobacterial emergence and the emergence of leaves (megaphylls) in Devonian.

There is now robust evidence for a very warm Archean/early Proterozoic (50-70 deg C) (aside from the Huronian) especially: the sedimentary chert oxygen and silicon isotopic record from the same samples [3] and evidence for nearly constant seawater O^{18}/O^{16} ratio going back into the Archean; higher weathering intensities; the apparent absence of deeply-rooted mesophiles/ psychrophiles on molecular phylogenetic trees; high atmospheric pCO_2 prior to the first evidence of atmospheric methane at 2.8 Gya, consistent with apparent requirements for Mn-bicarbonate cluster formation leading to oxygenic photosynthesis; and the progressive increase of biotic enhancement of weathering from the Archean to its present value emerges as a model result with plausible limits on continental growth and outgassing rates [1]. Organismal emergence times occur at surface temperatures corresponding to the maximum growth temperatures of their living models, while atmospheric pO_2 levels alone cannot explain the big delay in the appearance of the "Higher" Kingdoms. Within abiotic constraints that have included the steady rise of solar luminosity, modest growth of the continents and decline of carbon outgassing, surface temperature history has been determined by the evolving carbonate-silicate biogeochemical cycle, declining from an early hot climate to much cooler conditions during much of the Phanerozoic.

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HIERARCHY OF BIOLOGICAL COMPLEXITY AND ITS EVOLUTIONARY EMERGENCE

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Basing on the notations "referents" and "hierarchy of referents", a presentation of the biological realm is proposed to describe the hierarchy and interrelations of different biological organizations often referred as the levels of biological complexity. Each referent is considered as a "primer element" (entire representative) of a given level of biological complexity. At the same time, any referent can be considered as the system of referents belonging to one level down in the hierarchy, and, on the other hand, it is a constituent of more complex referent belonging to a system associated with higher level of biological complexity. In this context, the hierarchy of biological complexity emerges as an up-ward dictate of features of referents from the lower to the higher levels.

In formalization of the referent representation, the hierarchical topology of an ultrametric space can be used to describe hierarchical interrelations and hierarchical evolutionary dynamics of the biological complexity. The evolutionary dynamics of the entire hierarchy of referents is described by means of pseudodifferential equations defined on the field of p-adic numbers, thus expanding considerably the scope of the possible application of the representation. It is necessary to emphasize, that any description of biological evolution by ultrametric processes may be solely justified if the basic concept is positioned beyond the gradualistic evolutionary paradigm. This circumstance requires a peculiar definition referred to "complexity", as well as a peculiar model of "transitions" between different levels of biological complexity. To satisfy this requirement, a model of the referents was constructed by such a way that cyclic iterations of reproduction, differentiation, mixing, and integration processes may result in rise in biological complexity. Although transitions to higher level demand complete composition of these processes, the fundamental importance is emphasized firstly to differentiation, and then – to integration. Exactly as a result of integration the referents of higher levels can be formed. The structure and dynamics of referents of different complexity are discussed.

AUTOCATALYTIC REACTIONS AND NATURAL SELECTION AT PREBIOLOGICAL STEPS OF THE EARTH EVOLUTION

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The main sufficient distinction of living matter from nonequilibrium abiogenic chemical systems seems to be the existence of a biological memory which allows the natural selection and thus an adaptive evolution of living systems. The known carriers of that biological memory in the currently existing terrestrial living systems are only the DNA and RNA molecules. However, the existence of a primitive “memory” without a DNA or RNA support is characteristic of autocatalytic systems having the properties of chemical mutation of autocatalysts. For this reason such autocatalytic systems may be considered as a real abiogenic predecessor of life on Prebiotic Earth. The most interesting among the known autocatalytic systems with the “mutation” properties appears to be the Formosa reaction, i.e. autocatalytic aqueous synthesis of monosaccharides from formaldehyde in the presence of calcium(+2) cations. One can expect that the Formosa reaction could initiate the abovementioned prebiological evolution resulting in appearance of ribose which is known as a key element of both RNA and DNA molecules. Recently, the possibility to increase the selectivity of biologically important monosaccharides synthesis in the presence of some calcium phosphate containing minerals has been found that confirms the importance of such synthesis for appearance of the RNA or DNA molecule prototypes.

**ECOSYSTEMS AND BIOSPHERE EMERGENCE
(EVOLUTION AND DEVELOPMENT)
ACCORDING TO BIOGEOCHEMICAL PRINCIPLES
OF VERNADSKY AND ENERGY CRITERIA**

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The main unifying feature of natural and artificial ecosystems is their biotic turnover (cycling) of substances which are induced with energy fluxes. To study biotic cycles, we need to develop and use an integrating approach which join many scientific disciplines. This approach is connected with extensive studies of Biosphere by Russian academician Vladimir Vernadsky. He developed and used “empirical generalizations” based on innumerable observations, comparisons and reflections. His “biogeochemical principles” of Biosphere and ecosystems development have more qualitative than quantitative nature. Quantitative criteria to evaluate the efficiency of natural and artificial ecosystems are to take into account energy fluxes and their use in ecosystems of different types. At least, three of them are of value for estimation of natural and artificial ecosystems’ functional activities. (Energy Principle of Extensive Development – (EPED), Energy Principle of Intensive Development – (EPID) and Main Universal (generalized) Criterion – (MUC). The last Criterion (Principle) characterizes the specific cycling rate of limiting chemical elements in multi-organism systems, developing under external energy fluxes. Its value can be a quantitative measure of effectiveness for every ecosystem functioning, including our global Biosphere. Different examples of these (above mentioned) integrated criteria actions are presented and analyzed in the paper. Comparisons of these criteria with main “empirical generalizations” and “biogeochemical principles” of Vladimir Vernadsky are given in generalized table.

BACTERIA – ACTIVE PARTICIPANTS OF THE SILICON CYCLE IN LAKE BAIKAL

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Diatoms play a dominating role in the global silicon cycle (Lisitsin, 1972; Nelson *et al.*, 1995). Every year, about $5.6-7.8 \times 10^9$ T Si is transformed in the ocean from its dissolved state into biogenic silica of diatom frustules, but about 50 % of this silica is re-dissolved in the upper 100 m water layer (Nelson *et al.*, 1995), and only 3 % reaches the bottom (Tréguer *et al.*, 1995). Hence, understanding of the processes which determine the preservation of diatoms while they sink in the water body, as well as during the diagenesis in the bottom sediments is important for the interpretation of sedimentary records of changing climates and environments (Regueneau *et al.*, 2000). Participation of bacteria in the cycle of Si in the ocean was for the first time proven by Bidle and Azam (1999). Progressive degradation of the organic coating of diatom frustules was identified as the major reason of the increase of the rate of silica dissolution during the sinking in the upper 20-80 m layer (Bidle *et al.*, 2003).

Analysis of Baikal sediments belonging to the Holocene and the Late Pleistocene by means of scanning electron microscopy revealed a different extent of preservation of diatom frustules which did not depend on the time after burial. Diatoms exhibit a variable extent of preservation in sub-recent sediments collected in the three deep basins of Lake Baikal and in its shallow opposite the major tributary, the Selenga River. Frustules of some diatom species abundant in the modern plankton of the lake are absent from the sediments.

To elucidate the role of bacteria in the degradation of diatoms in Lake Baikal, we isolated bacterial strains from the water body of the lake and from its sediments. We also studied bacteria co-existing with the diatom *Synedra acus* in a laboratory culture raised from a sample of phytoplankton collected in Lake Baikal. Fluorescent *in situ* hybridization (FISDH; Gloeckner *et al.*, 1996) revealed that bacteria associated with diatoms in the water body of Lake Baikal – *Proteobacteria* α and β belong to the same phylogenetic groups as those associated with diatoms of the plankton in the ocean (Bidle *et al.*, 2003). Bacteria associated with cultured *S. acus*, as revealed by fluorescent DAPI staining and transmission electron microscopy (TEM), were diverse in localization and morphology: (1) attached to entire diatom surface; (2) present in mucilage connecting diatom cells; (3) penetrating inside dead diatoms. Sequencing of 16S rRNA genes revealed that the diatom-associated bacteria belong to α -*Proteobacteria*, β -*Proteobacteria*, γ -*Proteobacteria*, *Cytophaga-Flavobacterim-Bacteroides*

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(CFB) and to *Bacillus*. The isolated strains differed in their action upon diatoms. Bacteria isolated from growing cultures of *S. acus* did not suppress the growth. ICP-MS revealed that strains of *Bacillus* isolated from the sediments and the water body of Lake Baikal accelerate the dissolution of Si of homogenized diatom frustules.

Hence, bacteria can be active participants of the Si cycle in Lake Baikal. Stability of live diatoms towards bacteria can help preservation of frustules in the sediments.

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RELICS OF THE TETHYS SEA FAUNA IN THE RECENT OCEANS

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In tropical and two subtropical zones of the recent oceans the distribution of bottom animals' relic taxa is cleared. Their ancestors are found in ancient seas of the western and eastern parts of Tethys.

It is shown that the distribution of relic genera (among brachiopods, molluscs, echionoderms and coelenterates) divides the recent low-latitude fauna into Atlantic part and Westpacific one. This two parts of fauna are isolated and well differ each other but also use to be connected from time to time.

The faunistical centre which took place in the western part of Tethys changed its position after the northern part of the Atlantic Ocean opened, and now we can find west-tethyan relics at the West-Indian (Central American) region.

The cause of changing in disposition of the Atlantic faunistical centre is in disposition of all recent faunistical centres in the western parts of the oceans because of an asymmetry in hydrological structure of the World Ocean. And this asymmetry depends on planetary peculiarities of the Earth.

To know about the planetary asymmetry of the World Ocean in the biogeography is useful for palaeogeographical reconstructions, and some examples are ready to be demonstrated.

AMMONOID EVOLUTION IN MARINE ECOSYSTEMS BEFORE P/T CRISIS

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The Permian was marked by the global climatic restructuring (the cool glaciation climate of the Late Paleozoic was replaced by the warm, glaciation-free Mesozoic climate), mainly produced by the Late Hercynian tectonic and volcanic processes. The general regression characteristic this time was complicated by smaller, relatively regressive-transgressive cycles. The last Paleozoic epoch was rich in abiotic events of various ranks and was terminated by a vast biotic crisis. The analysis of the morphological evolution and taxonomic diversity of ammonoids in the Permian allows the recognition of four major stages, which are based on the (1) dominating groups at the level of orders and families, (2) achieved level of the morphological complexity in the evolution of the suture, and (3) predominance of certain morphotypes. The first stage was termed Propermian, because it largely retains diversity of the Carboniferous history. The Permian stage in the evolution of ammonoids almost entirely fits into two subsequent stages (Eopermian and Mesopermian). The conclusive, (Metapermian) stage predefined the Mesozoic evolution of the subclass. Taxonomically, the ammonoid communities of the Propermian stage were moderately diverse. At the Eopermian stage, the generic diversity reached its maximum. During the Mesopermian some groups reached an unusually high morphological complexity, and the first ceratitids appeared. At the Metapermian the Paleozoic orders decreased, while ceratitids experienced an explosive radiation. The Propermian and Eopermian stages are characterized by sharp dominating in nekton and nectobenthic forms. During the Mesopermian stage morpho-ecological structure of ammonoid biota was changed, it shows maximum values for the planktonic taxa. A sharp increase in the proportion of the benthic taxa occurs because of the decrease of nekton in the Metapermian stage. Each of this stage was terminated in a deep crisis followed by considerable renewal of the morphological and taxonomic structures of the communities. The relationship between the taxonomic diversity of the Permian with transgressive-regressive cycles is not linear. A stronger correlation exists between these cycles and changes in the morpho-ecological structure of the ammonoid biota. The profound change in the Mesopermian ammonoid biota was caused by both biotic and abiotic events. This changing took a place beforehand the unprecedented Permian/Triassic crisis.

PALAEOPROTEROZOIC PETRIFIED OIL FIELD (SHUNGA EVENT)

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Significant accumulation of autochthonous organic matter (OM) preserved in Palaeoproterozoic rocks is rare. One of the largest and most remarkable occurrences is the deposit at Shunga, in Karelia, NW Russia. There, ca 1000 m-thick volcano-sedimentary sequence enriched in matured OM covers an area of 9000 km²; an estimated total C_{org} reserve exceed 25·10¹⁰ tonnes. This enormous accumulation of C-rich rocks is part of the world-wide Shunga Event. The integrated data suggest that the OM was most likely derived from planktonic microorganisms. This remarkable accumulation of OM and inferred generation of giant volume of petroleum took place in the aftermath of the ca 2330-2060 Ma Lomagundi – Jatulian Event – the largest positive excursion of $\delta^{13}\text{C}_{\text{carb}}$ of sedimentary carbonate in the Earth's history. The Onega Basin in Karelia is well-known for its vast volume of C_{org}-rich sediments that represent a giant, petrified oil field, including petroleum source rock, joint-trapped metamorphosed oil, veins of migrated petroleum, redeposited subaerial oil spills, and organo-siliceous substances forming diapers. OM occurs in the form of shungite showing a considerable depletion in ¹³C. Abundant diagenetic ¹²C-rich carbonates and sulphide concretions associated with the shungite rocks suggest the emergence of a 'modern-style' recycling of OM. The Shunga deposit is a rare example of an ancient oil field that underwent metamorphism and petrification. The occurrence of pyrobitumen in cracks and caves suggests that oil formed at a relatively early stage of burial, and probably at a relatively shallow depth. Early oil generation might have been caused by enhanced heat flow in a volcanically active rift setting. Large joints and intraformational cracks filled with pyrobitumen imply macro- and meso-scale oil migration. Abundant pyrobitumen clasts and 'pancake intraclasts' (originally petroleum) in the rocks overlying the C_{org}-rich strata very likely originated from an oxidised oil spill occurring either sub-aqueously or sub-aerially. The formation of shungite carbon and its diagenetic, catagenetic and metamorphic transformation are related to fundamental problems of biological evolution, global carbon cycle and the earliest oil generation. What caused a radical change in the biogeochemical recycling of OM and controlled large accumulations of OM worldwide at around 2060 Ma remains poorly understood.

SYNTHESIS OF ORGANIC MOLECULES DURING IMPACTS AT ACCRETION OF THE EARTH AND PLANETS

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Organic molecules can be produced by various natural processes and can be found in interstellar clouds, meteorites, comets, planets, etc. An impact of a meteorite into the Earth is generally considered as destructive process for organics because of the action of two factors: 1) extremely high temperatures, and 2) oxidizing conditions in the forming plume due to thermal dissociation of silicates. A number of works investigate the possibility of survival of original organics during impacts [e.g., 1]. The present paper considers the possibility of synthesis of organic species from initially inorganic carbon and hydrogen during simulated impact-induced vaporization of silicates.

Our simulation experiments were performed using standard laser pulse (LP) technique [2]. Experiments show a rather efficient synthesis of complex organic molecules even at oxidizing conditions. The earlier experiments have shown a rather efficient synthesis of volatile organic molecules during simulated impact-induced vaporization of various silicates [3]. The formation of nonvolatile organic components in such processes was indicated by the abundance of carbon with C-C and C-H bonding during investigation of the forming condensates by methods of X-ray-photoelectron-spectroscopy (XPS) [4].

The amount of formed organic species is orders of magnitude higher than gas phase thermodynamic equilibrium [5]. We claim for heterogeneous catalysis on the surface of glass nano-particles which are condensing everywhere in the spreading cloud. The possible mechanism here can be the Fischer-Tropsch-type of synthesis since more than a half of carbon during vaporization is converted to CO [3,5] and the dissociation of H₂O also produces a certain amount of H₂ and H. Organic materials were mainly highly polymerized hydrocarbons with low solubility in solvents. XPS analyses also have shown that amino- and carbonyl- groups were also present in correlation with C-H bonds in the condensate in some LP experiments [6].

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A NOVEL SCENARIO OF PREBIOTIC STAGE OF EVOLUTION OF LIFE BASED ON THE UNIVERSAL MECHANISM OF ORGANIC COMPOUND SYNTHESIS IN THE PLASMA TORCH OF METEORITE IMPACT

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A new idea of possible synthesis of the complex organic compounds (OC) in super-high velocity impact (SHVI)-generated plasma torch were proposed and experimentally confirmed. Previously unknown and found experimentally new feature of impact generated plasma torch have allowed to develop the original concept of the prehistory of life. According to this concept the intensive synthesis of complex OC arose during heavy meteoritic bombardment in first 0.5 billion years after formation of planets. This the most powerful and destructive action in the Earth history could play the decisive role and prepare the conditions for origin of the life. In the interstellar gas-dust clouds the synthesis of simple OC may be explained by identical process occurring in the plasma torch SHV-collisions between the dust particles.

In-depth study of physical processes occurring during the plasma torch fly away make it possible to advance a hypothesis according to which the plasma-generated unbalanced asymmetric electric and magnetic fields and circularly polarized plasma emission may lead to the initial insignificant breaking the mirror symmetry in processes of isomer generation in this medium and determinate the "sign" of symmetry of bioorganic world.

Laboratory experiment of modeling of SHV-impact plasma torch by influence laser, working in Q-switch regime has shown the possibility of synthesis of high-molecular ~4000 a.m.u OC by impact of micrometeorite with effective diameter 100 mkm composed of only H, C, N and O. The obtained mass-spectra evidence to the high velocity of chemical reactions of synthesis characteristics of catalytic processes and to the some signs of self assembly and regularization. This allows to conclude that the torch plasma possessing huge local density of energy and matter may be the optimal medium for synthesis of complex OC, needed for the origin of the simplest apparatus for replication.

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PHYSICAL CONDITIONS ON MERCURY IN COMPARISON WITH SATELLITES OF THE EXTRASOLAR PLANETS CONSIDERED AS POSSIBLE HARBOR OF LIFE

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Search of analogues of the terrestrial group planets remains far beyond reached technically possibilities: the Kepler speed of the Sun produced by the Earth makes $0.09 \text{ m}\cdot\text{s}^{-1}$ only. At the beginning of 2007 the total number of discovered giant planets at other stars exceeds 200, and many of them are of «hot jupiters» types, whose major semiaxis of the orbit lies within the limit 0.15 AU. It would be naive to suppose existence of life (in known to us amino-nucleic acid form) on the massive gas-liquid extrasolar giant planets. Nevertheless conditions for onset and evolutions of life can be realized on their hypothetical satellites. Recent publications were dedicated to the possible habitability of bodies like satellites of an exoplanet in rather low orbit. Of interest is to compare physical conditions on these hypothetical satellites of the «hot jupiters» and on the planet of Mercury for which orbital distance is close to that of the middle period of giant «hot jupiters» type planets.

All giant planets of the Solar system have a big number of satellites, exceeding 50 for Jupiter and Saturn each. Part of them consists of very large bodies, comparable to planets of terrestrial type, but including much more significant share of water ice. Some of them have a rarified atmosphere. Formation (or capture) of satellites is a natural phenomenon, and satellite systems definitely should exist at extrasolar planets. If the way of search of such satellites will be found, their detection can become the important event for bioastronomy.

As for massive giants they are met practically in all orbits. In «a habitable zone» (from 0.8 up to 1.1 AU) few planets have been found with a small orbit's eccentricity (less than 0.12) that provides approximately constant stellar radiation at a level of a solar constant, during the whole planet's year.

Let's assume that there is a massive giant planet at a distance of about 0.4 AU from a Sun-like star. A hypothetical satellite of the planet, with a dense enough atmosphere and hydrosphere, should be very hot. The daytime surface temperature of Mercury (having spectrally averaged surface albedo about 0.2) is about 600 K, and drops up to 80-90 K during the nighttime. This range is far the limits of our notion about what the terrestrial biosphere could withstand. There should be a cloud blanket with the albedo less than 0.1 and no greenhouse effect in the atmosphere. Otherwise the body should be placed at least as far 0.7 AU from the Solar type star. Only the late K and M classes stars could have a habitable zone at the Mercurian orbit.

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The nature of a hypothetical satellite of the planet obviously would have special features. A body at the planet with a 3 Jupiter mass, in an orbit in size of the Jovian satellite's Europe, will have the period about 2 days, according to the Kepler's third law. The body would have rather long period of rotation, synchronous with its revolution period. Nevertheless the period would be considerably smaller, than that of the Moon; due to the extrasolar planet's high mass. Interestingly, if the inclination of polar axis of the planet to a plane of its orbit is not too big, at midday long eclipse of a star will be observed on a regular basis (in the shown example – by duration for about 3 hour). The eclipses will be observed only on one hemisphere of the satellite. The feature is a result of huge diameter of a planet and that orbits of satellites are usually placed close to its equatorial plane.

There are also other interesting features, – for example, a small, on 2 %, distinction in a stellar constant for two hemispheres of the satellite. All these features cannot, however, hamper the chances for a long pre-biological evolution of this type satellites and onset on them of life and biosphere.

WAS NITRIC OXIDE THE VANGUARD MOLECULE FOR DIOXYGEN IN BIOLOGICAL ENERGY CONVERSION?

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Biological energy conversion provides the crucial fuel for life. In most extant (non-photosynthetic) organisms, this energy is harvested from redox equilibration between strongly electronegative electron donors and strongly electropositive acceptors. In the Hadean and early Archaean environment prior to the production of O₂ via oxygenic photosynthesis, the presence of the latter substrates, *i.e.* high potential redox centres in their oxidised state, seems unlikely. However, molecular phylogenies of several of the enzymes involved in bioenergetic electron transfer towards these substrates indicate origins pre-dating the divergence of Archaea and Bacteria [1,2, Duval, Nitschke & Schoepp-Cothenet, ms in preparation]. These enzymes thus seem to be older than their substrates. A prominent example of this class of ancient bioenergetic complexes are heme-copper oxidases, the key enzymes in aerobic respiration. The superfamily of the heme-copper oxidases encompasses, in addition to at least three distinct O₂ reductase subgroups, a "freak" outgroup, the NO-reductases. Recent molecular results concerning crucial redox active groups in the diverse subgroups of oxygen reductases suggest that the O₂-reducing reaction in these subgroups may have evolved independently several times starting from ancestral NO-reductases. This finding indicates that NO rather than O₂ was the ultimate electron sink in many bioenergetic chains existing prior to the Archaea/Bacteria cleavage. NO likely was produced in large amounts by electrical discharge (lightning) from CO₂ and N₂ during the Hadean and the early Archaean [3]. In contrast to most other terminal electron acceptors, NO therefore doesn't depend on the presence of oxygen to become an available bioenergetic substrate. The redox potential of the NO/N₂O couple (+1.18 V) is even higher than that of the O₂/H₂O couple (+0.82 V). We therefore propose that energy conserving electron transfer chains ultimately reducing NO have evolved long before O₂ appeared on this planet. Atmospheric CO₂ concentrations are considered to have substantially diminished in the course of the Archaean entailing dwindling NO production rates until about 2.2 Gyrs ago [3]. By that time, photosynthetically produced O₂ would have turned (by adding a single redox-active aa residue) NO- into O₂ reductases.

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KVATARONS - PRECURSORS OF ELEMENTS OF LIVING MATTER

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The main idea of a new hypothesis is that kvatarons are precursors of the primary elements of living matter. This idea is resulted from surprising coincidence of the size of voids in kvatarons and each nitrous compound (adenine, guanine, cytosine, thymine, uracil) and phosphate groups. In this case it is natural to suppose that kvatarons, formed in supersaturated water vapors, are original reactors (“molds”) for synthesis or selection of such components of living matter from the environment. Then the scheme of abiogenesis in the framework of kvataron conception is the following:

Formation of water kvatarons in atmosphere → capture and preservation of atoms H, O, C, N and P in the voids of kvatarons, which is necessary to form nitrous compounds, phosphate groups, D-ribose etc. → condensation of kvatarons with “guest” atoms, molecules (possibly with already formed functional groups) → interaction and aggregation of “guest” atoms and molecules, nitrous compounds in condensed water, polymerization and formation of RNA and DNA molecules → formation of nucleic acids capable to self-replication, synthesis of protein origin of protocellular life → formation of unicellular organisms.

In this scheme there are no improbable and super-difficult processes. All the processes at each stage proceed according to universal laws of Physics and Chemistry. Life is determinate and appears as a result of regular and inevitable processes of evolution of physical and chemical system of certain content in non-equilibrium conditions. This process can repeat many times and occur in many places. It is likely to occur now in places with appropriate conditions.

The suggested kvataron hypothesis of life origin has much in common with existing theories (living matter originates on the Earth, not somewhere else; non-randomness of the process etc.). At the same time it differs fundamentally in mechanism and place of primary concentration of chemical elements, synthesis and assembly of polymer molecules. This hypothesis does not require ordered hard (crystalline) structures either as precursors, or as a matrix.

In conclusion we note that the suggested scheme of consequent evolutionary events resulting in life origin (carbon-based) is universal and do not depend on the place of its origin in the Universe.

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MAXIMUM ENTROPY PRODUCTION AND GENERAL TRENDS IN BIOSPHERIC EVOLUTION

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The Earth's biosphere is a dissipative system which produces entropy in steady state by utilizing low entropy sunlight for photosynthesis and subsequently respiring the assimilated organic carbon compounds into high entropy heat. The principle of Maximum Entropy Production (MEP) states that sufficiently complex non-equilibrium thermodynamic systems maintain macroscopic steady states at which entropy production is maximized under the relevant constraints, such as the energy- and mass balances. This principle can potentially inform us about what the emergent structure and function of the biosphere should be, and how it should have evolved in time in concert with environmental constraints: biospheric activity is – and has been maintained – at a maximum given the relevant constraints of light, temperature, water, and other biogeochemical elements (Kleidon 2004).

Here, I start by assuming that MEP characterizes Earth system evolution sufficiently well, infer how the biosphere should have evolved over time and how this interpretation can provide a reasonable and consistent view of Earth's reconstructed past. The most important driver of change in these simulations is the gradual increase in solar luminosity, which is amplified within the Earth system through feedbacks that involve the planetary albedo and thereby affect the planetary rate of entropy production. Episodes of drastic change, such as the transition to an oxic atmosphere 2.3 billion years ago or the evolution of vascular land plants 400 million years ago, can be understood as phase transitions to a biosphere of substantially higher productivity, higher forms of organization and diversity of the Earth's biosphere and accompanying intensifications of global biogeochemical cycles.

From this perspective, anthropogenic change, which is presently altering the Earth system at a rapid rate, can be seen as the next transition to a biospheric state that is dominated by human actions and is associated with even higher levels of dissipation. This thermodynamic perspective of Earth's biospheric evolution extends the views of Vernadski (1926) and Lovelock (1972) and puts it on a quantitative foundation.

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ADAPTIVE EVOLUTION OF GENETIC SYSTEMS

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Increase in the complexity of the structural-functional organization of organisms is a global trend of evolution. The process is uneven: long periods of relative stability of morphology (stasis) are replaced by brief, in geological terms, “evolutionary bursts” when new structural designs (archetypes) arise. The different rates and scales of evolution form an evolutionary cycle: aromorphosis→ cladogenesis→ anagenesis→ stasigenesis. During aromorphosis, the tightness of correlative relationships that form the archetype during organism ontogenesis becomes much weaker. This makes possible rearrangement of ontogenesis through the formation of new archetypes (cladogenesis) and adaptation to new ecological niches. Then, purifying selection decreases variation range – the scales of evolution reduce (although their rates may increase – progressive specialization). Finally, ontogenesis loses its flexibility, and stasis lasts up to a new evolutionary burst – aromorphosis - or up to extinction. What may be the molecular mechanisms of this cycle?

Any character of an organism is the result of function of gene networks, of a group of genes that are coordinately regulated by the central regulator (CR). Three mutational types that affect the CR are conceivably possible: 1) mutations in the regulatory region of the CR gene that alter its expression; 2) mutations in the coding part of the CR gene that alter the structure of its molecule and thereby the signal parameters (the distance and rate of morphogene action, for example); 3) mutations of coregulators modulating CR activity. Mutations that change the CR profiles (duplication and neofunctionalization of one of the CR paralogs) must be noted. Study of the protein coding parts of the CR genes (morphogenes, transcriptional factors) of development according to Kimura’s criterion revealed that their adaptive evolution correlates on the phylogenetic tree with large aromorphoses (the appearance of large bilaterian taxa, the emergence of vertebrates on land), that their adaptive evolution is frequently associated with the formation of paralogs and, as a rule, coincides with the adaptive evolution of their receptors and other coregulators. Significant changes in ontogenetic parameters are possible only when embryogenesis is of the morphodynamic type, when the gene networks at its different stages can affect the dynamics of each other through feedbacks. In contrast, the gene networks with negative feedbacks can accumulate mutations in a mode close to neutral. The genes in such a regulatory circuit must evolve saltatorily: a long accumulation of mutations must be replaced by a brief hypermanifestation of the entire mutation spectrum after the breakdown of the regulatory

circuit. It cannot be excluded that selection will promptly test a set of accumulated mutations. We propose to call this mode of evolution the “adaptive optimization” in contrast to the classical scheme of positive adaptive selection in which case the mutations are tested immediately after their appearance.

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ECOLOGICAL EVOLUTION OF THE PHLOEM OF DICOTYLEDONOUS PLANTS

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2300 plant species belonging to 850 genera and 126 families from 8 subclasses of dicots have been subjected to comparative analysis of the structure of their terminal phloem. These studies have been the basis for the construction of a typological data base. It includes morphological, ultrastructural and biochemical information as well as characteristics of the natural habitats, region and time of collection of the plants used for anatomical and ultrastructural analyses. The report presented here is based on the evaluation of these data.

Taxonomic analysis supports monotypic nature of phloem endings in taxa ranking from species to family. Parallelism of series of structural types could be shown within orders and subclasses. Families with similar structure of terminal phloem have been identified. By analysis of the palaeobotanical data on the age of these plant families, a specificity of the types of terminal phloem and associated morphological and functional features has been revealed for groups of plant families of the same phylogenetic age. The ancestral type of terminal phloem is widespread among the families of Prodicots which appeared during the Cretaceous period (145.5 – 65.5 Ma). The symplastic type is characteristic of the families of Eudicots and biomes that appeared in the Paleogene (65.5 – 23 Ma), and the apoplastic type is characteristic of the families and biomes that appeared in the Neogene (less than 23 Ma). We have demonstrated the existence of the relationship between the changes in structural features and the dynamics of climate in the Phanerozoic.

The results of these combined analyses of phylogenetic and zonal series of the structure of phloem endings in dicots have revealed their similarity. The evolution of dicots with symplastic phloem loading – the plants with the most effective transport and growth which appeared in early Eocene and have been dominating up to now in tropical biomes (about 100 000 plant species) – is finished. The establishment of the younger group of dicots with apoplastic phloem loading (more than 20 000 plant species) which is associated with the appearance and expansion of meadow-steppe biomes at the end of the Miocene could be continued. The results are discussed in the context of the problem of global changes in climate and vegetation.

PATTERNS OF RETICULATE EVOLUTION IN PLANTS AND ANIMALS OF THE BOREAL ZONE

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Divergent evolution is traditionally considered as the main mechanism of biological evolution. At the same time there is considerable amount of data about hybridization among species within plant and animal genera including cases of formation of novel species and extensive zones of hybridization. In many instances an appearance of intermediate or 'chimeric' phenotypes in some organisms is explained by their hybrid origin, but conclusive results can be obtained only by using molecular markers proved to be effective tools for identification of natural hybrids and studying of their system of reproduction. Two groups of boreal and subarctic organisms, woody plants and fish are particularly interesting in the aspects of frequency of hybridization and patterns of reticulate evolution. Based on our data own on boreal conifers (*Pinus*, *Picea*) and coregonid fishes (*Coregonus*, Salmoniformes) and on extensive world literature (conifer genera *Pinus*, *Larix*, *Picea*, *Abies* etc, and fish species of the order Salmoniformes, genera *Salmo*, *Salvelinus*, *Coregonus*) we demonstrated that interspecific hybridization is especially common phenomenon in these natural zones and play an important role in evolution and adaptation. Unstable ecological conditions at the higher latitudes cause situation when species need to possess high genetic variability, and interspecific gene exchange among congeneric species is an efficient mechanism of rapid creation of new variation serving as a material for natural selection. High heterozygosity at many genes including those that are monomorphic within species and related somatic heterotic effects promote spreading of F₁ hybrids. At the same time as far as reproductive systems are concerned hybrids are often inferior as compared to parental species (*Pinus sibirica* x *P. pumila*). Several evolutionary scenarios are possible for hybrids: 1) F₁ formation with no introgression and subsequent generations, 2) F₂, F₃ etc. formation with separation of the new species of the hybrid origin, and 3) backcrossing with one or both parental species leading to clinal variation and formation of broad or narrow introgression zones. Direct and indirect evidences for these scenarios are discussed with respect to fish and tree groups in focus. Significance of reticulate evolution in creation of biodiversity is becoming more and more evident with development of molecular tools able to trace this process in natural populations.

ICDP FAR-DEEP – SCIENTIFIC DRILLING THROUGH THE ARCHAEO-PALAEOPROTEROZOIC TRANSITION: PROGRESS REPORT

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Research into the critical intervals in Earth history when the biosphere, hydrosphere and atmosphere were changing in a planetary-scale fashion, has intensified during the last decade. Two scientific drilling projects initiated recently (Archean Biosphere Drilling Project and Deep Time Drilling Project) focus mainly on the early evolution of life. The ICDP Fennoscandian Arctic Russia – Drilling Early Earth Project (FAR-DEEP) will address several global events that occurred during Early Palaeoproterozoic time and led to the emergence of the modern, aerobic Earth. The project involves the drilling of 15 boreholes (c. 4,000 km in total) through several key intervals in the Palaeoproterozoic sedimentary and volcanic successions on the Russian part of the Fennoscandian Shield. The scientific drilling will enable us to obtain fresh rocks recording global intracontinental rifting, the oldest known glaciation(s), atmospheric oxygen rise, change in redox-state of the mantle, the Earth's greatest perturbation in the global carbon cycle (Lomagundi-Jatulian Event), modern-style recycling of carbon, sulphur and phosphorus, generation of the oldest giant oil deposits (Shunga Event), and other fundamental events that heralded the emergence of the modern, aerobic Earth (Melezhik et al., 2005). The drillcores will enable us to address several fundamental questions of the Earth system evolution with an international research group by using a multidisciplinary approach. A progress report will be made on the first phase of the project, based on the drilling operations that are due to commence in May and should be accomplished by the end of November 2007.

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**GEOLOGICAL AND BIOTIC SETTINGS
FOR THE ORIGIN AND EVOLUTION OF MAJOR CLADES
IN THE EARLY PALEOZOIC BIOSPHERE (540-440 My)**

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Early Paleozoic (Cambrian, Ordovician) is a transitional stage between the primordial, locally distributed Precambrian-type ecosystems and the mature, tiered Phanerozoic-type ecosystems. The Cambrian and Ordovician periods mark the two fundamental revolutionary events that determined the principal structural-functioning and spatial parameters of marine ecosystems: 1) the appearance of major skeletal hydrobionts and the explosion of biotic diversity in benthic communities dominated by grazing heterotrophs (trilobites and soft-bodied worm-type organisms) in the Early Cambrian; 2) in the middle Ordovician – the rapid diversification of benthic groups of filter-feeding fauna (cnidarians, bryozoans, crinoids, brachiopods, etc.) and small-sized trophic generalists (ostracodes), the rise of a new group of autotrophs (chitinozoans), specialized groups of zooplankton (graptolites, radiolarians) and nektonic predators (conodontophores, nautiloids, early agnostids), the flourishing of colony-grade organisms, being an effective means of ecospace conquering and food resource utilization. The principal chorological and trophic restructuring in marine ecosystems in Cambrian and Ordovician was controlled by: 1) the changes in the biological productivity and spatial (tiered) distribution of autotrophic components in food chains (benthic cyanobacteria being replaced with phytoplankton), the formation of a vertical vector and a system network in trophic conveyers; and 2) the emergence and rapid diversification of new ecological guilds in the benthial and pelagial, thereby facilitating the diversity of trophic specializations, the amplification of the system of depositing, transportation and spacial distribution of food resources, and the dominance of detritivore-based food webs over grazer-based food webs. The report discusses biological and geological prerequisites for the origin of major clades, the ecosystem restructuring, and the explosive biotic diversification in the Early Paleozoic biosphere: 1) the importance of the supporting carcasses (skeletons) as a novel adaptive resource (the ability to form diverse defensive, locomotary and trophic mechanisms, as well as the optimal morpho-functional organization of hydrobionts); 2) the role of the evolutionary ephemera as precursors of flourishing ecological guilds; 3) the role of the trophic factor in speciation within coherent and incoherent ecosystems; 4) the importance of the progressing oxygenation as a major factor of global ecosystem restructuring (replacement of oxyphobic organisms by diverse oxyphilic organisms). This work was supported by the Russian Academy of Science Program 18 “Biosphere Origin and Evolution” and the Russian Foundation for Basic Research Grant no. 05-05-64509.

PALEOBIODIVERSITY AND PALEOCLIMATOLOGY

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The application of the taxonomic diversity of the Paleozoic marine biotas as paleoclimatic indexes is examined. Regular increasing in the taxonomic diversity of the communities from the polar and temperate to the tropical climatic realms is one of the most significant features of the climatic environments in recent biosphere. For example, the fluctuations in the forams taxonomic diversity are used successfully to estimate the climatic changes (ice- and interice-ages) for subdivision and correlation of the Upper Cenozoic ocean sediments.

The positive correlation between fluctuations in genera taxonomic diversity in the Paleozoic (Ordovician – Permian) and major global climatic epochs (greenhouse-icehouse) defined by sedimentological and oxygen isotope data is obvious. Detail comparison of the genera ammonoid biodiversity and species conodont diversity dynamics in the biostratigraphic zones scale permits to propose the existence of the global climatic fluctuations with periodicity in about 40, 12, 7 and 3,5 myars.

Diversity dynamics of the Silurian cephalopods shows remarkable difference in various climatic zones (Fig.1).

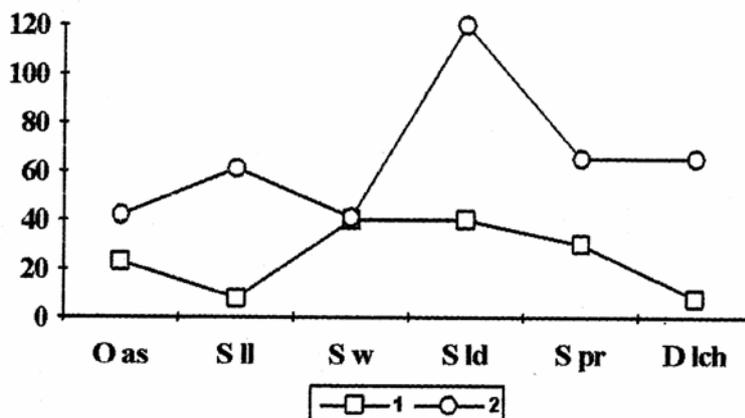


Fig.1. Dynamics of the Silurian cephalopod diversity: 1 - temperate climatic zone; 2 - warm-water zone.

In temperate climatic zone in the Llandoveryan the diversity decreases in corresponding to global trend of the temperature changes at the end of Ordovician. Increasing of the diversity in warm-water zone at the same time is connected with migration of the cephalopod from temperate zone.

Thus the studies of the marine biotas diversity could be used for detail global paleoclimatic reconstructions and in the various climatic zones.

MESSINIAN SALINITY CRISIS EVENTS AND BIOTA HISTORY

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The Messinian chronology and salinity crisis events restored enough detail now due to paleontological, sedimentological studies and accurate astronomically calibrated timescale (Krijgsman et al., 1999; Roveri, Manzi, 2006 et al.). Major reasons of the crisis were tectonic and glacioeustatic ones: the northern Betic Corridor shallower and closed 7.5 Ma and the southern Rif Passage existed before 6.58-5.96 Ma. According to Roveri, Manzi (2006) scenario, limited sea level fall (up to 150 m) took place at 5.96 Ma, when the lower primary evaporates had been sedimentated in marginal basins. Catastrophic sea level fall is proposed from 5.61 to 5.51 Ma, when halite salts up to 2 km thickness deposited in deep depressions of the Mediterranean and main river valleys were cut up to 1.5 km. Overall transgressive trend existed from 5.51 to 5.33 Ma, when filling of the Mediterranean depressions took place under continental river flow influence (Lago-Mare facies).

These data allow revaluating the fauna history. Some genera and species of very rich specific Pontian – Late Messinian fauna was formed in the Aegean basin under influence of more ancient Paratethys brackish fauna of the Pannonian basin. This fauna of bivalve mollusks and ostracodes inhabited the Aegean basin during the mid-Messinian, from 6.3 to 6.0 Ma (Popov, Neveeskaya, 1998; Snel et al., 2006). At level 6.15 Ma they migrated into the Eastern Paratethys and inhabited the whole Euxine-Caspian basin during the beginning Pontian. The Pontian fauna became the most diverse and abundant at the Portaferian time (beginning late Pontian) as in the Euxine-Caspian as in the Pannonian basins (15 genera of lymnocyprids in the Euxinian basin, 17-19 – in Dacic and 18 – in Pannonian ones). At the late Pontian these fauna migrated into the brackish Lago-Mare Mediterranean basin.

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EVOLUTIONARY MODEL OF RADIOLARIA IN A NORMAL OR REGRESSIVE PHASES AND SOME GENETIC MODIFICATIONS

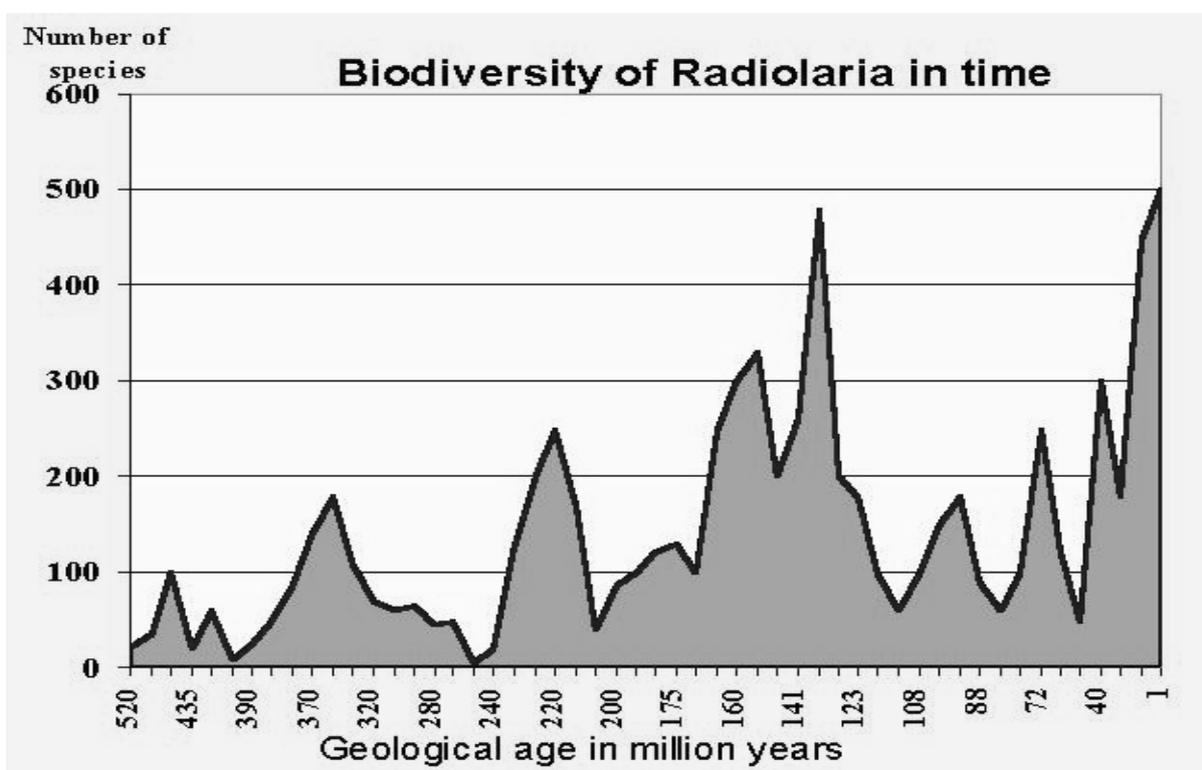
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Radiolaria are protozoan microorganisms with siliceous shell. On the earliest stages of evolution more than 500 Ma ago Radiolaria elaborated ability to synthesize cell skeleton due to extracting of silica. Only Radiolaria and Diatoms among spongy, mollusca, equisetaceae and others achieved high-level perfection in application of SiO₂. Radiolaria similar to Diatoms, Foraminifera and Silicoflagellates are well preserved in sediments. Due to siliceous skeleton Radiolaria safed in deep-water media where calcareous skeleton dissolves and no other fossils occur. Rock formed by Radiolaria called as radiolarites, which are monument of radiolarian organisms for ages. Radiolarian rocks or stone archived information about Radiolaria of past. Recent knowledge about Radiolaria based on species descriptions collected over all world.

Owing to strong siliceous skeletons Radiolaria are quartz clock of our Earth. Biodiversity of radiolarian species in geological time shows several peaks and drops (figure).



Geological record fixed at list 8 great mass extinction of Radiolaria. The evolution of inner spicular apparatus of spherical radiolarians gone from 4 to many rays in Paleozoic-Early Mesozoic to microsphaera in Mesozoic-Cenozoic and to loss of siliceous inner

apparatus or skeleton in Recent time. The development of the axoplast from inner spicules is of fundamental importance in Nassellaria. The shorter ranging genera gave rise to many rapid speciations. The bloom of Willriedellidae with submerged cephalothorax as well as eccentrically arranged microsphere, twisted spines, siamese twins in Radiolaria at crisis levels are considered as major mutations or genetic modifications which related to the strong environmental stresses. A decrease in the size, number of chambers and increase in volume and size of porous is also fixed in progressive evolution of Radiolaria.

The major part of radiolarian investigations devoted to description of their skeletons. Physiology, biochemistry and living cycle are not enough studied.

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BIOMINERALIZATION AND MAIN DIRECTIONS OF DEVELOPMENT OF RADIOLARIAN SKELETONS

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The development of any skeleton is controlled by previously formed organic matrix, which serves as a cast or mould of the shell to be formed and which provides its development as a single structure through the interactions of the organic and mineral skeletal components. Research on the organic and mineral constituents of radiolarian skeletons provided a basis for the development of a hypothetical model of skeletal biomineralization. It begins with the appearance of dense primary opal globules in the radiolarian skeleton that are deposited within an organic matrix enclosed by a living cytoplasmic envelope called a cytokalymma. These primary biomineral particles are progressively grouped within hierarchically interrelated ultrastructural skeletal units. In radiolarians, the skeletal-enclosing cytoplasmic envelope, called a cytokalymma, serves as a mold where the organic matrix is deposited and by its dynamic molding action, determines the ultimate shape of the siliceous skeleton.

A new scheme of the successive stages of the formation of radiolarian skeletons is proposed. The development of the skeleton in *Polycystina*, *Phaeodaria* and *Collodaria* may pass through several stages and occur in various ways: 1) appearance of the skeleton occurs simultaneous on the polysaccharide plates over the entire volume of the organic matrix of the future shell; 2) primary development of the skeleton occurs in two ways: *pellicular growth* and *bridge growth*; 3) final stage of the skeletal development is finalized in two ways: *bridge growth* and *rim growth*. All types of the skeletal growth may be observed in the same individual at different ontogenetic stages, or one of the patterns may be dominant.

The main variants of skeletal shells are combined in two major types according to the growth pattern of skeletal tissue, i.e., (1) the latticed, cellular, and spongy shells formed by the *bridge growth*, and (2) the porous and lamellar shells formed by the *rim growth*.

A new scheme of successive stages of a radiolarian spine formation is offered. It is shown that the main difference between the radiolarian skeleton and the spicules of sponges is in the direction of skeleton formation: spines of spiny radiolarians grow spirally, whereas spicules of sponges show a centrifugal growth.

The study was supported by the Program of the Presidium of the Russian Academy of Sciences "Origin and Evolution of the Biosphere" and the Russian Foundation for Basic Research (project nos. 06-05-64859, 07-04-00649).

NUCLEOTIDE COENZYMES IN PRIMITIVE EVOLUTION

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The insight to abiotic origin of nucleotides and the nucleotide-like coenzymes is of key significance for evolutionary studies: structurally belonging to “RNA world”, these molecules play a role of catalytic cofactors and the photon sensors for proteins. Here we describe some new models of abiotic synthesis and transformation of nucleotide coenzymes.

The problem of ATP origin comprises two aspects: (1) synthesis of adenine nucleotide, and (2) phosphorylation reactions yielding the energy-rich phosphoanhydride bonds of ATP. The sole source of the de novo biosynthesis of 5'-AMP (and of purines per se) is a multistage enzymatic process in which phosphoribosyl scaffold is used to assemble purine heterocycle from Asp, GluNH₂, formate and CO₂. We showed that practically identical set of precursors (ribose, phosphate, Asp, GluNH₂, formate and HCO₃⁻), when subjected to thermolysis gave rise to formation of 5'-AMP. Besides contributing to the problem of ATP origin, these results indicate that abiotic formation of metabolite and the development of a route of its biosynthesis can proceed within the same chemical milieu.

Several ways of photochemical regeneration of terminal phosphoryl group in ATP were demonstrated. One of the models, in which ADP was phosphorylated by orthophosphate (Pi) to form ATP with the yield of ca. 40 % involved the substrates adsorption on clay particles and was driven by UVA radiation. The other model which utilized photons of both UVA and visible (blue) spectral area was based on the photochemical activity of flavoproteinoid microspheres, the structures formed by aggregation in an aqueous medium of products of thermal condensation of a Glu, Gly and Lys mixture and containing amino acid polymers and abiogenic flavin pigments. Irradiation of microspheres in the presence of ADP and Pi resulted in ATP formation with the yield ca. 30%. The system was active both in aerated medium and (in the presence of H₂O₂ or an electron acceptor alternative to O₂) after deaeration. Photophosphorylation mechanism seems to involve interaction of free-radical form of reduced flavin and ADP.

Pteridine derivatives when adsorbed on mineral surface and subjected to thermal treatment were shown to partner nucleotides in oligomerization process. The treatment of FMN and 5'-AMP mixture adsorbed on clay particles yielded FAD along with oligomer products. The evolutionary consequence of the coenzyme copolymerization with oligonucleotide is dualistic: the polymer gains a redox photocatalytic function, but loses a resistance against photodegradation [1]. Supported by Basic Research Program No 18 of Presidium RAS and grant 07-04-00460-a from Russian Foundation for Basic Research.

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ANOXIGENIC PHOTOTROPHIC BACTERIA OF THE EXTREME WATER RESERVOIRS - MODERN ANALOGUES OF ARCHEAN ECOSYSTEMS

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During Archean and beginning of Paleoproterozoic era the concentration of atmospheric oxygen was very low. At this period (3.5 – 2.3 Ga) shallow water reservoirs and local places with increased geothermal activity might be widespread on the Earth. These conditions favored the development of microbial mats with the dominance of anoxygenic phototrophic bacteria (APB): (purple, green sulfur and green filamentous bacteria). As electron donors modern APB can use reduced sulfur compounds, hydrogen, nitrite, iron, some organic substances and, probably, manganese. As a result, in ancient phototrophic communities there were no production of oxygen, but sulfates, sulfur, pyrite, oxides of iron and manganese should be deposited. Benthic phototrophic communities played an important geochemical role at different stages of evolution of water ecosystems, what is confirmed by massive development of stromatolites. The role of APB in production of organic matter, formation of caustobiolites and deposition of some minerals is obvious. Epicontinental soda lakes represent another unique evolutionary significant water ecosystem. According to opinion of G.A. Zavarzin these oldest water reservoirs played a role of the centers of biodiversity formation of prokaryotic microorganisms. According to hypothesis of E. Degens a number of facts testify that the primary ocean was alkaline that attracts attention to study of soda lakes as relict ecosystems. Endogenous formation of hydrogen and sulfide is observable today in rift zones and in areas of modern volcanism. A number of geological and paleolimnological data shows that stratified water reservoirs with anaerobic and aerobic zones existed in history of Earth. Purple sulfur and green APB form colored bacterial plate in chemocline which serves as a filter for toxic reduced compounds and protecting inhabitants of aerobic zone in modern conditions colonized by multicellular organisms. Thus, our attention has been focused on studying of biodiversity and geochemical activity of APB in microbial mats of alkaline and acid hydrotherms, littoral zones of seas, hypersaline reservoirs and epicontinental soda lakes. In the report our own data on study of communities of APB of Black Sea and meromictic lakes of a different origin will also be presented. Investigated water ecosystems can be considered as relic and the data obtained during their research gives the information on biogeochemical processes occurring at different stages of geological history of the Earth.

ROLE OF BIOGENIC FACTOR IN PLATINUM ACCUMULATION BY OCEANIC IRON-MANGANESE CONCRETIONS

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As a result of detailed studies of the oceanic iron-manganese nodules (OIMN) composition, it has been revealed that they are largely enriched in Ni, Cu, Co, Mo, and Pt as well, being in fact the new economical type of deposits. The OIMN complex study was carried out in the Clarion-Clipperton deep-water field and Lamont guyot (Pacific Ocean). Precious and trace element concentrations were determined by atomic absorption and neutron-activation methods and XRF-SR as well (Institute of Nuclear Physics SB RAS). In addition, SEM, microprobe analysis and activation autoradiography techniques have been widely employed. The experiments were made with the use of Pt, Au and Ir radionuclides (technique of radioisotope tracers).

The obtained data on Pt, Au, Pd, Rh, Co, Ni concentrations in the Lamont guyot OIMN are fully compared with the results of OIMN previous studies in other regions of the Pacific Ocean. High stable concentrations of Pt in the Lamont guyot OIMN are fixed from the tenth parts up to 1 ppm Pt.

A series of experiments that modeled interaction of the OIMN matter and seawater containing Pt and Au were carried out. The artificially prepared seawater, where either Pt or Au marked by the radioactive isotopes in form of chlorides were added depending on experiment, with the concentrations 3 mg/l Pt and 1.125 mg/l Au, was used. The image reflecting Pt spatial distribution (on radionuclides Pt-195m, Pt-193m and Au-199) on the concretion section surface is fixed in the autoradiograms that were obtained from the IMC preparations after the experiment of interaction with Pt-containing seawater. Pt irregular distribution with maximum enrichment of concretion marginal parts in some cases as well as microfissures and microinclusions is established. In addition, Pt-concentric-layered distribution with enrichment of the layers with predominantly Mn and Fe hydroxides is clearly observed.

The colonies of microorganisms, i.e. microscopic fungus of class Deuteromycetes, genus *Penicillium*, subsection *Lanata* actively absorbing Pt from seawater solution originated during the experiment in solution with concretions. Several micro fungus colonies originated were used in the experiment of their interaction with seawater that contained Au marked as Au-198. Subsequently, their gamma-spectrometrical analysis was carried out, and autoradiograms that fixed Pt and Au distribution in fungus colonies were obtained. It was found that fungus colonies extracted Pt more actively (~ by 2 orders) from seawater compared to Au. The maximum Pt concentrations have been observed in the peripheral parts of fungus colonies, in band 1-2 mm

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thick that corresponds to sorptional mechanism of Pt extract from seawater. In the central parts of the colonies, Pt content is significantly less, and it is concentrated in hyphas, but much less than in the marginal parts of the colonies. In addition, Pt microinclusions and microisolations have not been revealed in fungal mycelium. In contrast, the numerous isolations that correspond to particles of micro- and nano-size, mostly being confined to the marginal parts of the colonies have been found for Au. In addition, some Au is regularly distributed in the mycelium of fungus colonies or enriches hyphas.

The following peculiarities have been established based on results of SEM study: (1) Pt distribution in fungus colony is irregular. The areas of hypha thickening and intergrowth occur, ones of the highest Pt and Cl concentrations being associated with them. In addition, ratio of Cl and Na does not testify to NaCl presence in them; (2) Pt is absorbed by the hypha walls and then concentrated in their central parts without forming the metal isolations, and attributing to Pt participation in biotrophic cycle of fungus vital activity; (3) conidia are maximally enriched in Pt; (4) except filamentous fungi, colonies of microscopic tubular biogenic formations have been found, they also maximally absorb Pt along with Cl and S (Na not fixed). In addition, the concentrations of these elements are 4-5 times more in the inner parts (pipes) compared to the walls; (5) Au is only fixed as micrograins in fungus colonies.

Oceanic floor microbiota contribution to the process of concretion formation was discussed in literature, and firstly, the role of bacteria as catalysts in Mn^{2+} oxidation was considered. By the reference data, the ratio of Pt and Au average contents in the oceanic iron-manganese concretions and crusts equals about 1-2 orders. The same can be suggested by the difference in Pt and Au content in iron-manganese concretions normalized to the contents of these metals in deep water sediments and oceanic water. At the same time, the significant variety in Pt and Au concentration from seawater was established in microorganisms that were observed during the experiment. Pt concentrations up to the first percents were determined by SEM in the microorganisms that were in contact with Pt-containing solutions, i.e. Pt accumulation ten thousand times more occurred. Au concentrations were less than 0.1% (Au accumulation less than 1000) in the microorganisms that were in contact with Au-containing solutions. The highest estimate of Au concentration from solution was given 50 times based on gamma-radiation activity of the original solution and colonies of microorganisms. Thus, activity of microorganisms that inhabit OIMN on the ocean floor can determine selectivity in Pt concentration from water by concretions and crusts. Pt maximum observed in the marginal parts of concretion preparations during the experiment is significantly well agreed to the all above. The surface of the concretion can be considered as the area inhabited by microorganisms and therefore most actively extracting platinum from solution. The results obtained attribute to the biochemical mechanism of Pt selective concentration by the oceanic iron-manganese concretions.

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BIOGEOLOGICAL PROBLEMS IN RECOGNITION OF MULTICELLULAR ORGANISMS IN LOWER PROTEROZOIC

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The Udokan fossil biota constitutes a special subject matter in shaping the view on the early Proterozoic evolution of the biosphere. The Udokan fossil biota represents an assortment of organisms fossilized in the metamorphosed sedimentary sequence of the Lower Proterozoic Udokan Gr and the correlative strata of the Khani Fm, south-western block of the Aldan Complex. The fossil assemblage of the Udokan Gr comprises microfossils, stromatolites and microphytolites, but it is best known for *Udokania* – the cylindrical mineralized objects from stromatolitic limestones, as well as for the discoidal structures and systems of ramified ridges preserved on sandstone bedding surfaces. The succession of the Udokan Gr is regarded as the parastratotype of the Lower Karelian (Lower Proterozoic). The minimum radiometric age of the Udokan Gr is constrained by the U-Pb dates of 1867±3 Ma (China Gabbroid Massif) and 1876±4 Ma (Kodar Granite Complex). This renders the Udokan fossil assemblage as one of the oldest complex macroscopic biotas.

Recognition of multicellular organisms in lower Proterozoic strata (such as the Udokan Gr) is linked to a problem of recognizing fossilized life systems in general. Thus, if *Udokania* represented a life system, it would provide an early Proterozoic age for both the origin of Metazoa and the advent of biologically controlled mineralization. However, *Udokania* does not fit the morphospace of accretionary growth skeletons and demonstrates an array of remarkably rigorous geometries, therefore its metazoan affinity remains doubtful.

Neither complex morphology nor macroscopic size provides an unequivocal line of evidence for distinguishing between fossilized multicellular organisms and fossilized colonies of microorganisms. Under conditions of nutrient deprivation, microscopic unicellular organisms (bacteria, protists, fungi) are well-known to form macroscopic colonies that typically occur as discoidal mounds, spheres or honeycombs with complex and elaborate morphologies. Importantly, the discoidal and ramified structures in the Udokan sandstones are preserved on bedding surfaces that formed as a result of sediment biostabilization by benthic microbial communities. The microbial nature of the substrate is suggested by various sedimentary structures, reflecting processes of microbial colonization of the sediment surface

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(shagreen texture), erosion of the microbial substrate (flattened pedestals) and degradation of microbial mats (shrinkage crack infillings). The Udokan discoidal and dendritic fossils, that are often interpreted as Ediacara-type fossils of multicellular organisms, could thus represent fossilized microbial colonies of bacteria, protists or fungi.

PREBIOTIC CARBOHYDRATES AND THEIR DERIVATES

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Carbohydrates and their derivatives play an inestimable role in organic life since they constitute the building blocks of various biomolecules indispensable for the living organisms (DNA, RNA, ATP, cellulose, chitin, starch, etc.). Among carbohydrates the main emphasis is placed on ribose, since the "RNA-world" [i] is the most reasoned hypothesis on the prebiotic chemical evolution and origin of life. We summarize and discuss the most significant experimental results on the plausible prebiotic synthesis of carbohydrates and other vitally important organic substances from carbohydrates as initial substrates for such synthesis.

There are two points of view on the origin of first carbohydrates on Earth: i) carbohydrates were synthesized in the interstellar space at low temperature under action of UV-irradiation or cosmic radiation and were delivered on Earth with comets and meteorites [ii]; ii) the prebiotic carbohydrates synthesis embodies the catalytic processes in the aqueous solutions of simple substances such as formaldehyde or glycolaldehyde [iii, iv]. We support last hypothesis. The synthesis of monosaccharides from formaldehyde and lower carbohydrates (glycolaldehyde, glyceraldehyde, dihydroxyacetone) is catalyzed by different compounds such as natural minerals, phosphate and borate ions [v-vii]. Ribose can be selectively synthesized from glycolaldehyde and glyceraldehyde in the presence of borate-containing minerals or Zn-proline complexes [viii, ix]. Lower carbohydrates necessary for the synthesis of monosaccharides can be formed in formaldehyde aqueous solutions under the action of UV-irradiation [iii]. Higher monosaccharides can be formed directly from formaldehyde in the course of the combined photochemical and catalytic reactions in plausible prebiotic conditions [vii]. Aminoacids and heterocycles can be obtained from carbohydrates and NH₃ in the presence of thiols [iv].

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ON THE POSSIBLE ROLE OF ORGANIZED MEDIA AND SPIN AND MAGNETIC EFFECTS IN PREBIOLOGICAL PERIOD OF THE EVOLUTION

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“Host-guest” complexes and the micelles formed by natural self-organized molecular systems have been shown to affect the direction (selectivity) and the rate of radical reactions involving molecules present in the nature (oxygen, ozone, carotenoids, alkaloids, amino acids). Since in the prebiological period, the natural sources initiating chemical transformations include light, heat and radiation, the investigations of the processes involving free radicals in organized media are of special interest. Additionally, these studies are motivated by the achievements of spin chemistry which demonstrated the possibilities of the effect of external and internal magnetic fields on the rates and sometimes on the direction of reactions in the pairs of radical particles. In the present work, NMR, spin chemistry and optical spectroscopy were used to study the aggregation processes of naturally occurred complexing agents (triterpene glycosides, arabinogalactan). The effect of the complexes and micelles on the fine mechanisms of photoinduced redox transformations of carotenoids, dihydropyridines (NADH analogs), alkaloids and amino acids has been demonstrated. It has been shown that the presence of organic compounds in the inclusion complexes or micellar solutions significantly alters the stability and reactivity of the guest compounds as compared to homogeneous solution, especially, in the case when the reactivity is vividly dependent on the medium. Thus, one might conclude that from the viewpoint of prebiological evolution the detected properties would allow the self-organized inclusion complexes and micelles to control the solubility of complex organic molecules in aqueous media, their protection from the destructive external factors (radiation, ozone impact) and simultaneously to play a role of microreactor that changes the direction of the chemical transformations of the guest compounds.

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FORMATION OF RNA-OLIGONUCLEOTIDES ON THE MINERAL SURFACE PRELIMINARY IRRADIATED BY UV LIGHT

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Probable source of organic molecules is perhaps the surface of mineral particles where the formation of an organic matter occurs which then gets on a surface of planets. The volcanic activity on the ancient Earth, characteristic for many planets, was much more intensive, than now, so it is possible to assume, that in the top layers of an atmosphere owing to volcanic eruptions a plenty of volcanic dust (ashes), clay and gases has been concentrated. Thus, the opportunity of oligonucleotides synthesis on a surface of particles of volcanic ashes, clay and SiO₂, preliminary irradiated by UV light was studied (the solar spectrum was modeled). The results coincide with earlier obtained upon synthesis of these molecules on a surface of particles of clays or SiO₂: on irradiated by UV mineral surface the biologically important biopolymers (in our case – oligonucleotides) are formed. We have shown, that on the surface of particles of the volcanic ashes preliminary irradiated by UV light, there took place the formation of similar polymers from the adsorbed AMP molecules while in the absence of UV irradiation it did not occur. Besides it is necessary to say, that formation of oligonucleotides occurs not because of specific properties of AMP, because in some experiments with GMP the same results were obtained. Some additional experiments for revealing the possible molecular mechanism of oligonucleotides formation has been conducted also. It has been revealed, that upon nucleosides monophosphate adsorption (which generation from water and gas under any energy exposure is possible in relevant conditions) on preliminary irradiated with UV light mineral surface, the formation of linear oligonucleotides occurs. Thus formed linear molecules of nucleic acids (in our case – RNA) could play a corresponding role for evolution and formation of the Earth and prebiological structures.

NATURAL MONTMORILLONITE CLAY AS PREBIOTIC CATALYST

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A characteristic hallmark of life is its homochirality – biology uses only one enantiomer and not the other. The question of how chirality arises in nature and how it is transferred from simple to complex compounds is a clue to the understanding of the origin and evolution of life on earth. Even if we assume that the first chiral molecules came from space, the transfer of optical activity from small abiotic molecules to more complex molecules essential to the emergence of life remains an open question.

One of the possible mechanisms responsible for the formation of complex optically active compounds at the dawn of life generation on earth might include chirality-preserving intra- and intermolecular transformations of simple compounds in the presence of the then existing natural catalysts, among which clays were certainly most accessible.

To model these processes, we chose the natural clay askanite-bentonite as an acid catalyst and labile natural terpenoids as substrates.

We have found that in the presence of natural clay, oxygen-containing terpenoids generally undergo multistage rearrangements. Although the rearrangements involve the asymmetric centers of molecules, they lead to the formation of optically active products. Using aldehydes (including those that occur in nature) as the second reaction components in reactions with terpenoids made it possible to obtain complex polyfunctional optically active compounds from simple starting compounds on clay catalysts.

Thus our studies have clearly demonstrated that complex transformations of natural compounds can occur in the presence of natural acid clays and that optical activity is preserved in the products. The significant dependence of the reactivity of terpenoids even on minor changes in their structure, found in this study, suggests that clay is an enzyme-like catalyst.

RECONSTRUCTION OF PALEOENVIRONMENT AND CONDITIONS OF THE HABITABILITY OF THE ANCIENT MAN BY THE EXAMPLE OF NORTHWESTERN ALTAI

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1. The purpose of the study was to reconstruct the structure and dynamics of Pleistocene mammal communities and environmental dynamics. Research problems are: to reveal the structure of recent mammal population in the Anui Basin; to determine mammal remains in the Pleistocene beds of Paleolithic sites; to recognize the stages of mammal communities development in the Pleistocene; to estimate the effect of Paleolithic man on the biota. It was established, that the general pattern of the recent population of small mammals in the Anui valley is defined by voles of the genus *Clethrionomys*, which dominate at all altitudinal levels and in the majority of biotopes. The second numerous group is gray voles, represented in river valleys by *Microtus oeconomus* and *M. arvalis* and on high mountain meadows by *Stenocranius gregalis*. An important position is occupied by the zokor *Myospalax myospalax*, which occurs from flood plain biotopes to high mountains. All biotopes are inhabited by shrews and the mole *Asioscalops altaica*, chipmunk (*Eutamias*) and squirrel (*Sciurus vulgaris*) are common. Gentle slopes with low-density herbage are inhabited by the long-tailed ground squirrel *Spermophilus undulatus*. Recent biota of the northwestern Altai is of forest (taiga) pattern but includes isolated steppe and nival elements.

3. In Pleistocene fauna of Anuy valley prevailed voles (*Stenocranius gregalis*, *Alticola strelzovi*), inhabitants of dry steppes and tundras or high-mountainous steppes. *Clethrionomys* submitted at all temporary levels, though, the number of these voles during Pleistocene was steadily reduced. The Asian wood mice *Apodemus uralensis* and *Ap. peninsulae* are extremely rare in Pleistocene sediments of Denisov cave. In a modern Anuy valley they have the majority in some biotop. The same Pleistocene species were absent in recent fauna, for example, marmot, Eversmann hamster, *Ellobius*, lemmings and steppe lemmings. The quantity of *Lagurus* by the end of Pleistocene accrues.

4. The fossil and recent faunas are steadily kept endemic of this territory: Altai mole, *Asioscalops altaica* and zokor, *Myospalax myospalax*, some characteristic west Siberian species - longtail ground squirrel, chipmunk, Siberian red vole, *Alticola*, daurien hamster. It is evident that the changes of ecological structure of communities proceeded on a background stable as a zoogeography situation. The changes of structure of the population of investigated area occurred mainly at the expense of mobilization of internal resources of Altai Mountain and neighboring territories.

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5. Against the background of gradual changes in natural assemblage, displayed by materials from Paleolithic sites of Anuy, a sharp decrease in the abundance of bats at the transition from bed 22 to bed 19 and other overlying beds in Denisova cave attracts attention. Forest species of small mammals decrease in number at this boundary, while the proportion of steppe species increases. The composition of large mammals also changes significantly. Among the carnivores, bear dominates in bed 22, while, in the upper part of the Pleistocene strata, cave hyena prevails. In the upper part of the Pleistocene strata, ungulates increase in number. In addition, above bed 22, the number of artifacts sharply increases, which is evidence of increased activity of the Paleolithic man.

6. All this suggest the following model. Judging from the small mammal fauna, during the formation of beds 21 and 20, the area of open landscapes increased, while the forest vegetation reduced. As a result, the area and biomass of grassland communities increased. The increase in area and efficiency of pastures caused an increase in number and species diversity of ungulates, which, in turn, resulted in the growth of population density of the Paleolithic man. A large number of coal pieces and other signs of fireplaces in beds 21—9 indicate that humans spent much time in the cave and kindled fire. This disturbed and produced a negative effect on bats and other inhabitants of the cave. Human activity affected considerably the population of large carnivores. This suggests that humans occupied the ecological niches of hyena, bear and cave lion.

EARLY HUMAN HABITATION OF NORTH ASIA

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The latest available archaeological, anthropological and genetic evidence suggests that Africa is the motherland of humankind. The most ancient human sites with stone tools of the Oldowan type dating from 2.6 to 2.0 Ma are located mostly in the area of the East African Rift. Around 2 Ma ago, early hominids crossed the boundaries of Africa and colonized a considerable portion of Eurasia. The earliest human populations of the first migration wave seem to have moved along two major routes: via the Near East to Southern Europe, including the Mediterranean Sea and the Caucasus Mountains, and via Western Asia toward the east. The eastern route is likely to have had two main branches: along the southern slopes of the Himalayas and Tibet across the Indian Subcontinent to Eastern and Southeastern Asia, and via the Middle Eastern plateaus to central and northern regions of Asia and the Far East.

Paleolithic studies in the areas situated in the border zones of large geographical regions are especially important for reconstructing migration routes of early hominids. The Altai Mountains are situated along the presumed northern migration route in the area bordering Central and Northern Asia. The Altai Paleolithic is the best-studied part of the Quaternary history of Northern Asia. Archaeological research in the Altai has yielded stratified sites allowing for the construction of chronological sequences covering the Middle and Upper Pleistocene. This time span encompasses the development of human culture and environment from the Lower to the terminal Upper Paleolithic. Archaeological materials from the Altai sites suggest a continuous development of prehistoric cultural traditions throughout all the major stages of the Paleolithic.

For instance, the Karama stratified site has yielded the earliest pre-Acheulian pebble tools in Northern Asia. These archaic tools have been recovered from red early Middle Pleistocene sediments dated to 600 – 800 ka BP. The early Middle Paleolithic layers at Denisova Cave yielded the earliest remains of early Homo sapiens in association with the numerous stone tools. The culture-bearing horizon of the initial Upper Paleolithic, dating to about 50 ka BP, has yielded a collection of personal body adornments made of animal bones and teeth, ivory, ostrich egg shell, and stones.

THE EASTERN REGION OF DISPERSAL OF THE CULTURE OF THE EARLY HOMO SAPIENS

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The region (Transbaikal and Mongolia) is viewed as the easternmost territory where the early Upper Paleolithic complex appeared quite early. Its chronology is relevant for adjacent regions as well. While the Transbaikal and Mongolia Upper Paleolithic sites are rather numerous and probably representative, it is so far difficult to assess the beginning of this epoch due to the insufficiency of materials, lack of reliably dated profiles, absence of a detailed technical or typological characteristics of industries, etc. More than 100 absolute dates are available for the Upper Paleolithic complexes, based on traditional as well as new dating techniques (14C, RTL, AMS, thermo-gravimetry methods).

In recent years, we have discovered and examined new series of Middle and Early Upper Paleolithic sites in the Transbaikal and Mongolia region. Chronologically divergent sites have been found using geoarchaeological methods, with intent to elaborate detailed local chronostratigraphic and cultural-historical schemes. The tentative scheme of organization of the Middle and Early Upper Paleolithic complexes suggests the existence of several technological trends. Cultural modifications of the Early Upper Paleolithic represent two evolutionary trends: the predominant one based on blade technologies; and the secondary one based on other reduction techniques. The pattern is less clear and more variable with the preceding Middle Paleolithic stage. In our view, there is little if any continuity between the Middle and the Upper Paleolithic assemblages. Generally, cultural complexes associated with anatomically modern humans appeared in the region around 40,000 BP [Kamenka, Varvarina Gora (level 3), Khotykh (layers 3 and 4), Podzvonkaya, Tolbor, etc.].

There is a viewpoint that in Siberia Middle and Upper Paleolithic sites co-existed for a long period, at about 43,000-27,000 BP. Obviously, more work need to be done in order to understand better the chronological and archaeological patterns of this process, as recently shown in the discussion of Eurasian records on the MP/UP transition and origin of the Upper Paleolithic, especially with last discovery in China.

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PALEOLITHIC PEOPLING OF THE MOUNTAIN BELT OF SOUTH SIBERIA

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The patterns of human colonization identified in Siberia (that may consider as a natural corridor for migrating populations into Eastern Asia) are not only important for reconstructing Siberian prehistory but also for developing models about human dispersal in the Pleistocene and the formation of culture of the anatomically modern humans. From at least 800,000 years onwards, there is evidence for continuous human occupation of the Altai Mountains region. The goal of this report is to highlight the adaptive response of early humans to changing environmental conditions and determine the main trends in the development of industries and behavioral systems in mountain belt of South Siberia during the first half of the Upper Pleistocene with an emphasis on the Altai Mountain region and Transbaikalia. This geographical choice is determined by several reasons: these regions contain the highest density of currently known Middle Paleolithic and Early Upper Paleolithic sites in Northern Asia. The available information is sufficient for the reconstruction of an Upper Pleistocene cultural sequence; the main characteristics of the human material cultures during the Early Upper Paleolithic from these regions are very similar. This combination of attributes makes the mountains of South Siberia uniquely suited for exploring patterns of Paleolithic occupation and landscape use in the heart of Asia. Recent multidisciplinary research in Altai has identified numerous archaeological sites indicating a lengthy Paleolithic occupation in a rich, protected and highly mosaic environment. Middle Paleolithic technology (in many features closely resembling Mousterian of the West Asia) arrived by at least the last interglacial. The earliest Upper Paleolithic sites present in Altai with dates around 43-48 thousands years BP. The following stage of expansion of the Initial Upper Paleolithic industries is illustrated by the Makarovo-4 (Upper Lena River basin) site in the Cis-Baikal area, more than 39 ka BP. In 40 ka BP, Upper Paleolithic culture appeared in the Transbaikal region. In the Altai, subsistence technology and other kinds of behaviour (except of appearance of personal ornaments) have undergone only minor changes compared with the more pronounced changes in the lithic industry during the Middle-to-Upper Paleolithic transition. However, the general trend may signify regional continuity in the development of Altai Paleolithic industries, contrary to sudden appearance of Upper Paleolithic in Transbaikal. In the new epoch, the Transbaikal populations have had more 'Upper Paleolithic' behavioural features than those in the Altai. In Transbaikal, these changes reflect the responses of migrating populations to the more open, arid and severe environmental conditions and less predictable resources.

PROBLEM OF CROSS-BREEDING AT LATE STAGES OF HUMAN EVOLUTION

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Modern anthropology has rejected aramorphose theory for the human origin, implying the gradual evolution throughout the successive stages of archanthrop, paleoanthrop and neoanthrop. The world anthropology more and more tends to cladogenetic origin of Human, with multiply migration and metisation events.

- It is commonly accepted to divide all erectoid forms into the 3 species: Homo erectus - the Asian forms (pithecanthropus and sinanthropus), Homo ergaster - more ancient forms from Africa, Homo heidelbergensis - African and generally the European progressive forms.

- The Neanderthal Man has returned its specific name Homo neanderthalensis. As a species the Neanderthal is traced only in periglacial zone of the Western Europe 70-30.000 BP.

- The mtDNA data showed the common ancestors of the Homo sapiens and Homo neanderthalensis had probably existed nearby 500-600.000 BP. Neanderthal men most likely weren't involved directly into the evolution of modern humans.

- According to recent studies Homo sapiens had originated as a species on the Africa continent or passed there the initial stages of formation. Numerous remains of ancient humans anatomically similar to modern ones, have been found on the African continent; they are dated as 150-130.000 years. As the species with the certain pattern of apomorphic characters, Homo sapiens would probably appear to be more ancient then the Neanderthal man.

- Nowadays the representatives of polymorphous species Homo heidelbergensis are considered to be the common ancestors of Homo sapiens and Homo neanderthalensis

- West Asia was on the route of continual migration from Africa to the East and from the East to the Europe. Most likely, different directions of migrations did not allow new human species to originate allopatrically in this region. Therefore Homo ergaster initially, and probably Homo heidelbergensis later, having had some morphological characteristics of sapiens or/and Neanderthal people, formed here various mixed variants maximum stabilized only on underspecies level. Most likely area of migration and metisation included not only West Asia but also Central Asia. Such findings as Teshik-Tash and Obi-Rakhmat can be undoubtedly named "neanderthal-sapiens", regarding that such mosaic trait combination was not the result of cross-breeding between species.

- The findings from Krapina and Vindjia are dated from the time of the beginning of direct contacts between two species of Wurm hominids, approximately 35 thousand years ago. The high fragmentation rate of remains from Ortu IV and Okhoz does not allow to determine their species affiliation. And so-called transformed or mixed forms (from Velika Pechina, Khaneferzand), can easily appear to be metises, but most likely, at the same level as in West Asia. Most likely, at this time continual movements of the population from Africa to the Europe by water through Gibraltar and Sicily in a number of populations prevented from the allopatric speciation. They create a layer of so-called neanderthal-sapiens metises on underspecies level. Genetic researches of mtDNA demonstrate that in such a forms there are sites of both sapiens and Neanderthal man. But yet it's not clear how could such similar sites of mtDNA be presented in ancestor form of both species in question - Homo heidelbergensis.

DISCOVERY OF NEW DEEPLY DIVERGENT MICROBIAL DIVISIONS AT A MODEL SITE FOR AN EARLY EARTH ENVIRONMENT

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Warner Valley, Oregon (USA) is a model environment that contains hydrogeological conditions thought to occur early on Earth when life originated. This region has an alluvial system containing numerous geothermal springs and evaporative alkaline lakes, hosted by saltic flows and sedimentary deposits from Pleistocene Lake Warner. Anderson Lake in Warner Valley is an alkaline (pH 8.3-10.5), Na-Cl dominated system (brackish/saline), enriched in arsenic (0.4-16.6µm). A 16S rDNA library was constructed with the recovery of 1,085 clones that exhibit an anomalously biologically diverse ecosystem containing previously unknown deeply divergent microbial divisions. Despite a large library size, only a 61% redundancy level was obtained indicating that this environment is one of the most diverse sampling sites documented on Earth. Most significantly, this diversity spreads through 27 *Bacterial* phyla and division candidates as well as *Archaea* and *Eukarya* domains. Although, the most surprising feature of the biological diversity in this lake manifests itself in the levels of divergence presented by some of the phylotypes, several phylotypes show a divergence level high enough to qualify them as possible representatives of brand new phyla (or candidate divisions). For instance, *Candidate Division Eximius*, has *Candidate Division OD1* as the closest Division, expanding significantly the 'as yet uncharacterized microbial world'.

Specific probes were designed and used to recover additional representatives of the new *Eximius* candidate division at Anderson lake and in various other locations within Warner Valley. These attempts were successful in identifying 41 phylotype representatives of this new candidate division. The observed divergence within *Eximius* is higher than any defined bacterial phyla, being only equaled by *Candidate Division OP11* which is one of its closest relatives.

SIMILARITY OF MITOCHONDRIAL DNA PATTERNS IN ANCIENT AND MODERN INDIGENOUS WEST SIBERIAN POPULATIONS

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According to anthropometrical data, an undifferentiated protomorphic type of humans of the Northern European race became fixed from the Neolithic period over the territories of Western Siberia. It is intermediate between Mongoloid and Europeoid morphotypes. The process by which the protomorphic type formed remains unclear. From ~ 3000 BC to ~ 800 BC, the human population of this area included the sequentially changed representatives of the Krotovo, Andronovo and Irmen' cultures. Development of the Krotovo culture (~ 3000 - ~1300 BC) was accompanied by migratory flows of humans from the east, south, and southwest (archaeological and anthropological data). Here, we analyzed haplotype diversity of mitochondrial DNA (mtDNA) in samples of ancient DNAs from skeletal remains of Krotovo culture humans. Samples of skeletal remains referred to all the developmental periods of the Krotovo culture were collected (Baraba steppe, Sopka-2 burial site). Using the polymerase chain reaction (PCR), followed by direct sequencing of PCR products, the sequences of the first hypervariable segment of the mtDNA control region (HVS1) from the ancient DNA samples was determined. Assignment of the haplogroups to the ancient mtDNA was based on comparison with the Cambridge reference sequence (CRS). Additional analysis of markers in the coding part of mtDNA was performed for certain samples. It was demonstrated that the West Eurasian haplogroups (H, T, V, and U5) significantly prevailed over the East Eurasian (haplogroup C) in the mtDNA pool of the Krotovo population. The mtDNA haplogroups, which are widespread among the modern aboriginal population of this area, were frequent in mtDNA pool of the ancient population.

FROM REPLICATION TO TRANSLATION ONLY USING HYBRIDIZATION: A THERMAL, ENZYME-FREE HAIRPIN REPLICATOR

Philipp Baaske and Dieter Braun

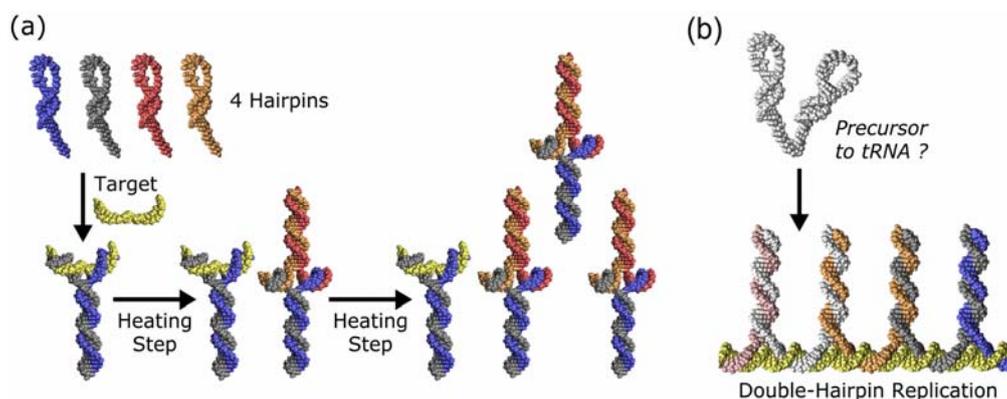
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Introduction. Understanding replication is at the core of understanding molecular evolution. Required is a robust replicative machinery which directly points to mechanisms of contemporary biology. We propose a mechanism, backed by preliminary experiments, which replicates solely by hybridization in a thermal convection. Possible settings are pores in precipitates near the mounds of hydrothermal vents. There, molecules strongly accumulate by thermophoresis and convection [1]. Moreover, convective temperature oscillation was shown to drive the protein-assisted DNA replication reaction of PCR [2].

Mechanism. Generally, replication reactions that mimic conditions of an RNA world are driven by the chemical energy of unstable activated groups. Our proposed replication mechanism in Figure (a) is only driven by the hybridization energy which is kinetically stored in secondary RNA structures (hairpins) after fast cooling. A hairpin pair is catalyzed by target RNA to form a duplex. The target unbinds after a heating step. The duplex remains stable and presents the first replicate: a single stranded region complementary to the target. This region can catalyze the duplex formation of a second hairpin pair, leading to a quadruplex. Another heating step unbinds the quadruplex into two duplexes, each presenting replicated target and its complement. Temperature cycling leads to an exponential growth of quadruplexes without poisoning the substrate. We show first experimental results for such a hairpin replicator.

Outlook. The same mechanism can replicate larger sequences using double hairpin structures [Figure (b)]. These show a striking resemblance with the cloverleaf structure of tRNA and form a persuasive bridge from replication to translation. Technically the method might allow faster DNA detection than PCR with millisecond temperature oscillations.



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**DNA DIVERSITY IN EAST EUROPEAN POPULATIONS IN VIEW
OF DEMOGRAPHIC HISTORIES AND ADAPTATION**

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East European region is an area of great interest for human biology because of long-time contact between Caucasoid and Mongoloid groups that has been affected upon the formation of the gene pool. The region studied includes territories with very different ecological and climatic conditions. The interaction of the human genome with the changing environment moulded the genetic structure of human populations. DNA diversity analysis has long been focused on studying the relationships and demographic histories of human populations. Lately this work has taken on considerable importance for studies of genes, underlying common diseases and involving in adaptation processes.

We have examined normal variability of autosomal mini- and microsatellite loci, Ins/Del, SNPs polymorphisms and the haplotype diversity in geographically diverse populations from Russia and neighbouring countries. Basic tendencies in variability were investigated both for single loci and their haplotypes, concerning specific types of polymorphism. The results reveal marked differences in the allele spectrum of each locus between East European populations and those from the Asian part of Russia. Populations inhabit the Ural region had other values of these characteristics. These differences may be caused by natural selection and various demographic histories. For some loci we have studied the possible effects of climatic-geographic factors on the allele and haplotype frequencies. The existences of these correlations provide evidence for a possible effect of both adaptation to natural environmental factors and large-scale population movements on the specificity and diversity in gene pool of the region investigated.

TOWARDS THE STRUCTURE OF CELLULOSES FROM EVOLUTIONARY VARIOUS SOURCES

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In connection with the extensive discussion of the biosphere development and evolution [1] the definite attention is given to the most abundant biopolymer on the Earth – cellulose (C) [2]. Biosynthesis of C was carried out as long ago as the most ancient organisms – cyanobacteria [3]. As a consequence of intensification in the last years the conceptions about the supermolecular organization (SMO) of C and also the problems of ecology and the deficit of C for its numerous employments the necessity for use of C from the evolutionary various sources and the more complete investigation of its SMO [4-6] increased. At present work the molecular and structural characteristics of cotton cellulose (CC), alga *Cladophora rupestris* (AIC), *Acetobacter xylinum* (CAX) and animal C (AC) extracted from a tunic of ascidia of the class *Styelidae* have been investigated during the solution of their in trifluoroacetic acid (TFAA). It was shown that all samples had the essentially different time of achievement of the molecular dispersed state with an increasing in the row CC, AIC, CAX, AC that was related with the growth of their structural regularity. X-ray analysis indicates the more perfect network of intra- and intermolecular H-bonds in the mentioned row of the initial samples. Analysis of the diffraction patterns from the oriented and non-oriented films obtained from TFAA solutions showed that the meridian reflections [even and uneven order 00l ($2\theta \approx 19^\circ$, 27° and 36°)] could be explained by the change of conformational characteristics of the chain skeleton of macromolecule at the rupture of intrachain H-bonds and the transition from curved to twisted chains. Analysis of an equatorial range of oriented samples demonstrates the relatively low degree of an intermolecular order of flexible chains and it is characterized by only one diffuse reflex at $2\theta \approx 20^\circ$.

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THERMAL CONDITIONS OF THE EARLY EARTH'S SURFACE RELATED TO SYNTHESIS OF PRECURSORS OF ORGANIC COMPONENTS

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In the framework of Safronov's accretion model (Safronov, 1969) a molten surface model of the growing Earth was proposed by Matsui and Abe (1986). However Mukhin and Pimenov (2002) showed that during accretion the surface of the growing Earth remained at low temperatures because of the high cooling rates driven by forced convection in the thin surface layer of impact craters.

They estimated that only 2.5% of the total surface will be hot. Moreover, this value will become less as the assumed accretion time increases. Calculations based on local convection instead of a global convection model demonstrated that under these conditions, water will immediately condense on the cold surface and the greenhouse effect will be determined only by CO₂. As was shown by Moroz and Mukhin (1977), and later by Pollack (1979), it is necessary to accumulate approximately 1 kg/cm² of carbon dioxide in the atmosphere to reach the melting point of water ice. At this point CO₂ dissolves into the liquid water and forms carbonates. Therefore, in the frame of the cold accretion model, the early Earth never had a steam atmosphere and magma ocean. The main greenhouse components - water vapor condensed on the surface and carbon dioxide - could not create a noticeable blanketing effect. This proposed scenario of impact crater hot spots and massive cold traps on the surface of the growing Earth looks attractive for prebiological evolution because some precursors of important organic molecules formed during impact events (Mukhin et al., 1989) would be preserved and accumulated in cold areas.

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EXTREME MICROBIAL COMMUNITIES AS AN EXTRATERRESTRIAL LIFE MODEL

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A number of bacterial communities inhabiting perennially and temporarily ice-covered Antarctic and Arctic (Spitsbergen) lakes, glacier ice sampled over Lake Vostok (Antarctica) and hydrothermal vents of Kamchatka were studied using microbiological, biogeochemical, and molecular biology methods, as well as by microscopy and X-ray microanalysis techniques. The taxonomic structure of the studied communities was investigated by means of clone libraries. The numbers of the determined phylotypes varied between two and five. Clone dominants (oligodominants) were found in four springs: I (60°C; *Sulfurihydrogenibium* sp.); II (43°C; nonculturable organism of the class *Gammaproteobacteria*; III (40°C; species related to *Rhodoferrax ferrireducens*); IV (37°C; species related to *Chlorobium tepidum*). Molecular biological analysis of Antarctic ice using two-stage PCR approach has not produced any positive results.

The physiological status of microbial cells contained in ice samples and bacterial mats from thermal springs was determined microscopically and on the basis of the elemental composition of cells. Resting forms, unlike vegetative cell, were characterized by low contents of P and K, and high Ca content, as well as by low values of P/S ratio and a high Ca/K ratio. Also, we found mineral particles – bacteriomorphs – that resemble microbial cells in their form and size. However, these particles consist, for the most part, of silica.

A mathematical model of the biogeochemical processes of the carbon and sulfur cycles in the Antarctic Fryxell Lake has been developed. These processes were described using differential equations with partial derivatives of the diffusion type. The model was advanced enough to describe the concentration profiles and intensities of the processes of major organic and mineral compounds, as well as to predict the rates of their biological transformation during the first half of an Antarctic day.

We believe that extremophilic photo-, chemoautotrophic, and chemoheterotrophic bacteria and archaea which are responsible for the main biogeochemical/microbial processes in Antarctic lakes and terrestrial hydrotherms can serve as analogues of microbial communities inhabiting hypothetical lake and hydrothermal ecosystems of Mars.

COMPARATIVE ANALYSIS OF HISTORICAL ZOOGEOGRAPHICAL AND MOLECULAR DATA SUPPORTS EARLY DIVERGENCE OF THE BASIC MAMMAL LINEAGES

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When the global historical tetrapod zoogeography was first developed and associated with contacts and isolation between faunas inhabiting particular landmasses, it provided surprisingly early dates of divergence of a number of therian lineages (Kalandadze and Rautian, 1980, 1981, 1983, 1992, 1995). In particular, the split of the therian stem into Metatheria and Eutheria, which coincided with the separation of faunas of the southern and northern blocks of continents, was dated Early Jurassic (200-190 Ma). The lineages of certain extant groups, such as Xenarthra, Condylarthra, Caviomorpha, and Platyrrini, differentiated not later than 132-121 Ma. Recent paleontological studies provided new fossil data on Early Cretaceous and Jurassic therian mammals (Rich et al., 1999; Flynn et al., 1999; Rauhut et al., 2002; J et al., 2002), which reduce the gap between zoogeographical estimates and data of the fossil record. In addition, molecular evidence for the early divergence of mammals, in particular, placentals were reported by a number of research groups during the past ten years. The dates for particular nodes of mammalian phylogenetic trees range depending on the material, technique, and calibration points used; however, they are much closer to the dates obtained on the basis of tetrapod zoogeography than the dates derived directly from the fossil record. For example, the divergence between placentals and marsupials is dated from 120 to 180 Ma. However, these molecular-based estimates are still younger than what is predicted by zoogeography. This is not surprising, because they are also based on particular calibration dates that mark the appearance of taxa in the fossil record. In actuality, divergences between lineages always occurred somewhat (or much) earlier than the earliest known records. In this respect, it is interesting that the molecular date that is closest to zoogeographical estimate was obtained when the divergence between synapsids and diapsids (ca. 310 Ma) was taken for calibration (Kumar and Hedges, 1998). This is additional evidence for the fact that mammals reached biological progress rather late in historical development and were less completely represented in the fossil record than other tetrapod groups.

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BIOMINERAL WORLD, ITS STRUCTURE AND IMPORTANCE FOR DEFINING THE MECHANISMS OF BIOSPHERE ORIGIN AND EVOLUTION

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The sources of biological structures and functions come from the mineral world. On the other side, biological organisms, having been a powerful geological factor for a long (not less than 3.8 billion years) period of the Earth history, played and continue playing a great role in mineral substance formation and transformation; in lithosphere formation. For the upper lithosphere layers, the main mineral formation processes are biogenic. Minerals, formed by living organisms and also with the help of organisms and organogenic substance, are called biominerals. More than 300 biominerals are known in the Earth lithosphere. Their number is rapidly increasing as a result of new geological object study and new research technique appearance.

Bio-mineralogical research can give fundamental information for understanding life origin mechanisms on the Earth and biosphere evolution. The basis of many recent life origin concepts is the idea of mineral biostarting role. Due to the studies of natural hydrocarbons of nonorganic origin, it can be noticed that prebiologic informational structures and gene predecessors should be looked for not among ionic minerals, completely different from biological structures both in their composition and constitution, but among condensed hydrocarbon molecular systems (solid bitumens) and organic molecular crystals, abiogenic synthesis of which takes place both in the Earth and space conditions.

Hydrocarbon molecular crystals are the most suitable prebiologic systems both for informational genetic apparatus formation and for the development into the simplest bioorganisms. On their basis, it's possible to model an autonomous cell, in which RNA (DNA) assembly and protein synthesis take place. Not random events but quite defined laws of natural process development contributed to life appearance, and life formed as something whole, integral, but not as isolated components, connected with each other at random. The concept of mineral organismobiosis and life carbon crystallization, explaining the structural-functional development of ordered molecular hydrocarbon systems- protoorganisms into biological organisms, is being developed by us.

MINERAL PROTECTION OF NUCLEIC ACIDS IN HOSTILE PRIMORDIAL HABITATS

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The appearance in a primordial era of a nucleic acid-like polymer able to undergo Darwinian evolution marked the beginning of life on our planet and perhaps any other [1].

The hypothesis of an origin of life based on nucleic acid, or nucleic acid-like molecules, is strongly affected by the hostile environmental conditions probably present in the early Earth. In particular, strong UV and X-ray radiations, and high temperatures, could have been a major obstacle to the formation and evolution of first biomolecules.

In 1951, J.D. Bernal first proposed that clay minerals could have served as the sites of accumulation and protection of ancient biopolymers [2], providing a suitable physical setting for the evolution of more complex systems. Numerous experimental studies in the last years have reinforced the hypothesis of a mineral-mediated origin of genetic material [3].

In this work, the behaviour of nucleic acid constituents in a mineral environment, and the ability of different minerals to protect DNA and catalytic RNA (ribozymes) from various degrading agents (e.g. UV irradiation, temperature, etc.) was experimentally evaluated. In particular, adsorption experiments of nucleotides on different mineral surfaces, including the Murchison meteorite, were performed. Moreover, self-cleavage activity of the hairpin ribozyme ADHR1 [4], and transforming capacity of chromosomal DNA, were analyzed after UV irradiation of the two nucleic acids at 254 nm. Results obtained showed that mineral-protected nucleic acids retain their biological activity after irradiation much more than the same molecules free in solution.

These observations suggest that a clay-rich environment could have favoured not only the accumulation of precursors and the formation of first genetic molecules, but also their evolution towards increasingly complex molecular organization.

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STROMATOLITES IN THE DESERT: ANALOGUES TO OTHER WORLDS

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Freshwater stromatolites with non-thermophilic temperature gradients environments are relatively rare. Environments such as this are good proxies for early earth environments. Stromatolites and various metabolites are prominent in a central Mexico hydrologic field site, the Cuatro Ciénegas basin (CCB). The CCB is a system of springs, streams, and pools (pozas) in the Chihuahuan desert of Coahuila (México) located within an evaporitic basin with ~150 mm annual precipitation. Of particular interest to this project, the aquatic system exhibits the lowest phosphorous content reported in continental waters (Elser et al., in press).. We have sampled both oncoïd metabolites and stromatolites from two different spring sources; one a free flowing river system, the Rios Mesquites, and the Pozas Azules, a spring-fed, thermally heated pool that has been protected from anthropogenic contamination. The metabolites in each of these systems are morphologically distinct and yet preliminary microscopic investigation indicates they have relatively similar microbial constituency. We have performed metagenomic viral community assessment on the two metabolites. Our results indicate that:

- 1) The two viral communities are very different (Pozas Azules versus Rio Mesquites);
- 2) Pozas Azules has a large number of marine-like phage, including sDNA and *Prochlorococcus* cyanophage sequences; and
- 3) Pozas Azules has over-representation of proteins that protect against oxidative stress whereas the Rio Mesquites appears to be denitrifying.

Understanding the metabolic ability of these communities will help to understand the diversity of ecologies that stromatolitic microbial growth has played throughout our planets history and the likely roll a similar strategy would provide extra terrestrially.

BACTERIAL EDUCATION OF MINERALS IN TRAVERTINES OF THERMAL SOURCES OF BAIKAL RIFT ZONE

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The geomicrobiological study of travertine sediments from hot springs of nitrogen sodium-sulfate and carbonic sulfate-hydrocarbonate calcic waters in the Baikal rift zone demonstrated the decisive role of bacterial mats in their formation. Bacteria also participated in large accumulations of humus-sapropelite organic matter, including coal seams associated with travertines.

Microorganisms are highly diverse in microbial mats and sediments of the Zhoigon carbonic spring in the East Sayan province, where calcitic travertines contain abundant lithified films of bacterial mats. Microscopic study of the mucous ocherous sediment accumulated in mat near the discharge area of this spring revealed the presence of abundant filamentous ferruginous bacteria close to *Leptothrix* sp. and *Gallionella* sp. associated with cyanobacterial mats. Cyanobacteria include dominant *Phormidium tenue* and subordinate *Phormidium valderiae* f. *pseudovalderianum* and *Oscillatoria tenuis* f. *woronichiana*.

Mats of nitrogensodium-sulfate waters are composed of filamentous cyanobacteria *Phormidium angustissimum*, *Annabaena contorta*, and *A. minutissima*. In addition, spring hosts abundant thermophile filamentous green bacteria *Chloroflexus aurantiacus*. Their most intense growth was recorded at T = 40-55 °C and pH = 8.0-8.5.

Prior to the formation of travertine, bacterial mats stimulated differentiation and changes in the chemical composition of primary nitrogen sulfate solutions. The early stage of travertine formation from the colloidal system was marked by the appearance of organic-clayey-carbonate aggregates with carbonaceous ore accumulations, which subsequently served as centers of calcite crystallization from true hydrocarbonate solutions.

Bacterial organomineral associations in the examined dolomitic travertine carbonic sulfate-hydrocarbonate calcic bodies: amorphous silica, smectite, hydromicas, hematite, pyrite, sphalerite.

Aragonite-calcite travertines that are younger than their dolomitic varieties form small (up to 10x5 m), thin (1-30 cm) bodies in discharge areas of hot (43-44 °C) waters.

Rubbly-pebbly sediments of the riverbed represent a main substrate for development of stratified travertine domes. One of the domes includes eight successive microlaminae (10 mm thick in total) composed of structureless siliceous, carbonate, siliceous-carbonate, and siliceous-clayey-carbonate matter.

Siliceous-smectite-calcite laminae contain abundant rods of lithified microorganisms (approximately 0.1%, on average) that form small accumulations at boundaries between calcite and smectite aggregates. Some rod-shaped bacteria are replaced by transparent fibrous smectite with simultaneous formation of a siliceous envelope around them. In the course of metabolism, bacteria probably decompose smectite and produce a shell of amorphous silica around bacterial cells. Simultaneously, ore elements are released from the organic matrix and concentrated in pyrite, magnetite, ilmenite, and galena. Another part of bacteria is replaced by pelitomorphous carbonaceous ore matter with a rim of iron hydroxides.

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**STRUCTURE AND MOLECULAR EVOLUTION OF THE RIBOSOMAL
DNA EXTERNAL TRANSCRIBED SPACER IN THE COCKROACH
GENUS *Blattella***

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The ribosomal DNA (rDNA) cluster of insects contains several hundred repeating structural-functional units and, therefore, is a typical example of a multigene family. Eukaryotic ribosomal RNA (rRNA) genes (18S-, 5.8S-, and 28S-like) are arranged in tandemly repeated clusters in the nucleolus organizers, separated by several spacers, namely the nontranscribed spacer, external transcribed spacer (ETS), and internal transcribed spacers. The nucleotide sequences of the ETS of the three closely related *Blattella* cockroach species, *B. germanica*, *B. asahinai* and *B. lituricollis*, were determined and compared. The three species had relatively similar ETS lengths, and sequence differences among them could be explained by two types of rearrangements, namely deletions of subrepeats and nucleotide substitutions. Minor ETS variants in *B. germanica* differed from the major variant in the same way that the major ETS variants of the three *Blattella* species differed from each other. Concerted evolution and the birth-and-death models, which often invoked to explain the diversity and evolution of the multigene families of rDNA clusters, are discussed in the light of our data. A new model is proposed to explain the evolutionary reorganization of the ETS region: evolution of rDNA by “magnification-and-fixation” is characterized by magnification of minor subrepeats, which become adaptive in a new rapidly changed environment, and subsequent fixation of this variant type as a major component of the multigene family of a new species.

COMPLEMENTARY SYMMETRY AND ORIGIN OF THE GENETIC CODE

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If the genetic code table is rearranged in a manner that puts complementary codons vis-à-vis each other, the latent mirror symmetry of the code is revealed with respect to the two sterically mirror modes of tRNA recognition by class I and class II aminoacyl-tRNA synthetases (aaRS), – from the minor or major groove sides of the acceptor stem, respectively (Rodin & Rodin, 2006). The symmetry is consistent with the “frozen stereochemical accident” (Yarus, 1998). A closer analysis of the corresponding complementary anticodons with adjacent invariant U and R at the 5’ and 3’ sides together with the updated phylogenetic analysis of tRNA and aaRSs suggest that the ribozymic precursors of the two aaRS exhibited precisely the same complementary modes of tRNA recognition. This complementarity is consistent with the origin of two p-aaRSs from the opposite strands of the same ancestral gene (Rodin & Ohno 1995; see also Carter & Duax 2002; Pham et al. 2007). Furthermore, this striking instance of RNA–protein molecular mimicry provides a new insight into the mystery of the RNA→RNP transition, is consistent with the fingerprints of codon/anticodon-like triplets in the acceptor stem (Rodin et al. 1996) and might represent the missing link between the classic genetic code embodied in anticodons, and the “second” (RNA operational) code of aminoacylation embodied mostly in the acceptor stem of tRNAs (Schimmel et al. 1993; Schimmel & Beebe 2006).

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THE EMERGENCE AND EXPANSION OF THE GENUS HOMO: A BEHAVIOURAL PERSPECTIVE

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Anthropogenesis and hominization represent the trajectory of one primate line. It highlights an evolutionary pathway exploiting a hitherto unoccupied adaptive niche and growing reliance of non-biological means. The genus *Australopithecus* shows diagnostic hominid traits such as bipedal stance and locomotion, and dentition since at least 4.2 my. The genus *Homo* appears between 2.5-2.0 my, showing increased stature, encephalization, handedness, toolmaking and skill, a broader omnivorous diet including a carnivorous exploitation of ungulates. An outstanding question for human palaeontology and Palaeolithic archaeology is tracing and explaining hominization trends between early *Homo* and *H. sapiens*. Resolution is hampered by empirical and theoretical difficulties: Some argue for *Homo* cladogenesis into separate species before *H. sapiens*; others see *Homo* as a single species evolving as a network of shifting biological parameters by anagenesis; Practical limits in direct evidence, like the scarce, fragmentary fossil human record, compounded by overlooking principles of population sampling; Differential preservation of Palaeolithic cultural evidence. Modern humans constitute a single polymorphic species resulting from microevolution by genetic drift, selection, mutation and hybridization. Cladogenesis thus faces the challenge of providing robust support to establish a *Homo* evolutionary bottleneck into a single *H. sapiens* species.

A model focusing on key interrelated aspects of hominid behaviour, namely *ecological polymorphism* and *culture*, is more compatible with anagenesis, however. Ecological polymorphism indicates a trend since early *Homo* to fit and expand into a wide range of habitats, unlike other primates. Hominids developed culture, namely the “domain of interpretation and meaning, that transforms the actual reality of objects, events, activities into an emergent *human reality*”. Its biological capability roots are traced to early *Homo* encephalization, particularly “the expansion, elaboration and growing complexity of the cerebral cortex of neural structures” or ‘biological hardware’. The cultural contents, or ‘behavioural software’, technological, social organizational and cognitive are transmitted by social learning. Culture played a distinct, non-biological function, creating a *new environment* to which hominids adapted and depended on. Despite preservation limits, Lower Palaeolithic evidence and contexts in Africa and Eurasia indicate an early, growing trend in ecological polymorphism and reliance on cultural means. Ancient hominid broad-spectrum foraging subsistence exploited ecosystems at different levels of the trophic pyramid in the most productive ecotones. Eurytopic adaptability, and cumulative learning fostered colonizing different biomes by interconnected mating network groups. These contributed in maintaining a single *Homo* evolving species.

IN-SITU ANALYSIS OF BACTERIA IN POLAR PERMAFROST OF DIFFERENT AGE

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Different approaches for in-situ analysis of microbial communities are currently applied in environmental ecology. In this research high resolution microscopy (SEM, AFM, epifluorescence microscopy) as well as lipid biomarker's analysis were used to investigate native microbial communities in arctic and Antarctic frozen sediments of age from ten's thousands to 1,8 mln of years (age of permafrost in frozen state). All sediments were highly populated by prokaryotic and eukaryotic microorganisms up to 10^8 of bacterial cells per g and 10^6 fungal spores per g. Also microorganisms with sub microbial scale were detected and investigated. Lipid biomarkers analysis enables to recognize the taxonomic structure of bacterial communities in permafrost of different age and genesis. Bacterial cells in-situ revealed features of dormancy or hypometabolic state. One of the main tasks of this research was to investigate in-situ morphology and cell surface parameters depending on the main physiological status of cells using different modes of atomic force microscopy.

MULTIELEMENT ICP-MS MICROANALYSIS IN BIOMINERAL STUDIES

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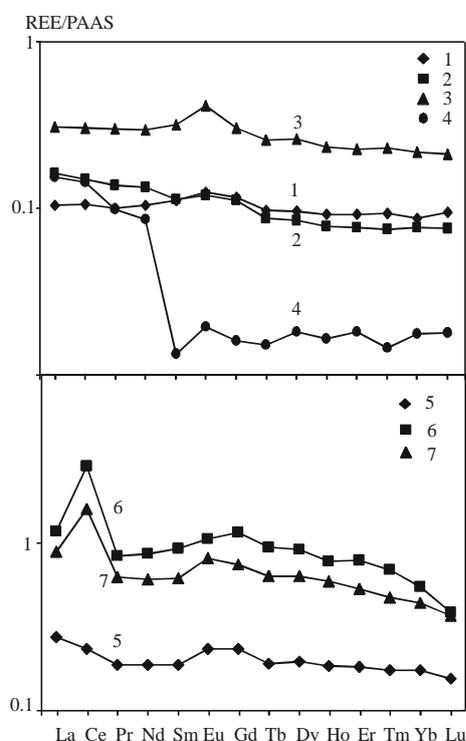
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Biominerals are well-known for their ability to accumulate and store trace microelements to which organism is exposed, and prospects of using microelement composition as a geo-indicator (for example, *Biom mineralization*, 2003). This publication is devoted to the development of sample preparation method and multielement microanalysis of biominerals by quadruple ICP-mass-spectroscopy. Modern cyano-bacterial mats (hydrotherm thermophilic communities from lake Uzon, Kamchatka, salty lagoons halophilic communities from Sivash and Koyashskoe, Crimea, soda lakes alcaliphilic communities from Dabas-Aur, Buryatia) and fossil stromatolitic formations of different ages (Mongolia, upper vend and lower Cambrian; Australia, lower Cambrian; Karelia, etc) have been studied. In order to reduce trace and ultratrace analysis blank level analytical procedures have been carried out in the special laboratory complex using special equipment; organic constituent removal at the stage of sample preparation and analysis on mass-spectrometer ELAN 9000 regarding organic matrix effects are examined.



PAAS normalized REE distributions in mats and stromatolites are shown in figure (1-4 - Koyashskoe, Sivash, Dabas-Aur, Uzon; 5-7 - various zones of Australia sample). Lithological-geochemical indicators of depositional environment, recording provenance peculiarities and palaeogeodynamic environment (LREE/HREE, (La/Yb)_{norm}, Eu/Eu*), volcanic exhalation components presence ((Fe+Mn)/Ti), palaeosalinity (Sr/Ba), and redox conditions (Mo/Mn, V/(V+Ni), V/Mn, Mo/Co, V/Co, U/Th, V/Cr, Ni/Co, Ce/Ce*) have been analyzed for samples investigated. Several different lithological-geochemical types of sediments have been figured out.

The study was supported by the program «Origin and Evolution of Biosphere» and by the Russian Foundation for Basic Research (07-05-00097).

ESR AND LUMINESCENT STUDY OF BIOCARBONATES

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Biocarbonates have been tested as markers of geological events using ESR and luminescence (for example, *Cazenave et al.*, 2003; *Franco et al.*, 2003); various paramagnetic impurities Mn^{2+} , Fe^{3+} , TR^{3+} , etc and ion-radicals CO_2^- , CO_3^{3-} , O^- , etc have been identified in them; effects of manganese and iron on carbonates luminescence have been described. This publication is devoted to ESR and luminescent study of stromatolite-containing limestones and dolomites from the main South Urals Riphean formations series with age ranging between 0.5 and 1 billion years. The scheme of calcite and dolomite classification based on the data of ESR, thermo- and X-ray luminescence (in the temperature range 77-400 K) of the typical impurity Mn^{2+} -ions replacing Ca^{2+} (Mg^{2+})-ions in carbonates is under consideration. The scheme is based on the statistical analysis of biocarbonate of the different content and age. Numerical ESR and luminescence databases have been created. It has been shown that analytical spectroscopic Mn^{2+} line widths, their intensities and their dynamics under the temperature changes varied in the samples essentially and depended on the minerals content and their structure defectness. Suggested scheme of carbonates classification has been used for the analysis of limestones (dolomites) containing various types of stromatolites (*Gaya ircuskanica* Kryl., *Conophyton metula* Kirich., etc) from South Urals Riphean formations series.

Besides the main carbonate minerals investigated rocks contain insoluble organic matter (IOM). For such a material ESR appears to be a valuable analytical tool (Binet et al. 2002), for it can be applied to raw rock samples with no need to isolate and concentrate a highly degraded macromolecular organic matter. In some of the investigated rocks an ESR line with no hyperfine structure assigned probably to organic radicals in the macromolecular organic matter has been observed. The variation of the signal lineshape with age, type of stromatolites and thermal laboratory treatments has been estimated. The results obtained have been compared with those for ESR study of IOM in extraterrestrial and terrestrial rocks age 0.045-3.5 billion years (Binet et al. 2002; Courier et al. 2004). The experimental spectroscopic data have been analyzed using the results of computational modeling for calcite and dolomite.

The study was supported by the program «Origin and Evolution of Biosphere» and by the Russian Foundation for Basic Research (№07-05-00097).

POSTER PRESENTATIONS

THE MS OF CARBONYL COMPOUNDS GENERATED FROM TITAN ATMOSPHERE SIMULATIONS CONTAINING CARBON MONOXIDE

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Experiments have been carried out to determine the role of solar ultraviolet radiation in initiating reactions in gas mixtures that simulate the atmosphere of Titan. Identifying the “volatile” compounds in Titan’s atmosphere formed by solar UV is of interest since their structures will suggest the structural units present in the Titan haze. The experiments are carried out in a flow system, irradiating at 185 nm and the products collected via vacuum line techniques. The analysis of the reaction products from a Titan atmosphere simulation experiment (mixing ratio of Nitrogen 0.98, Methane 0.18, Hydrogen 0.002, Ethylene 0.0003, Acetylene 0.00035, Cyanoacetylene 0.000017, and Carbon Monoxide 0.003) by direct GC/MS measurements led to the detection of relatively few simple carbonyl compounds. CO reacts with radicals generated by photolysis of other atmospheric constituents to generate these carbonyl compounds. After the product mixture had been derivatized with 2, 4-dinitrophenylhydrazine (2, 4-DNPH), HPLC (Reverse phase C-18, THF / acetonitrile / water system) and LC/MS enabled the detection and identification of 25 products with a further similar number tentatively so. Mass spectra were obtained using electrospray ionization in negative ion mode. MS/MS measurements were made throughout to enable structural confirmation. GC/MS and LC/MS experiments were carried out for the analysis of the reaction products. Electron ionization allowed for the detection of small carbonyl compounds. LC/MS was performed on 2, 4-DNPH derivatives. Atmospheric pressure chemical ionization was unable to ionize these compounds as well as ESI(+). ESI(-) mass spectra showed $[M-H]^-$ ions for the majority of the products. The identification of the derivatives of saturated species such as formaldehyde and acetaldehyde was expected; the formation and identification of 2:1 adducts (2 DNPH molecules per molecule of carbonyl compound) from unsaturated carbonyl compounds was resolved by prompt measurements to avoid their re-equilibration. The identification of isomeric derivatives from unsaturated compounds such as acrolein, methyl vinyl ketone and butenal was assisted by the presence of Z- and E-isomers of the hydrazones. For example, the geometrical and structural isomeric nature of the derivatives of methyl vinyl ketone and butenal: they all have the same mass, but the identification of four materials of this mass confirms the presence of the isomeric carbonyl compounds. The detection of materials related to ketene and diketene products is hitherto unreported. Ketene was identified by the detection of the acetyl derivative of 2, 4-DNPH as the derivatization product. Its structure was confirmed by its synthesis from acetic

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anhydride and 2, 4-DNPH. Ketene also formed a 2:1 adduct. Diketene, a synthon for acetoacetic acid, formed both a 1:1 and a 2:1 adduct with 2, 4-DNPH. Further accurate mass measurements are in progress to distinguish between isobaric species. The MS data enable a direct probe into the feasible mechanistic steps taking place. Relatively few free radicals need be invoked to describe the formation of all the products identified to date.

The results may be useful in the interpretation of the spectroscopic and mass spectral data obtained by the Huygens probe.

**ENDOSPORE-FORMING GRAM-NEGATIVE BACTERIA ISOLATED
FROM SOIL AND SPRINGS OF THE VALLEY OF GEYSERS
(KAMCHATKA)**

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Aerobic endospore-forming bacteria of *Paenibacillus* genus (FAME analysis, 16S RNA) with Gram-negative staining at all cultivation stages and a cell wall of Gram-negative type have been found in samples collected in different areas of the Valley of Geysers (Kamchatka). Phenotypic characteristics and results of phylogenetic analysis of nucleotide sequences of the bacterial 16S rRNA gene fragment allow us to refer them to new gram-negative bacillus, which are probably endemics of the Valley of Geysers. The obtained strains of Gram-negative endospore-forming bacteria are of great interest for fundamental study of evolution and speciation of microorganisms.

The work was supported partly from the grants IPP-DOE CRDF RUB2-10618-NO-04 (LBNL) and Interdisciplinary Integration Project #114, SB RAS.

THE FEATURES OF BENTHIC COMMUNITIES DEVELOPMENT DURING SILURIAN IN THE NORTH URALS PALEOBASIN

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In the history of the Earth there have been no basins with similar characteristics. The North Urals paleobasin had its own unique features. The dominant benthic organisms of basin ecosystem during the Ordovician and Silurian periods were corals and stromatoporoids. The uneven distribution of stromatoporoids and coral fauna through the section indicates frequent modification of biota states and its cyclicity. During the Ordovician and Silurian in the North Ural basin there've been several tipping points in the benthic ecosystem evolution, connected with the changes of depositional conditions. At the close of the Ordovician the diversity of coral-stromatoporoids biota reduced dramatically which subsequently was replaced by algal communities. The diversity of corals and stromatoporoids gradually restored with the evolution of the Llandovery transgression in biocenosis. The buildups in Middle Llandovery was accompanied not only by the reduction of benthos diversity but also by the wide-spread distribution of cyanobacteriaes and stromatoporoids. Within the Llandovery there was the decrease of taxonomical benthic fauna diversity with the preservation of stromatoporoids prevailing function. The Wenlockian transgression contributed to the fauna renewal. In the Ludlow numerous lagoonal conditions and active formation of buildups favored a wide-spread distribution of coral and stromatoporoids fauna. At the close of the Silurian the coral-stromatoporoids communities were replaced by ostracod communities, and the value of other groups of fauna was increased. The development and morphological peculiarities of stromatoporoids and corals made it possible to reconstruct the local paleoecological depositional environment in the Late Ordovician and Silurian in the Subpolar Ural. The coral-stromatoporoids communities exemplify the adaptation to different conditions of sedimentation and have long existence.

The coral-stromatoporoids communities played a key role in the development of trophic composition of the Late Ordovician and Silurian biocenoses of the North of Urals. The euryfacies stromatoporoids species were among the first to cultivate paleobasin territory after global events. The development analysis confirms the ecosystem reorganization boundaries, coinciding with the geological events in the North Ural paleobasin.

LOPIAN (UPPER ARCHAEN) MICROFOSSILS FROM KARELIA (KHIZOVAAR GREENSTONE STRUCTURE)

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Traditionally the first appearance of eukaryots refers to Gunflint time of the Early Protherozoic (Sergeev et al., 1998). Trustworthy finds of fossilized remains of eukaryots (acritarchs belong to them as well) in Archaean rocks practically were not locked in. The work of B.V. Timofeev (1982) is among few exceptions. Moreover, this publication probably is the only one in which the finds of fossilized eukaryots, including acritarchs, were locked in. Archaean rocks are mainly represented by highly metamorphized volcanogenic and volcanogenic-sedimentary rocks. Finds of fossil microorganisms in the Archaean is not common and, so that every new find has a great significance. The samples under our investigation (from the weathering zones, from quartz arenites and from tufa-genic – sedimentary rocks and carbonaceous shales, lying upon arenites) came from the Lopian (Upper Archaean) of Northern part of Khizovaar structure (Northern Karelia) that is a part of the Parandovsk-Tikshosersk greenstone belt. The age of studied rocks is about 2.7-2.8 GA. It was determined that there are 3 types of such biomorphic structures in ancient rocks:

1. structures found in situ, in other words microorganisms even-aged with rock matrix, that is real Archaean fossils,
2. endolithic biomorphic structures, that is to say forms inhabited early formed rocks, and
3. younger than Archaean-Protherozoic mineralized microorganisms, that is later contamination.

The real Archaean structures were under our examination. Practical investigation of ancient microorganisms from Green-Stone-Belt of Northern Karelia turns to be very perspective. It shows that even in such ancient time as Archaean ancient diverse world existed. Moreover probably such relatively highly organized forms as cyanobacteria and perhaps eukaryotic forms existed in Archaean world. All recognized microbial pseudomorphs are represented by filament, wandering, and coccoidal forms.

1. Filaments and rod-shaped forms are met in carbonaceous shales, quartzites (metasandstones) and tufa-genic - sedimentary rocks. The main part of these forms are represented by filaments with diameter about 3-5 mkm. Their length can reach, even exceed, 100 mkm.

2. Coccoidal forms in Lopian rocks of the Khizovaar Structure also are found both in carbonaceous shales and in tufa-genic – sedimentary rocks. These forms are represented by several modifications.

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3. Peculiar oval-flattened forms (with length reaching 5 mkm, width about 3 mkm) are also found in tufa-genic – sedimentary rocks. The study indicates the presence in the Late Archaean of Northern Karelia various microorganisms of bacterial and cyanobacterial nature, and possibly even eukaryotic forms.

This research forms part of the Russian Academy of Sciences program “Origin and Evolution of the Biosphere” and RFBR grants 05-04-48008, 03-05-64499 and NSH-974.2003.5.

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THE STRUCTURE AND FUNCTIONING OF THERMAL SPRINGS MICROBIAL COMMUNITIES IN RIFT ZONE

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The microbial communities of hydrotherms are interesting from the point of view of the biosphere's evolution and as analogs of the communities, which prevailed in early development stages of life on the Earth. The diversity of microbial communities in alkaline hydrotherms of Baikal rift zone (30-92 °C, pH 7-10) and in shallow hydrotherms of the western coast of Pacific Ocean (19-95 °C, pH 7-8) was studied. There are two types of hydrotherm's microbial communities: with phototrophic microorganisms domination and with chemotrophic microorganisms domination. Between the phototrophic and chemotrophic communities there is a boundary which is determined by natural's conditions, in the first place, by temperature and by illumination. The upper temperature limits for phototrophic microbial mat in the springs with pH 5-10 are 61-73 °C. The chemotrophic communities are developed at higher temperatures or in the absence of light.

Changes of physical and chemical conditions and succession of cyano-bacterial, purple, green and sulfuric microbial communities are observed on the downstream of thermal springs. The rate of total photosynthesis in the mats of hydrotherms reaches 3.65 g C/m² per day, chemosynthesis reaches 1.1 g C/m² per day. In the mats of shallow sea hydrotherms the rate of total photosynthesis reaches 3.7 g C/m² per day, chemosynthesis reaches 0.86 g C/m² per day. $\delta^{13}\text{C}$ in the microbial mats of sea hydrotherms are -21.9 – -22.1 ‰, terrestrial hydrotherms – -5.93 – -22.34‰ and $\delta^{13}\text{C}$ vents of Lake Baikal are -30.7 – -41.6 ‰. In the terminal destruction process the large part of the organic matter is used for the bacterial sulfate-reduction. The metanogenesis is minor process. The hydrotherm's microbial communities play the leading role in the processes of travertine and geysers formation in the area of thermal waters head.

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COMPARATIVE ANALYSIS OF CROSSINGOVER FREQUENCY AND DISTRIBUTION IN MAMMALS

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Recombination is a process that promotes gene shuffling in the progeny and insures genetic uniqueness of each individual. Crossingover performs two main functions: it 1) provides an orderly segregation of homologues, and 2) generates new combinations of alleles.

The aim of our work was to analyze frequency and distribution of recombination events along the chromosomes of four carnivores species domestic dog (2N=78), domestic cat (2N= 36), silver fox (2N=34) and American mink (2N=30) and to compare their recombination patterns with those of other mammals studied.

Sites of crossingover were located on synaptonemal complexes (SC) pachytene chromosomes with antibodies to mismatch repair protein MLH1.

We found that foxes and minks were characterized by critically low crossingover frequency which was just sufficient for orderly chromosomes segregation, while cats demonstrated extremely high level of recombination. This high crossingover frequency in the domestic cat was apparently determined by very weak crossover interference. Average distance between crossover sites in the cats was shortest among all mammals studied so far.

Overall crossingover frequency in the dog was rather low, but due to large number of chromosomes (2n=78) the number of freely recombining blocks of genes was close to that in humans (2n=46).

Interspecies differences in recombination process apparently resulted from evolutionary history of these species and peculiarities of their ecology.

This work was supported by research grants from the Programs of RAS "Biosphere Origin and Evolution" and "Biodiversity", INTAS and RFBR.

CHROMOSOME PAIRING AND RECOMBINATION IN HYBRIDS BETWEEN TWO CHROMOSOME RACES OF THE COMMON SHREW (*Sorex Araneus* L., Soricidae, Eulipotyphla)

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Hybrid zones occur when genetically distinct forms (races or species) make contact and produce the high frequency of hybrids. Hybrid zones have been considered ‘natural laboratories’ for evolutionary study, since natural selection against unfit hybrids may cease gene flow between hybridizing forms, promote assortative mating and then speciation. The common shrew, *Sorex araneus*, shows one of the most remarkable chromosomal variation in mammals and forms numerous hybrid zones between chromosome races with different karyotype.

To understand the role of chromosomes in reproductive isolation we analyze chromosome pairing and recombination in Tomsk and Novosibirsk chromosome races and their hybrids heterozygous for complex Robertsonian translocations. We show that interracial hybrids had a 10-times higher frequency of synaptic abnormalities compared to non-hybrid animals (Fig.1), although recombination was not impaired in cells with normal synapsis. We suggest that the observed meiotic aberrations should severally decrease fertility of the hybrids and, therefore, suppress the gene flow between two chromosome races of the common shrew.

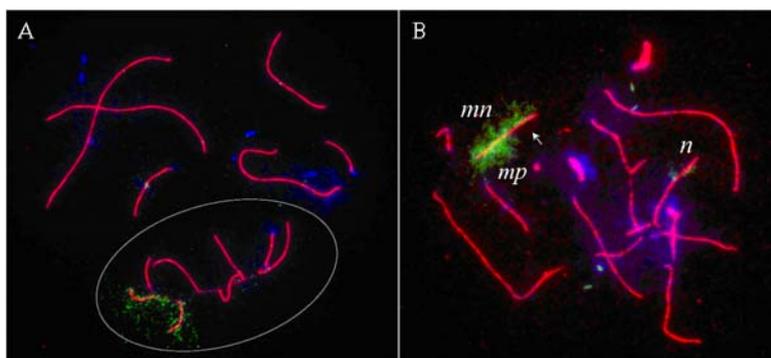


Figure 1. Examples of normal (A) and abnormal (B) synapsis in hybrid shrews.

Synaptonemal complexes are shown in red, DAPI in blue, the DNA probe to chromosome *mn* in green. Ellipse indicates the complete chain of nine chromosomes involved in Robertsonian translocations. Arrow points to the area of nonhomologous synapsis between chromosomes *mn* and *mp*.

This work was supported by research grants from the Programs of RAS “Biosphere Origin and Evolution” and “Biodiversity”, INTAS and RFBR.

INFLUENCE OF EVOLUTIONAL CHANGES OF INTRON LENGTH ON RNA SECONDARY STRUCTURE

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The most of the coding genomic sequences of eukaryotic organisms contain introns. In many works the participation of introns in gene expression is suggested, but the true intron function remains unknown. To determine the influence of intron length on the evolution of exon-intron genes structure we have taken 2 or 3-intronic genes of *A. fumigatus*, *A. thaliana*, *C. neoformans*, *C. elegans*, *H. sapiens*. The series of model experiments were performed on RNA secondary structure with the help of Mfold by M. Zuker. The influence of intron length on a free energy (ΔG) of RNA molecule was established. In the presence of introns the conformation of pre-mRNA molecule becomes more stable due to ΔG decrease. After the shorter intron excision free energy insignificantly increases and RNA secondary structure changes slightly, i.e. RNA structure still looks like pre-mRNA. The excision of the longest intron dramatically changes RNA molecule conformation. The RNA secondary structure and value of a free energy become closer to mRNA ones in spite of other introns are still present. All introns have the similar values of lengths within one gene of lower organisms, for example *C. neoformans*. It is interesting, that the length of one of introns is several times more than the length of other introns within one gene of *C. elegans* and *A. thaliana*, and ten times more than in genes of *H. sapiens*. Thus, the longest intron is the critical element that totally changes the secondary structure from pre-mRNA to mRNA. The deviation of fC, fG, fA, fT (nucleotide frequencies in coding one strand DNA) in exons and introns we studied by calculating delta: $\Delta = fC/fG - fA/fT$. The delta of exons of *A. fumigatus*, *A. thaliana*, *C. neoformans*, *C. elegans*, *H. sapiens* is not equal to zero. Delta of introns is close or equal to zero. We propose that the nucleotide content of introns influences on the RNA secondary structure and a free energy. To confirm this fact the natural intronic nucleotide sequence was shuffled. The secondary structure of pre-mRNA with original nucleotide sequence has been used as a control. After shuffling the RNA secondary structure became totally different. The significant grow of intron lengths from lower fungi to human confirms stabilizing role of introns. Therefore, established intron functions make clearer the influence of introns on RNA secondary structure.

HOW LONG CAN LEFT AND RIGHT HANDED LIFE FORMS COEXIST?

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Reaction-diffusion equations based on a polymerization model are solved to simulate the spreading of hypothetical left and right handed life forms on the Earth's surface. The equations exhibit front-like behavior as is familiar from the theory of the spreading of epidemics. It is shown that the relevant time scale for achieving global homochirality is not, however, the time scale of front propagation, but the much longer global diffusion time. The process can be sped up by turbulence and large scale flows. It is speculated that, if the deep layers of the early ocean were sufficiently quiescent, there may have been the possibility of competing early life forms with opposite handedness.

ON THE ORIGIN AND EVOLUTION OF METABOLIC PATHWAYS: THE HISTIDINE BIOSYNTHESIS PARADIGM

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The building up of metabolic pathways represented a key step in molecular and cellular evolution. In fact, if the Oparin's idea on the origin of life is correct, it is plausible that the exhaustion of the prebiotic supply of amino acids, bases, and other compounds due to the increase of cell concentration must have imposed a progressively stronger selective pressure favouring those primitive heterotrophic cells which have become capable of synthesizing by themselves those compounds whose concentration was decreasing in the primordial soup. Thus, the emergence of biosynthetic pathways allowed primitive organisms to become increasingly less-dependent on exogenous sources of organic compounds. Different molecular forces and mechanisms have played an important role in the assembly of metabolic pathways, in the arisal of regulatory mechanisms and in the organization of genes involved in the same metabolic route. Several theories have been proposed to explain how the metabolic routes have been assembled. Even though it is possible that different processes might explain the origin of metabolic routes, a large body of data concerning both sequence comparison and "directed evolution" experiments strongly supports one of them, that is the *patchwork assembly* theory. According to this idea, the extant metabolic routes are the result of the serial recruitment of relatively small, inefficient enzymes endowed with broad-specificity that could react with a wide range of chemically related substrates (Jensen, 1976). An excellent study-model is represented by histidine biosynthesis. There are many clues indicating the antiquity of this pathway, suggesting that it was completely assembled before the appearance of the last common ancestor and that its origin probably occurred in the early stages of molecular evolution. The availability of completely sequenced genomes from different (micro)organisms belonging to the three cell domains permitted a deep analysis of *his* genes, which revealed that paralogous gene elongation and duplication events occurred frequently and that they played a major role in shaping the pathway. Moreover, we found that (at least) seven *his* genes underwent different gene fusion events in some bacterial and eucaryal lineages, but not in Archaea, suggesting that the ancestral *his* pathway was constituted by mini-genes which underwent different rearrangements during evolution. Data obtained also suggested that some *his* genes are the descendants of genes encoding less specific enzymes, supporting the Patchwork hypothesis.

INTERACTION OF PEPTIDE PrP(92-138) AND MINERAL SURFACE

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We know, right now, that Prion pathogenic PrPsc could remain and contaminate soil for many years. Animals are infected through an airway, inhaling minerals present in dust/soil particles. This route which is a minor pathway has a more likely path, for ruminants, with the relative gastrointestinal absorption of minerals being much more plausible.

After observation of experimental PrPsc interaction on mica-muscovite (Vasina), we endeavour to understand how the mechanism of strong binding of the pathogenic peptide with the clay mineral surface is formed.

Starting from the PrPsc structure (Govaerts) we provided Molecular Dynamics computations to keep only the infection's moiety structural sequence of the PrPsc, say, PrP92-138. Molecular Dynamics was done with explicit water, therefore solvating the peptide, in a water box in contact with the cleavage mineral plan. A selection of a few structural orientations for the peptide, toward the clay mineral, was computed to select the best orientation giving a good explanation. A simple Montmorillonite without any "cationic substitution" to provide a 2D isotropic surface (pyrophyllite) was built. Then the cleavage plan was equilibrated by K^+ ions.

The beta helix of the PrPsc (pathogenic Prion) was not the best orientation to make a strong anchoring, but the peptidic surface holding LYS and HIS amino-acid residues was the best orientation to make strong adhesion. A few strong hydrogen bonds were computed, giving a stationary adhesion able to be stable for a long time. The formation was progressively stronger as K^+ ions were removed, from the mineral surface, favoring successive hydrogen bonds between LYS or HIS to the surface oxygen atoms of the clay siloxane cavities, so opening a new binding formation. During one nanosecond, 10 hydrogen bonds were formed, and oscillated around stationary distance and binding energy.

Phyllosilicates (~silicates too) are good models for interstellar dust mineral. Small peptides adhering to dust mineral (IDP too) should be a starting point for a better knowledge of the molecular mechanism for interstellar dust in forming the organic-mineral association.

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SOFTWARE CONSTRUCTOR 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. ChemPAK package consists of network database, computational modules and visual interface. User can create and edit systems of chemical equations with unlimited number of equations, translate systems of chemical equations to systems of ODE, add some new equations to the translated system and solve this system by using one of ChemPAK computational modules. Computational modules group consists of modules for PC and modules for cluster supercomputer. ChemPAK has some additional features for automatic generation parallel realization of code for ordinary differential equations (ODE) computational modules. The package was tested on the system of 8000 chemical equations. Total time of preparation of data and translation to system of ODE was approximately 10-15 minutes on PC.

The problem of modeling kinetics of Butlerov reaction in protoplanetary disk was solved with using of ChemPAK. Butlerov reaction consisted of 44 reversible chemical equations. Kinetics constants for this system were taken from experimental data.

Testing of ChemPAK package shows the efficiency of modeling of evolution processes of substance. This package can be used for solving problems of abiogenic synthesis of prebiotic compounds and for modeling of biological hierarchical systems.

UNDERGROUND BIOSPHERE AND ISOPRENOID HYDROCARBONS

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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. In accordance with local conditions and faults by which such fluids were coming they must have contained for some time various nonequilibrium compounds (fragments of hydrocarbon molecules, radicals, light hydrocarbon compounds with oxygen, hydrocarbons with multiple bonds), which in the course of fields formations were transformed into more stable compounds typical of hydrocarbon deposits. 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. Bacteria communities destroying oil hydrocarbons develop in oil deposits in close relation with the arrival of molecules which are oxidants coming to the deposits from the surface or a nearby reservoir. The process of oil deposit formation in terms of feeding microorganisms like *Methanobacterium thermoautotrophicum* and *Methanopyrus kandleri* is an income of feeding matter, which comes not from the surface but from deep underlying rocks.

Though in oils, more than one thousand biomarkers were discovered, the two types including chain isoprenoids of phytane structure and polycyclic isoprenoids play the major role. Originally those biomarkers were associated solely with plants but at present it has been shown that they are synthesized by bacteria in great amounts. It is estimated that hopanoids (polycyclic isoprenoids) are formed in the membranes of eubacteria, while phytanes and biphytanes (chain isoprenoids) are formed in archaeobacteria membranes.

The distribution of oils with depth obeys a certain regularity. Most deep-seated oils and gas condensate contain a very small amount of isoprenoid biomarkers, which makes less than 1 per cent. These oils can contain only micro amounts of biomarkers taken from scattered organic matter and the original set of pseudobiomarkers similar to those discovered in carbonaceous meteorites. Major components of such oils are n-alkanes. Optical activity in the oils of this kind is not manifested.

Less deep-seated oils with significant amount (more than 1 per cent) of chain isoprenoids of the type of phytane, pristane and their homologues are generated with deposits forming in rock mass in the presence of archaeobacteria consuming geofluid as substratum and in this case the temperature in which they develop may be more than 100°C.

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As a result, chain isoprenoids of the membranes of those bacteria find themselves in the oil. It is essential that the above-mentioned biomarkers formation is simultaneous with the formation of oil deposits and is not their further transformation after the genesis.

Oils that occur higher enriched with polycyclic hydrocarbons experienced subsequent bacterial oxidation by eubacteria and archaeobacteria community. Considerable amounts of hopanoids originated from eubacteria membranes testify to the development of eubacteria in oil reservoir at increased temperatures (but not more than 60 °C) and from the change of the relationship between hopanes and steranes in a deposit we can judge about the degree of development of bacteria. At this stage the decomposition of n-alkanes takes place.

BIOGEOCHEMICAL CYCLE OF METHANE IN EXTREME WATER SYSTEMS

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At the beginning of planet development on historical geological data the atmosphere of the Earth consisted mostly of carbon-dioxide, carbon-monoxide, methane, ammonia, hydrogen sulfide and hydrogen. It is assumed that gasotrophic prokaryotes played a sufficient role in biosphere evolution, where autotrophic methanogens and methane oxidizing bacteria took an active part. In extreme environments of terrestrial hydrotherms of islands of Pacific Ocean and Baikal rift zone, soda and salt lakes of Central Asia and Lake Baikal was found an intensive activity of both microorganisms group. In water, bottom sediments and microbial mats of those environments it was found significant abundances of cultivated and non-cultivated methanogens and methane oxidizing bacteria (Namsaraev and Zemskaya, 2000). The rate of biogenic methanogenesis reaches $543.7 \mu\text{l CH}_4 \text{ dm}^{-3} \text{ d}^{-1}$. In these extreme environments main part of methane is formed from CO_2 and H_2 . The bacterial oxidation of biogenic and volcanogenic methane is appeared both in aerobic and anaerobic sediments. The bacterial methane oxidation rate under aerobic conditions is $1180 \mu\text{l CH}_4 \text{ dm}^{-3} \text{ d}^{-1}$ and under anaerobic conditions – $12 \mu\text{l CH}_4 \text{ dm}^{-3} \text{ d}^{-1}$. In the upper layers of sediments of methane hydrate regions of Lake Baikal destruction of methane hydrates is observed. During this process the methane of methane hydrates are consumed by methanotrophic community. From 18 to 98% of methane carbon is oxidized to CO_2 , from 2 to 82% of methane carbon is converted to biomass and exometabolites. Metabolites and biomass of methanotrophic bacteria serve as a basis of trophic chain in the places with active methane oxidation in Lake Baikal. The data on definition of isotopic composition of organic matter of benthos animals ($\delta^{13}\text{C} = -61.2 \div -66.0\text{‰}$) and bottom sediments ($\delta^{13}\text{C} = -44.2 \div -49.5\text{‰}$) testify to this.

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THE VENDIAN BIODIVERSITY CHANGES: A VIEW FROM THE WHITE SEA

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The paper represents some results of taxonomic and statistical study of the Vendian Fossils Collection accumulated by the staff of the Laboratory of the Precambrian Organisms (PIN RAS) after thirty years of paleontological and stratigraphic research in the White Sea region. Only part of the Collection – over 3100 specimens from 20 stratigraphic levels - is put into the database so far. The Vendian shallow-water siliciclastic succession (>600 meter thick) has preserved a uniquely rich fossil record of the soft-bodied invertebrates, bioturbations, megascopic algae, organic-walled microorganisms, and bacterial mats. Time range of the documented fossil record goes well beyond the radiometrically dated interval 558-555 Ma. The stratigraphic distribution of the fossil taxa is controlled by the taphonomic, paleoecological and paleoclimatic factors that is reflected in the step-wise mode of the biodiversity change, punctuated occurrence ranges of the taxa, and severe alterations in the structure of the successive faunal communities preserved *in situ*. Distribution of the cosmopolitan taxa may be also related to the changes in the paleobiographic connections of the Vendian palaeobasin. Beside, the fossil records of the fauna and flora are represented in different degree. Nevertheless one can see the distinct trends in biodiversity. The metazoans diversity shows gradual growth followed by a leap, then by a period of stability, and then, by some decline by the end of the fossiliferous Vendian succession in the region. On this background we observe an increasing portion of the bilaterians represented by the body fossils and bioturbations. Decline in biodiversity by the end of the Vendian succession may be related to the regressive trends and to the change from the marine to the brackish environments.

The primary producers making the base of the food pyramid in the Vendian Ocean are represented by the cyanobacteria, bacterial mats, diverse eukaryotic phytoplankton and macroscopic algae. Biodiversity dynamics of the photosynthesizing eukaryotes and that of the metazoans went not in the concert during the Vendian. Maximum diversity of the tissue-grade algae is documented at the base of the succession (prior 558 Ma) marked by low metazoan diversity. On the contrary, the major leap in the metazoan diversity corresponds to the domination time (between 558 and 555 Ma) of the cyanobacterial benthic communities with low participation of the eukaryotic algae. The revealed biotic trends in addition to the high variety of the fossil groups provide a solid basis for the biostratigraphy of the Vendian as well as for the paleoecological reconstructions. The study is supported by the Program 18 of the RAS Presidium and by the Russian Foundation for Basic Research (Grant 05-05-64825).

THE PRIMORDIAL METABOLISM: AN ANCESTRAL COMMON ROUTE FOR LEUCINE, ARGININE, AND LYSINE BIOSYNTHESIS

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It is commonly assumed that early organisms lived in an environment rich in organic compounds spontaneously formed in the prebiotic world (Oparin – Haldane theory). Those primordial organisms had no need for developing new and improved metabolic capabilities since most of the required nutrients were available. However, their increasing reproduction would have led to the depletion of essential nutrients imposing a progressively stronger selective pressure favouring those microorganisms that had become able to synthesize by themselves the nutrients whose concentration was decreasing in the primordial soup. Thus, the origin and evolution of basic biosynthetic pathways represented a crucial step in cellular evolution, since it rendered primordial cells less dependent on the external source of nutrients. The growing number of completely sequenced genomes can give useful hints to disclose the origin and evolution of metabolic pathways and the possible interrelationships between different ancestral routes. In this context, the comparative analysis of the structure and the organization as well as the phylogenetic analysis of genes belonging to the same route from (micro)organisms belonging to three cells domains (Archaea, Bacteria and Eucarya) represents a very powerful tool. The lysine, arginine, and leucine biosynthetic pathways represent interesting study-models for the following reasons: i) two apparently unrelated pathways have been characterized for the anabolism of lysine, that is the α -aminoadipate (AAA) pathway and the diaminopimelate (DAP) one; ii) genes belonging to the AAA and the DAP pathways are evolutionary linked to those involved in leucine and arginine biosynthesis, suggesting that the assembly of both the DAP and AAA routes might be explained as the outcome of a series of gene duplication events followed by specialization; iii) since the DAP biosynthetic pathway also provides essential molecules that can be found in the cell walls of extant bacteria (LL-diaminopimelate and meso-diaminopimelate), the comparative analysis of this metabolic route in the present-day (micro)organisms might also shed some light on the origin and evolution of bacterial cell wall. In this work an analysis of all the available genes involved in the three biosynthetic routes was performed, allowing to trace their history, to identify their ancestor pathways and the ancestral interrelationships occurring between them.

THE ROLE OF CYANOBACTERIA IN PRECIPITATION AND TRANSFORMATION OF DIFFERENT MINERALS

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The studying of the role of cyanobacteria in relict microbial communities with the analogy of the latter with ancient stromatolites is of supreme interest for the actual interpretation of geological and paleontological data.

In hydroterms of Kamchatka and Kuril the thermophilic mats and modern stromatolites were found. Process of silicification of different cyanobacteria was studied. The silicification was found to be dependent on species morphology and physical form of silica.

Alkaliphilic communities were found in soda lake Khilganta (Buryatia). Laboratory experiments showed the effect of alkaliphilic cyanobacteria *Microcoleus chthonoplastes* on the formation of magnesium calcites. The structure of sediments and shape and size of carbonate crystals depend on the experimental condition of cyanobacterial growth (in light or darkness). The formation and transformation of different carbonate mineral were studied in different conditions (photosynthesis, oxy- and anoxygenic destruction). The formation of dolomite domes is carried out in anoxygenic zone. The exomethabolites of cyanobacteria accelerate process of dolomite formation.

Process of carbonatization was studied on alkaliphilic cyanobacteria *Euchalothecae sp.* isolated from soda lake Magadi (Kenya). TEM-studying shows formation of different carbonate mineral. Unusual interaction of cells and mineral trona was found. A possible mechanisms of involvement of enzyme Carbonic Anhydrase in carbonatization of cyanobacteria is discussed.

Another model of a relict association is cyanobacterial mats from the hypersaline lagoons and shallow waters of saline lake of Crimea. Stromatolites were found near saline lakes Marphovskoe and Tobechikskoe. The comparative study showed the analogy between ancient stromatolites and modern mats structure in these lakes.

Process of phosphatization of *Microcoleus chthonoplastes* was also studied. The sequence of process (phosphatization of trichom or sheath) depends on the content of different polyphosphates in the cells. The laboratory modelling of mineralization processes and formation of the structures similar to stromatolites and oncolites in combination with the study of fossilized material proves the participation of cyanobacterial communities in the formation of phosphates and other minerals.

The study was supported by the Program of the Presidium of the RAS "Origin and Evolution of the Biosphere".

GENESIS OF SHUNGIT-LIKE ANTHRAXOLITE OF BAKYRCHYK DEPOSIT (EASTERN KAZAKHSTAN)

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The solid bitumens are well known in region of Kysyl fracture zone (KFZ) in Bakyrchik district. They correspond to higher anthraxolites on metamorphism degree. This deposit belongs to Late Paleozoic type of nonstratified linear-metamorphic shungite ore [1]. The organic substance migrated in rocks, and carbon content increases proportionally to a degree of rocks penetration. Temperature of the processes of Bakyrchik district carbon-rocks formation is characterized by values not higher than 350°C, and pH of surroundings changed from three to five [1]. In general, a source of bitumen organic substance is a debating point. In particular, there are two probability of KFZ carbonaceous substance origin: biogenic and abiogenic [1]. One way to determine a source of organic substance is amino acids analysis. We carried out the analysis of amino acid enantiomers extracted from rocks during acid hydrolysis by gas chromatography. Significant prevalence of L-forms of amino acids over D-forms in Bakyrchik anthraxolite was determined. It is the evidence of biogenic origin of the researched organic substance. High concentration of tyrosine can testify to significant bacterial oxidation of organic substance (biodegradation) [2]. By scanning electronic microscopy we found some formations in Kazakhstan anthraxolite which on their morphological and material features can be interpreted as fossil nanobacteria. Process of bacterial oxidation of Bakyrchik anthraxolite was putted on primary organic substance during migration processes.

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**EVOLUTION OF BIOGERM COMMUNITIES IN THE MIDDLE-UPPER
MIOCENE OF THE EUXINIAN-CASPIAN BASIN
(EASTERN PARATETHYS)**

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Biogerm constructions appeared repeatedly in the Middle and Upper Miocene (Early Chokrakian through the beginning of the Pontian) in the epicontinental seas of the Euxinian-Caspian Basin. Constructions of varying form, size, and composition of the framework builders formed in basins of different types (as defined by Neveeskaya et al., 2005) ranging from the marine with salinity close to normal to enclosed semi-marine ones. The marine Early Chokrakian and semi-marine Sarmatian basins have yielded the biggest and most original biogermes, up to 2-3 m in diameter and with Bryozoa as main framework-makers, which were characteristic of the shallow waters not below first tens of meters. The Early Chokrakian bryozoan biogermes were formed mainly by the bryozoan colonies dominated by *Membranipora* and *Schizoporella*, red algae, calcareous polychaetan tubes, and mollusks. The Sarmatian bryozoan biogermes were much impoverished being usually constructed by the only bryozoan species *Membranipora lapidosa* combined with Cyanobacteria and rare mollusks. In the long living (~ 4.4 myr) Sarmatian Basin, the bryozoan biogermes appeared at its different stages but mainly in the middle and the end of its existence. Some of these biogermes got adapted for and persisted in the changed environments of the beginning of the following Maeotian Basin. That time *M. lapidosa* has been replaced by *M. elliptica*, and the mollusk participation become considerable. Among the smaller biogermes (generally 0.5 m and less in diameter), noteworthy are stromatolithes of the Later Chokrakian and Karaganian formed in the stressed environments of the marine regime turning into semi-marine. Biostromes made by nest-like accumulations of complete shells of *Cryptomactra pesansensis* (Bivalvia), serpulid tubes, small gastropods, foraminifers, and oncoliths of supposedly cyanobacterial or rhodophyтан origin, are recorded earlier in the Middle Sarmatian at Zelensky Mt. in Taman' Peninsula and at Cape Pont Takyl in Kerch Peninsula. These biostromes has been formed at more depth in the sublittoral. In the brackish Late Maeotian Basin the cyanobacterial and serpulid nodules have been formed locally.

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ORIGIN AND EVOLUTIN OF BIOMINERAL SYSTEMS IN COASTAL-SEA ZONES OF PETER-THE-GREAT BAY

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Mineral matter and biota interact in the biosphere persistently through origination and degradation of biomineral systems. In the coastal-sea zone of the Peter-the-Great Bay, these processes go quickly and manifest themselves contrastingly. Hydrodynamics, composition of mineral deposits, and mobile sea-fresh water geochemical barrier are responsible for the long persistence and the extent of development of the systems.

Optimum conditions for their development include closed shallow-water bays, clayey deposits, and localization in the tidal zone.

The results of the phase diffractometric analysis of samples and determination of diatomic algae have been reported at the International Workshop "Biosphere Origin and Evolution" (2005, Novosibirsk, Russia). This paper puts forth the minor-element composition of samples and analyses of them on microanalyser JXA-8100 and scanning electron microscope EVO-50 XVP. The biomineral systems originate when the diatomic algae began to populate the estuarine deposits. The diatom mucus favors the deposition and accumulation of pelitic matter. The system, intensively sorbing minor elements, arises. Rather long existence of such system results in its thickness increase with diatom dying off and following work of bacteria.

The vital functions of sulfur-reducing bacteria are fixed by the formation of nest-like accumulations of pyrite framboids ($d < 1 \text{ mkm}$) in the samples from the tidal zone. Spatial relation of framboids with diatoms has not been established, though correlation of their amounts is observed. In this way the curing muds are developed. Regularly reinforcing flows and waves carry the mud into deep parts of bays and gulfs.

Outwardly similar to them black deposits originate in the bays overgrown with *Zostera*. As a rule, grass grows on the sandy bottom. When it dyes off and decays, the sand is soaked with fine-dispersed detritus. In these muds, diatoms are few, clayey minerals are almost absent, significant enrichment in boron is observed, and there are no pyrite framboids. Pyrites are absent also in the young muds of the river mouths, though they are enriched in diatomic algae. Gaseous hydrogen sulfide occurs in both types of mud, but the grass detritus decays, probably, under the action of other anaerobes.

EXON-INTRON STRUCTURE EVOLUTION OF FUNGI GENES

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In completely sequencing genomes of the lower fungi the share of genes containing introns changed from 0.7 up to 97.0%: *E. cuniculi* (0.7), *C. glabrata* (1.5), *K. lactis* (2.4), *E. gossypii* (4.5), *S. cerevisiae* (4.5), *D. hansenii* (5.0), *Y. lipolytica* (10.6), *U. maydis* (37.8), *S. pombe* (45.6), *M. grisea* (69.2), *A. fumigatus* (78.0), *N. crassa* (79.6), *C. neoformans* (97.0). The genome size of these fungi changed from 2,497 tpn (*E. cuniculi*) to 38,656 tpn (*M. grisea*) and chromosome number changed from 3 (*S. pombe*) to 23 (*U. maydis*). The density of genes decreased from 799 to 209 genes/Mbp at increasing of genome size. The share of genes containing introns corresponds to the distribution of the lower fungi by the phylogenetics lineages. For example, *K. lactis*, *E. gossypii*, *S. cerevisiae* and *D. hansenii* belong to Saccharomycetaceae and these genomes contain from 2.4 to 5.0% intron genes. The *M. grisea*, *A. fumigatus* and *N. crassa* belong to Pezizomycotina and contain 69.2 - 79.6% intron genes. The *E. cuniculi* and *C. neoformans* belong to distant taxons Microsporidia and Basidiomycota accordingly. They have greatly distinguished shares of intron genes - 0.7 and 97.0%. There is close correlation between exon length in one-intronic genes and the share of intron genes in 13 studied genomes of fungi despite of large difference of the share of intron genes in them. Average exon length changed from 193 to 880 n in one-intronic genes at correlation coefficient (r) 0.98 ($p < 0.001$). Genomes *E. cuniculi*, *C. glabrata*, *K. lactis*, *E. gossypii*, *S. cerevisiae* and *D. hansenii* have only one-intronic genes. The genes with larger intron number appear if the share of intron genes in genomes increases. In genomes having the share of intron genes about 40% and more there are genes with 10 and more introns. Average exon length decreases at increase of intron number in genes. These changes of exon lengths take place at decrease of the share of exon lengths more than 400 n and at increase the exons with length 60-100 n. The correlation between the sum of exon lengths (L_{ex}) and intron number (N_{in}) in genes is established, it is described by regression $N_{in} = aL_{ex} + b$, where a and b are the parameters of regression. There is the similar correlation between intron numbers in genes and gene length (L_{gn}) and it is described by equation $N_{in} = cL_{gn} + d$, where c and d are the parameters of regression. The correlations between the sum of exon lengths, gene lengths and intron numbers in genome higher organisms (*A. thaliana*, *C. elegans*, *O. sativa*, *H. sapiens*) were similar to the correlations of fungi genomes.

GLACIOEUSTATIC CYCLES AND CORRESPONDENT BIOTIC CHANGES IN THE LATE CARBONIFEROUS EPEIRIC SUCCESSION OF MOSCOW BASIN

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Introduction

A Late Carboniferous shallow-marine basin crossing the East European Craton between the Voronezh High on South and the Arctic Shelf on North has been regarded as a Volga-Kama or Moscow Basin. The width of this subtropical epeiric sea attained 1500 km during the Moscovian Epoch. The Moscovian-Kasimovian sedimentary succession under study provides the detailed record of high-frequency sea-level fluctuations and correspondent biotic changes, the former apparently driven by Gondwanan icesheet pulsations.

Cyclothems & unconformities

Seven major meter-scale cyclothems have been documented in the late Moscovian interval. These cycles are tracked at the distance of ca. 300 km in the southern Moscow Syncline and the Oka-Tsna Swell. The Myachkovian cyclothems are recognized in ca. 1000 km to the North in the western Mezen Syncline. Superposition of several orders of sea-level oscillations is evident from the levels of shoaling and 'ephemeral' subaerial exposure complicating the main transgressive and regressive trends. The major cyclothems are bounded by lowstand subaerial unconformities (diastems, geosols) that are used as principal correlative horizons (Kabanov and Baranova, 2007). The Kasimovian of the southern Moscow Syncline counts ca. 8 cycles of the same magnitude similarly complicated by minor pulsations (Alekseev et al., 2004).

Cyclothem paleoecology is being quantitatively tested at the late Moscovian interval with most detailed evaluation of the Domodedovo Cyclothem (Kabanov et al., 2006). Deepening and shoaling trends are revealed by lithofacies trends and decrease/increase in abundance of micritized grains, aggregates, oncoids, phylloid and dasyclad algae, conodonts, and ostracods. Facies shifts in response to sea level changes is also evidenced by distribution of brachiopods, bryozoans, and other macrofossils. The shallow subtidal normal marine, relatively oligotrophic intervals feature photozoan oryctocoenoses. Disphotic or even aphotic depths (? 50 m) with heterozoan benthic communities attained at highstands. A peculiar low-

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diversity community with mass brachiopods *Meekella* and the algae *Ortonella* established in the restricted lagoonal-to-intertidal settings.

Perspectives

The succession under study can be employed as a reference for glacioeustatic record with high potential for correlation with coeval cyclic successions of the World. The magnitude of sea-level rise can be appraised by quantifying the depth-sensitive particles such as green algae and micritized grains. The significant physico-chemical decoupling between Moscow seaways and the ocean is expected (Holmden et al., 1998). Extensive soil areas affected by transgressive abrasion must have caused eutrophication events, which can be revealed geochemically and palaeoecologically.

Acknowledgements

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**PALEONTOLOGICAL AND GEOLOGICAL EVIDENCE FOR
EXISTENCE OF A NEAR-VENT BIOTA IN THE EARLY CAMBRIAN:
AN EXAMPLE FROM THE VOLCANOGENIC SULPHIDE-ORE
FORMATION OF TUVA, EAST SIBERIA**

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Geological history of vent ecosystems constitutes a special interest in the studies of evolutionary process patterns – the data accumulated to date on taxonomic composition, evolution rates and structural-functional organization of these ecosystems in both recent and ancient oceans suggest that the vent ecosystems can be viewed as an alternative model of evolution of life (Kanygin 2002). The vent ecosystems are characterized by: 1) endogenic chemotrophic nature of primary production (as opposed to exogenic photosynthetic nature of aquatic and terrestrial ecosystems); 2) intimate connection with high-temperature hydrothermal vents confined to zones of volcanic activity (lava eruptions) and sulfide mineralization; 3) autonomous functioning and local oasis-like distribution amongst normal marine biotopes; 4) anomalously high biological productivity; 5) bacteriotrophic basis of trophic chains; and 6) punctuated ephemeral existence (in geological time scale). Type examples of fossil near-vent communities are known from the Silurian and Devonian of the Urals based on detailed paleontological, geochemical, petrological-mineralogical and facies-lithological studies. Similar type biotas are known from volcanogenic-hydrothermal formations of Paleozoic, Mesozoic and Cenozoic age. The fossil near-vent biota from the Kyzyk-Tashtyg Pb-Zn sulphide deposit of Tuva appears to be one of the oldest known. The associated archaeocyaths *Nochorocyathus khemtschikensis* Vologdin, 1940, *N. polyseptatus* Vologdin, 1940, *Dokidociathus* sp., *Rotundocyathus* sp., together with algae *Renalcis* sp. and *Epiphyton* sp. establish the Lower Cambrian age of the biota. The structural, petrogeochemical, facies, mineralogical and geomorphological indicators point to the similarities between the archaeocyaths- and algae-bearing formation of Tuva and the modern and ancient mounds formed in oceanic geodynamically active zones around high-temperature hydrothermal vents (“black smokers”). Taxonomic composition of the Early Cambrian near-vent biota corroborates a hypothesis of the origin of the heterotrophic tier in endogenic ecosystems through trophic adaptations to novel food resources at the cost of immigrants from the adjacent biotopes at each new evolutionary stage (Kanygin 2005). This work was supported by the Russian Academy of Science Program 18 “Biosphere Origin and Evolution” and the Russian Foundation for Basic Research Grant no. 05-05-64509.

**BIOCHEMISTRY OF LOWER PALEOZOIC MICROCEANOSIS
IN COMPARISON WITH BIOTA OF PROTEROZOIC
AND MESOZOIC MARINE BASINS**

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Lower and Middle Cambrian deposits of the Kuonamka complex occur in the east of the Siberian Platform. Its oil-generating rocks are anomalously enriched in organic matter (OM). Normal alkanes, isoprenoids and cyclohexanes have been identified. Analysis indicated the lack of significant concentrations of 12-, and 13-monomethylalkanes which are typical biomarkers of oils, generated by Upper Proterozoic deposits.

Homologs of sterane series (m/z 217, 218) have been determined. Ethylcholestane is dominated, as a rule, in the distribution of C₂₇₋₂₉ hydrocarbons. Triaromatic steroids (TAS) in the range C₂₀ to C₂₈ (m/z 231) have been identified, with TAS₂₈ being in maximum concentration. High contents of ethylcholestane and TAS₂₈, which are characteristic of biochemistry of microceanosis of Cambrian seas, seem to have been inherited from Precambrian biota. Besides, analysis of peaks in the fragmentograms m/z 245, 259, and 273 has shown that OM contains alkylated triaromatic steroids. Tricyclanes, tetracyclanes, hopanes and homohopanes have been identified in the fraction of terpane hydrocarbons (m/z 191). The distributions of homologs of these biomarkers are typical of Proterozoic and Phanerozoic aquagene organic matter. In particular, the OM composition of the Kuonamka Formation is similar to that of mainly aquagene OM of the Upper Jurassic Bazhenov Formation of West Siberia in principal molecular parameters. The difference is in slightly higher concentration of ethylcholestane. This fact allows the conclusion that initial producers of marine basins poorly evolved at the biochemical level.

The findings of saturated and aromatic hydrocarbons of bicyclic structure (m/z 123, 156, 179, 183, 193: sesquiterpanes; 1,6-dimethylnaphthalene; and cadilene) from the OM of the Kuonamka Formation are of special interest. These chemofossils are related to biosynthesis of higher plants usually. In the examined samples, their concentrations are low, but, nevertheless, they are unambiguously identified. Probably, as early as the Early Paleozoic, lipids of algal organisms began to take the features of biochemical habit, being characteristic of flora of later epochs.

DOUBLE FACED GLYCINE

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According to the reference data, glycine amino acid (glycocol), or – aminoacetic acid $\text{H}_2\text{N-CH}_2\text{-COOH}$ forms by the albuminolysis and synthesizes in organism. It is a predecessor of bioactive compounds: purin, porphytin, glutathione, kretine, hydroxiacetic and hippuric acids.

Glycine is known to be a base of collagen (an organic constituent of physiogenic biomineral formations of human being). Glycine prevails in amino acid composition of conchologin of shells and pearls. Studies of ammonite composition from Jurassic deposition have shown that according to the percentage, aminoacetic acid prevails over the rest of amino acids. It is significant for pathogenic biomineral formations (urolites, cholelites), which combine radial-beam and concentric types of the structure, to have considerable contents of glycine. It is a base of albumen in pigmental cholelites. Its content in gall-bladders can reach more than 65% of sum total of amino acids. The percentage of glycine, glutaminic acid in enamel of human being coincides with their content in uric acid and cholesterol gallstones. Studies of pathogenic and a physiogenic biomineral formation indicates more similarity, than differences in composition of amino acids between two groups.

The similarity in percentage of glycine between two groups of biomineral formations can be explained in that way. First of all, glycine is considered to be one of the abiogenous amino acids, formed from the prime elements (CO_2 , N_2 , H_2 , CH_4), which create the prerequisites for forming of the protoorganisms and for coevolution of the living and mineral worlds. In that way, its constructive function appears by forming of skeletal organisms. Secondly, according to our results, glycine creates crystallization medium in living organism, where formation of neogenic minerals occurs, and simultaneously, in the process of a biochemical transformation it turns into a mineral component of pathogenic biominerals.

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GENETIC FAMILIES OF UPPER PROTEROZOIC OILS AND THEIR RELATION TO BIODIVERSITY IN THE LATE PRECAMBRIAN

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Upper Proterozoic oils of the Siberian, East European, Arabian and Australian platforms are enriched in the light carbon isotope ^{12}C and have essentially aliphatic composition dominated by normal alkanes. Based on the composition of biomarker hydrocarbons, all the oils were divided into two families. Some of the oils from the East European, Australian and southwestern Siberian platforms were assigned to the first family. They are characterized by the absence of 12- and 13-monomethylalkanes. St_{27} - St_{29} steranes are almost in equal concentrations, low contents of tricyclanes in terpanes, and the $\text{Hh}_{35}/\text{Hh}_{34}$ homohopane ratio <1 . Oils of this family are similar to Phanerozoic marine oils, which are derived from lipids of prokaryotes and protozoan eukaryotes. The second family includes the most widely distributed oils from East Siberia, Oman and some oils from the East European Platform. They are characterized by the sharp predominance of ethylcholestanes in sterane distribution, high contents of tricyclanes in terpanes, and, frequently, the predominance of Hh_{35} homohopanes over Hh_{34} . Most oils of the second family (except the oils of the East European platform) contain 12- and 13-monomethylalkanes in anomalously high concentrations. There are no analogs of oils of this family among Phanerozoic marine oils.

The differences between these families of oils are related to the specific character of biochemistry of lipids of the oldest prokaryotes and protozoan eukaryotes in individual ecological niches of Precambrian seas. Some of such specific characters (12- and 13-monomethylalkanes) have disappeared as early as the Proterozoic and no longer manifested themselves in the Phanerozoic. Other features (e. g. the abundance of ethylcholestanes in marine oils and organic matter) are distinctly traceable later, at least, up to the Devonian. This diversity of biomarker composition in Upper Proterozoic oils could be probably considered as one of the evolutionary stages of biochemistry of living matter.

MORPHOLOGIC PATTERNS OF BIOLOGICAL AND BIOMIMETIC NANOSYSTEMS BASED ON THE SURFACE LAYER OF WATER

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The role of the surface layer (SL) of water is of great importance for the advent of life on the Earth and evolution processes of living matter as well as inexhaustible source of modular clusters of water which are necessary to forming of biopolymer structures. As it was shown previously, the two-dimensional crystal structure of the surface layer of water [1] constructed by the method of modular design from universal "structural units" (20 H₂O molecules, the D_{3d} symmetry) exhibits unique functional properties, which explained: (a) appearance of the surface tension of water and its dependence on the surfactant surface concentration; (b) the mechanisms of gas solubility in water and evaporation of water molecules through the SL of water; (c) impossibility of the transition of the SL of water to ice Ih in small capillaries and thin films; (d) high electroconductivity of the SL of water, formation of double electrical layer, and its penetrability by cations; etc. Moreover, the consecutive dynamic rearrangement of the water SL in the course of self-organization of a Langmuir monolayer on it and bilayer membranes is shown (4 stages of the water SL rearrangement are distinguished). These stages are consistent in the surface area per surfactant molecule with the corresponding experimental values of the inflection points of the Langmuir isotherms. This is important for the understanding of the mechanism of the monolayer self-organization.

In present work, on the basis of this model of the water SL, the possible morphologic patterns of the SL structure are considered such as cylindrical micelles and smooth closed surfaces with a positive Gaussian curvature. The role of the indicated morphologic patterns in the formation of biomineral biomimetic nanosystems and various nano- and mesoporous structures met in nature (bones, wood, vesicles, etc.) is extremely important.

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BIOMARKER HYDROCARBONS IN LOWER PROTEROZOIC SEDIMENTS OF NORTH EURASIA

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Lower Proterozoic organic matter (OM) of schungite-bearing rocks of the Onega synclinorium (the Baltic shield) and carbonaceous shales of Lower Khani graben-syncline (the Aldan shield) is overmature, judging from the low contents of chloroform-extractable bitumens (0.0007-0.021%), pyrolysis results (very low peaks S1 and S2), high concentrations of ¹³C ($\delta^{13}\text{C}$ value averages -25.3‰). Nevertheless, some samples preserved carbon isotope composition peculiar to normal-mature polymer-lipid marine OM (up to -31.4‰). In the extractable bitumens, the n-C₁₆₋₁₇ hydrocarbons have the highest concentrations of normal alkanes, and the CPI in the region n-C₂₂₋₃₀ varies within the range 1.0-2.0; Pr/Ph \leq 1. Besides, the lack of 12- and 13-monomethylalkanes is characteristic. Polycyclic isoprenanes show high concentrations of pregnanes and diasteranes (D/Reg 0.4-0.7), the predominance of St₂₇ cholestane in steranes and Hh₃₄ homohopane over Hh₃₅. High concentrations of tricyclanes (up to 75%) have been determined; the tricyclane index $2 \cdot (T_{19} + T_{20}) / (T_{23} + T_{24} + T_{25} + T_{26}) < 1$. By summing up the obtained data, it could be suggested that the plankton-derived and bacterial initial living matter (distribution of tricyclanes) with the input of marine phyto- and zooplankton (distribution of steranes) was buried in the depositional basin with a low content of carbonates in sediments (high concentrations of diasteranes) and underwent diagenetic transformations in the reducing environments without hydrogen sulfide contamination (Hh₃₅/Hh₃₄ < 1). Similar distribution of steranes and diasteranes was marked in some ancient oils of the Angara-Lena step and the Bakhta megasalient (Siberian Platform), Tishkovskoye field (East European Platform), McArthur basin (Australia), as well as in Lower Proterozoic chloroform-extractable bitumens of the Yenisey Ridge and the Baykit antecline.

MORPHOLOGICAL CHANGES OF GLOBOTRUCANIDS (PLANKTONIC FORAMINIFERS) AS THE RESPONSE TO CHANGES OF PALEOENVIRONMENTS (EARLY-LATE CRETACEOUS)

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During the early-late Cretaceous, the planktonic foraminifers experienced several episodes of major adaptive radiation. Each of this episode was characterized by the appearance of new and varied test morphologies – polytaxic phase. However, several short intervals were characterized by marked declines of diversity and a return to simple test morphologies – oligotaxic phase. Three of these intervals coincided with Oceanic Anoxic Events 1 (Barremian - Early Albian), 2 (Cenomanian - Turonian boundary), 3 (Santonian – Campanian boundary). The end of the Cretaceous (K/T boundary) was very dramatic event in evolution of globotruncanids, when practically 90-95% of them died out. These stages correspond to the subdivision of the Cretaceous into the four evolutionary episodes in the development of globotruncanids: (1) hedbergellid; (2) ticinellid; (3) marginotruncanid; (4) globotruncanid (Longoria, Camper, 1975). The first major adaptive radiation of globotruncanids was in the Aptian. During this interval a great variety of trochospiral forms appeared (*Hedbergella*), as well as the planispiral morphotypes (*Globigerinelloides*) and taxa with radially elongate chambers (*Leopoldina*). By late Aptian time, morphological features such as primitive apertural plates and accessory apertures (*Ticinella*, *Globigerinelloides*) had appeared. After OAE 1 the late Albian-Cenomanian time corresponded with rapid evolution of the family *Rotaliporidae* with diverse morphological features. *Rotalipora* species had a combination of relatively wide umbilicus, sutural supplementary apertures, keel, flattened chambers, and spiral-convex test (Gorbachik, Kopaeovich, 2002). After brief decline in globotruncanids diversity occurred during latest Cenomanian-earliest Turonian time (OAE 2) the new rapid diversification of the keeled taxa of the genera *Marginotruncana* and *Dicarinella* began (double keeled test, the main aperture with portici, and supplementary apertures). *Globotruncana* was derived from *Marginotruncana* by migration of the primary aperture towards an umbilical position and the replacement of the portici by tegilla. The evolution took place during Santonian and Early Campanian. The evolution of the *Globotruncanita* can be summarized as follows: at the end of the Santonian the primary aperture becomes umbilical in position, although the umbilical system remains composed of portici in contrast with that of *Globotruncana* (Caron, 1985).

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The species that became extinction at the K/T boundary were large, complex tropical and subtropical forms that dwelled in deep and intermediate water depths. The small cosmopolitan surface dwellers with simple morphologies survived and gradually disappeared in the early Danian. The K/T disappearance constitutes the most sudden extinction event in the history of planktonic foraminifers. However, it cannot be fully excluded that the earliest Danian forms may have their ancestors certain primitive and more resistant terminal Maastrichtian form.

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MACROFAUNA AND CHEMOFOSSILS OF THE CARBONACEOUS ROCKS

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The complexes of fauna and chemofossils from Kuonamka Formation (Molodo River Section) were investigated under the project «Research of fauna and chemofossils from Cambrian of the Siberian Platform». The complexes of fauna are submitted mainly by trilobites. Other groups of fauna (brachiopods, hyolithes) are very rare. Some layers contain a number of trilobites. Also take place intervals, where there are only single samples of the trilobites. Trilobites are submitted mainly by Agnostids and Oryctocephalids. The representatives of other trilobites families (Paradoxididae, Ptychopariidae and other) are present in insignificant quantities. The investigation of organic matter (OM) has shown that the rocks could be divided into two groups according to organic total carbon content (TOC) and chemofossil composition. The first group of highly carbonaceous black shales contains more than 10% TOC and is characterized by bimodal distribution of n-alkanes and predominance of tricyclanes over hopanes in the terpane fraction. The OM of the second group is characterized by lower content of TOC (< 10%), unimodal distribution of n-alkanes and higher concentrations of total hopanes as compared with tricyclanes. The alternation of the first and second groups of the rocks was caused by change of biota of Cambrian marine basin. When comparing the distribution of macrofauna remains with chemofossils in Cambrian deposits, it has been revealed that high-carbonaceous rocks are enriched with trilobite remains. The occurrence of these rocks in the section corresponds to the peaks in the curve of variation of carbonate carbon isotope composition. The reference intervals of the section could reflect the stages of favorable conditions either for fauna evolution in Cambrian seas, or for preservation of anomalous amount of OM and macrofauna imprints in sediments.

STRUCTURAL EVOLUTION OF NATIVE BITUMENS UNDER THE RADIATION CONDITION (BY IR-SPECTROSCOPY DATA)

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Knowledge of the structure of natural bitumens subjected to radiation impact is of significant fundamental and practical interest. However, the mechanism of structural transformations in them under the impact of high radiation doses, still remains unknown. It is undoubted that the main role in structural transformations of bitumens plays the temperature. At the same time, bitumens associate frequently with uranium-bearing minerals (thucholite). Consequently, the decay of radioactive elements can contribute much to structural transformations of bitumens. We have studied changes in the molecular structure of bitumens constituting the carbonization series (asphaltite–kerite–anthraxolite) under the influence of radiation (10 and 100 Mrad) by infrared spectroscopy.

Gamma radiation of up to 10 Mrad of the asphaltite substantially changed their molecular structures. In addition to the predominance of aliphatic components, the content of aromatic structures is also increased in the structures. An increase in radiation dose up to 100 Mrad results in further changes of the asphaltite structure, which are reflected by the substantial loss of some aliphatic, aromatic and heterofunctional groups. The IR spectra of kerites after radiation appeared to be generally identical to each other in terms of the intensity of absorption bands. However, in addition to areas with the aromatic structure, some segments with the aliphatic structure are also present in kerite subjected to radiation of up to 10 Mrad. The high radiation dose (100 Mrad) resulted however in the complete loss of aliphatic groups. Absorption bands disappear as a result of the increase in the carbon content in the bitumen structure and the consequent increase in the share of aromatic rings. Therefore, the IR spectra of anthraxolites after the radiation impact become similar to those of graphites.

The results show that, in addition to temperature, radiation can also affect the process of coalification. Using carbonization series as an example, we have established that traces of the influence of high-energy radiation on a substance are reflected in the modification of its structure and the appearance of features similar to those of graphite.

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THE CONDITIONS OF FORMATION AND FUNCTIONING OF MICROBIAL COMMUNITIES IN CENTRAL ASIA SODA LAKES

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Soda lakes are considered as places of a terrestrial relict microbial community's origin (Zavarzin, 1993). Investigation of shallow Central Asia soda lakes has revealed significant seasonal and interannual changes of hydrological, physical and chemical parameters of water. Annual fluctuations of temperature of air (between +40°C – -55°C) result in significant changes of a salinity and a chemical composition of water. During the droughty period alkaline environment are replaced on salty and then neutral.

Phototrophic and chemotrophic microorganisms formed benthic microbial mats in coastal shallow lagoons of the lakes. The rates of total photosynthesis in lake water reached 11 mg C l⁻¹ d⁻¹, in bottom sediments – 68 mg C l⁻¹ d⁻¹, and in microbial mats - 3860 mg C m⁻² d⁻¹. Dark CO₂ fixation in water of lakes was 1.9-2.7 mg C l⁻¹ d⁻¹, in bottom sediments – 8.6 mg C kg⁻¹ d⁻¹, and in microbial mats 41.4 mg C m⁻² d⁻¹. Values of δ ¹³C of soda lakes organic matter (-15.6 – -25.4 ‰) show that producers use metabolites of organic matter's microbial destruction. Aerobic and anaerobic prokaryotes (abundance of 1000-1000000 cells ml⁻¹) take part in organic matter destruction. The rates of cellulose and protein decomposition are 1-2 % d⁻¹. The highest sulfate reduction rate (69 mg S kg⁻¹d⁻¹) observed in silts at water salinity 3-30 g l⁻¹. The intensity of methane formation was low, up to 80.7 μl CH₄ kg⁻¹ d⁻¹. The main part of organic matter is used for bacterial sulfate reduction. Consumption of organic matter on sulfate reduction was 0.1-54.3 mg C kg⁻¹d⁻¹ and methane formation – 0.2 mg C kg⁻¹d⁻¹.

In the autumn and winter season's activity of microbial community is decreased. Nevertheless, processes of destruction are prolonged in brine under ice at temperature – 8°C that is caused by activity of psychroactive microorganisms and presence of water at a liquid state because of high salt content.

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**SIMULATION OF EVOLUTION IN HAPLOID CELLS COMMUNITY
BY USING THE "EVOLUTIONARY CONSTRUCTOR" PROGRAM**

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An original modeling tool called Evolutionary Constructor has been proposed and described. Evolutionary Constructor combines the advantages of both generalized and portrait modeling and, additionally, provides an option to modify a current model's structure. The evolution of syntrophic communities comprising a closed-loop trophic system with the horizontal transfer of metabolism genes occurring among the communities has been modeled and presented. It has been demonstrated that a prolonged increase in the fitness of any single community that forms part of that closed-loop trophic system of antagonistic communities will eventually lead that system to becoming absolutely dependent on environmental fluctuations. This result challenges the intuitive attitudes that the higher population fitness, the more stability is given to that population. Modeling for a system comprised by symbiotic communities has revealed that horizontal transfer confers a selective advantage not only on the acceptor population (which is up to expectations) but also on the donor population, if dwindled. It has therefore been demonstrated that horizontal transfer can be preserved by selection along evolution even without "selfish genes". Evolutionary Constructor allows any phenotypic character of a population, no matter what encoding is, which extends the applicability of this tool to various processes of information transduction among populations, should these processes appear to resemble horizontal gene transfer.

DYNAMICS OF EVOLUTION AND BIODIVERSITY OF THE MACROSCOPIC ALGAE ON THE PRECAMBRIAN-CAMBRIAN BOUNDARY

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In a recent scientific conceptions it is proposed that during the late Precambrian there was an algal flora gradual appearance of new and more advanced alga, more similar to Phanerozoic forms, rather than their predecessors.

After a detailed review of terminal Proterozoic algal assemblages, it seems that trends of their evolution were rather more complicated and not so gradual. The oldest of the diverse Vendian (Ediacaran) floras is Doushantuo flora. The Doushantuo assemblage includes algae with compact, laminated thalli of tissue-grade organisation. Many Doushantuo taxa are characterized by regular dichotomous branching and the presence of holdfasts or rhizoids for attachment to the substrate. The Laymtsa assemblage (Archyfasma flora) of the Eastern European Platform is contemporary to or slightly younger than the Doushantuo assemblage. Laymtsa taxa demonstrate thalli with tissue organization and differentiation into layers. The younger Redkino assemblage (Eoholynian flora) includes exclusively simpler, crust-like and bush-shaped thalli. A significant part in Redkino assemblage is represented by prokaryote taxa, such as oscillatorian cyanobacteria, which form biofilms. The uppermost Vendian Kotlin assemblage is typified by its Vendotaenian flora and cyanobacterial biofilms. The dominant eukaryotic taxa – members of family Vendotaeniceae - is more primitive when compared with older forms. Biodiversity is low – 1-4 taxa versus around 20 in the Doushantuo assemblage. The highly organised algae and diverse algal assemblages appear in geological record again only in Cambrian.

Thus there is a stage that falls outside the gradual trend for the overall evolutionary “progress” of eukaryotic algae. This stage corresponds to the second part of the Upper Vendian (558-543 ma). To understand the causes for this phenomenon further research is needed into such abiotic factors as the increased oxygenation of the environment, the brief periods of glaciation and related variations in carbon concentrations, and tectonics that affected the wide distribution of epicontinental seas with restricted water circulation.

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STUDYING THE INFLUENCE OF MICROORGANISMS ON ADSORPTION OF INORGANIC PHOSPHORUS ON SEDIMENTS OF LAKE BAIKAL

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Inorganic phosphorus in Lake Baikal is adsorbed on iron hydroxide and thus buried in the sediments. However adsorption of phosphorus is reversible [Likhoshvay et. al, 2006]. As phosphorus is one of the major nutrients, it is necessary for all live beings and microorganisms in particular. We attempted to estimate how much phosphorus is accumulated in microorganisms, living in the sediment. Therefore we calculated an aggregate number of microbial cells in sediments from two areas of Lake Baikal. For detection live cells of microorganisms we used an epifluorescent microscope (magnification x 3700) and fluorochrome dye DAPI. The number of microbial cells was found in seven layers: 0-1 cm, 2-3 cm, 4-5 cm, 6-7 cm, 10-11, 15-16 cm, and 20-21 cm below sediment surface (BSS). The sediment was sampled in Southern Baikal at a point having a water depth of 1400 m. The sediment has been fixed according to a protocol of Mussmann et al. [2006] I with formaldehyde. A minimal number of microbial cells ($2,8 \cdot 10^8$ cells/g) was found at 2-3 cm BSS; maximal abundance ($2,6 \cdot 10^9$ cells/g) occurred at 10-11 cm BSS. From these data it followed that the content of phosphorus in the biomass of microorganisms corresponded to $7,3 \cdot 10^{-2}$ - $7,3 \cdot 10^{-4}$ g of phosphorus per 1 gram of a wet sediment. We found in the experiments carried out with a radioactive label that the content of exchangeable phosphorus was $7,13 \cdot 10^{-5}$ g/g [Likhoshvay et. al, 2006]. Hence, microorganisms store a much greater fraction of phosphorus compared to that capable of exchange. To determine what microorganisms prevail in different sections of the sediment, were applied the method of hybridization in situ. Microorganisms of different phylogenetic groups were distributed irregularly: the highest abundances of sulfate-reducing were found at 4 and 20 cm BSS. Maximal abundance of archaea occurred at 6 cm BSS. The experiments supported by Program of Presidium RAS 18.10.

EVOLUTION ALGOFLORA IN THE CAMBRION PERIOD

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The evolution of algoflora outstripped cardinal reorganizations in global ecosystem of the Cambrian period, the basic event of which was the mass distribution of organisms with mineralized shells. Numerous algae association of Red and Green Cambrian algae have pressed Cyanobacteria in competitive struggle for places and resources of a feed. Fossil algae remained as organic-wall elastic makrophyta, insignificant part of which calcined in lifetime and took part in formation of reeves. The typical representatives of calcareous reef-building algae were two genera - *Epiphyton* and *Renalcis*, which nature remained debatable for more than 150 years.

The new morphological elements of the unique safety which has been found out by us recently in a genus *Epiphyton* (a cellular structure of filaments, traces of duplication, plasmodesmes, nematecies), have allowed confidently to place a genus in structure of Red algae. Besides it was established, that thallus of *Epiphyton* served nutritious substratum of calcite-precipitated Bacteria and Cyanobacteria communities, in which Bacteria represented itself as catalysts of circulation of alive substance. Thus a second calcareous covering of *Epiphyton* was formed hiding primary structure of algae, that complicated their taxonomy for a long time.

We have interpreted in a new fashion morphological model of group genera *Renalcis* – *Epiphyton* due to detection of close to *Renalcis* genus *Gemma* with "monospores" inside colony, which outside its limits formed an initial stage of growth called as a genus *Korilophyton*, then outgrowing to *Epiphyton*. On the basis of this fact the conclusion was made that the life cycle of a genus *Epiphyton* developed from of geteromorphic steps consisting at first of temporary phases of growth of the palmelloid forms – *Renalcis*, *Gemma*, *Chabakovia*, then passing into the first phase of dendrolitic forms named *Korilophyton*, which finally growth to bush *Epiphyton*. Thus, all the listed forms are considered by us as growth phases of only one genus` *Epiphyton*.

Evolution of Cambrian algoflora, model object of studying of which was the Siberian platform, directly depended on geodynamic events in the Paleozoic ocean, connected with the beginning of disintegration of uniform Precambrian continent Pangea 1. The situation in ocean was close to modern position in the West of Pacific ocean: in peripheral parts there was uniform paleogeodynamic system of island arches, which later (in the Middle Cambrian) has collided with Siberian craton.

THE ROLE OF COAGULATION PROCESS IN THE EVOLUTION OF THE GRAVITATIONAL INSTABILITY IN THE GAS-DUST PROTOPLANETARY DISKS

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In the frame of solving problem of abiogenous synthesis matter in solar system, one of the most important problems is forming of bodies with radii longer 100 km. According to the astrocatalysis hypothesis carbohydrates are synthesized on the surface of the dust particles in the circumsolar protoplanetary disk, which provide coagulation of these particles, and therefore bodies with radii 1-10 m appear. There is problem of principle mechanism of forming of 100-km-sized bodies, as meter-sized bodies are destroyed due to collisions when they are moving with orbital velocities.

There is a collisionless mechanism for solving this problem. The main point of it lies in possibility of appearance of gravitational instability in two-phase gas-dust environment. The probability depends on average particles mass. Thus it is necessary to study the influence of particles growth on increasing of the gravitational instability.

One of the most suitable instruments for studying evolution of the protoplanetary disk is mathematical modeling with numerical supercomputer experiments. Numerical model was developed with primary particle motion in the equatorial plane of the disk. The model describes gas dynamics and particle motion including coagulation process. Since the numerical algorithm is based on splitting method. It was made investigation of the influence of the coagulation rate on dynamics of gas-dust system for the initial conditions in which gravitational instability appeared. It was found that coagulation rate can increase the instability rate. For some parameters it can significantly influence on the structure of the disk.

ORIGIN AND EVOLUTION OF BIOSPHERE AND POSSIBILITY OF THEIR EXPERIMENTAL MODELLING

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Origin and evolution of living cells on the Earth (and other planets) can not be considered out of the scopes of origin and evolution of biosphere. It seems obvious however these two aspects of life origin are usually discussed separately.

Earlier we have suggested a geo-chemical (generally planetary chemical) cycle was an ancestor of biosphere [1]. Similar cycles exist due to thermal or light energy income and are to exist on different planet of the solar system. Chemical reactions of planetary cycle can be divided into two types: reactions driven by external energy, and reactions capable of spontaneous course with energy liberation. Reactions of the second type can be denoted as "base reactions" since their energy can be used for growth and proliferation of phase-separated autocatalytic systems (PSAS), which are considered as predecessors of living cells.

However origin and proliferation of PSAS rapidly decreases concentration of substances participating in the cycle turnover. Atoms of these substances turn into "chemo-mass" of PSAS, which is deadlock compound slowly degrading to parent substances by means physical-chemical, firstly geological processes. This implies initial PSAS were "chemo-autotrophic" systems and their evolution was directed to the capability of functioning at low concentrations of limiting substances.

Thence we can conclude that further evolution of "chemosphere" is associated with the origin of PSAS of new types: one – capable of utilizing "chemo-mass" of the first PSAS, and second – capable of effective utilizing additional external energy for accelerating planetary chemical cycle.

This view on the origin and evolution of initial chemosphere, and then biosphere allows to suggest criteria of optimality which drive the evolution of similar ecological systems with cyclic matter turnover.

The question on possibility of experimental verification of any hypothesis on life origin seems to be of great importance for scientific approach. From our point of view the experimental modeling of listed above assumptions is quite real.

This certainty is based on the fact PSAS are of so small size that the difference between the volume of experimental reactor and the volume of biosphere is not key limitation factor of the modeling. The main problem is extremely low rate of evolution in the biosphere. It essentially depends on its great buffer capacity. This problem is eliminated. On the other

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hand degradation and mineralization of wastes produced by PSAS can be intensified by modern technical means.

Specified schemes of laboratory installations on the base of flow reactor of ideal mixing for experimental modeling chemical turnover and evolution of PSAS are discussed in the paper.

Theses installations are designed for modeling initial stages of molecular chemical evolution leading to the origin of living cells and biosphere as a whole.

This work was conducted with the support of RAS Program #18.2 "Biosphere Origin and Evolution" and RFBR Grant #06-04-49016.

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MICROBIAL ANALYSIS OF LAKE BAIKAL BOTTOM SEDIMENTS FOR THE LAST 20 KA

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Lake Baikal is an ancient freshwater body. Of particular interest is the distribution of microorganisms in bottom sediments collected in the southern basin of the lake where, according to the data on seismic physical studies [Mats V.D. et al., 2000; Khlystov O.M. et al., 2000], an undisturbed regular sedimentation is recorded (Posolsk Bank). The thickness of deposits is 316 cm spanning 20 Ka. The distribution of the following bacterial groups in bottom sediments was analyzed: heterotrophs of genera *Bacillus* and *Pseudomonas*, and actinomycetes of genera *Streptomyces* and *Micromonospora*.

According to the diagram of microorganism distribution in bottom sediments of "Posolsk Bank", culturable heterotrophs prevail in surface layers of sediments (0-21 cm) where their counts make up from 35×10^3 to 200×10^3 cell/g. The genus *Pseudomonas* dominates in sediments at a depth of 75 cm where their abundance varies between 400 and 23000 cell/g. The number of *Pseudomonas* bacteria is reduced with the depth to zero.

The data on vertical distribution of actinomycetes and bacteria of the genus *Bacillus* in bottom sediments are also of great scientific interest. The analysis shows that most of them are concentrated in the surface layer (0-60 cm) at depths 280-333 cm. In surface layers, the abundance of actinomycetes makes up 600 cell/g, while in deep layers – 400 cell/g. Actinomycetes recorded in deep layers (105-336 cm) are represented only by the genus *Streptomyces*. The abundance of *Bacillus* bacteria in surface layers is 600-8000 cell/g, whereas in deep layers – up to 1200 cell/g. Taking into account sedimentation, all the studied groups are present in big quantities in Holocene sediments. In Pleistocene sediments referred to the last glaciation (18-25 thousand years ago, 250-350 cm), there are distinguished bacteria of the genus *Bacillus* and actinomycetes of the genus *Streptomyces*. At these depths, spore-forming microorganisms are likely to be preserved in a form of spores in sediments during hundreds of thousand years [Abyzov S.S. et al., 1990; Kochkina G.A. et al., 2001; Nichilson W.L. et al., 2000].

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**“EXPERIMENTAL EVOLUTIONARY MACHINES” ON THE BASE OF
MICROBIAL POPULATIONS AND ASSOCIATIONS**

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The idea of "experimental evolutionary machines" provides the possibility of a quantitative investigation of physical and chemical basis for natural selection. The processes of microevolution of microbial populations and associations can be studied in two main types of the open thermodynamic systems: stable flows – chemostat, stable organization – turbidostat and pH-stat. Different types of active mutants which are able to substitute initial form in the cultivator were obtained under different cultivation conditions. Natural selection acts in the chemostat in the favour of “K-strategy” forms which are able to utilize limiting substrates up to lowest concentrations. Prevalent mutants which are able to grow faster than initial form, so-called, “R-strategists”, have advantage under conditions of turbidostat or pH-stat cultivation. (Symbols are taken from well-known logistic equation). The dilution rate in turbidostat or pH-stat increases automatically, according to growth rate of new “conqueror” population. The rate of microevolution transitions is usually very high because of very short generation time of microbial populations. The kinetic canvas of microevolution processes is very diverse.

But general mechanisms characterized the increase of used energy flow by microbial populations and associations under study.

HYPERTHERMOPHILIC BIOGENESIS AND EARLY BIOSPHERIC EVOLUTION

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A wide range of recent research [1] supports both hyperthermophilic biogenesis and a hyperthermophilic Last Common Ancestor (LCA) of life. RNA world compatibility with hyperthermophilic biogenesis is consistent with highly saline Hadean oceans [2] and experimental evidence for RNA stability at high temperatures in saline solutions [3]. Likely impact reseeding during the Hadean [4] should have left deeply-rooted mesophiles if they indeed emerged soon after biogenesis, with their apparent absence implying both hyperthermophilic biogenesis and a hot Hadean climate. The robust anti-correlation of maximum growth temperatures (T_{max}) of thermophiles with their rRNA and tRNA phylogenetic distances from the LCA is consistent with the thermophilic T_{max} being close to the climatic temperature of each organism at emergence. Drawing on a plausible scenario of hydrothermal biogenesis near the seafloor [5, 6], we propose that a spectrum of Bacterial and Archaeal protocells, including ancestors of extant prokaryotes, emerged simultaneously in the thermal gradient between a hydrothermal source on the seafloor and the ambient climatic oceanic temperature, in Hadean time. A climatic temperature close to 80 deg C in the late Hadean/early Archean is consistent with the known oxygen and silicon isotopic record of marine cherts [2, 7]. Efficient repair of single and double strand breaks in DNA of early life is likely a consequence of emerging in the high temperature and higher radiation environment of intracellular K40 and C14 decay. Therefore the early accumulation of “clock-like” substitutions is possibly driven by this radiation dose as a function of time. We will present a test of this possibility.

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EMERGENCE OF CHIRALITY AND MOLECULAR EVOLUTION

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Since the article of Frank [1], several far-from-equilibrium models were developed, investigating the spontaneous onset of a non-racemic state from a symmetrical system. They are generally based on open-flow systems, incorporating autocatalytic reactions. However, recent works show how such models can be improved by replacing open-flows by activated recycling of compounds, and by allowing emergent network-autocatalytic behaviors rather than direct autocatalytic reactions [2].

This approach leads to the description of non-equilibrium chemical systems as subsets of direct matter fluxes and simple reactions cycles. A formalism can be developed on the basis of the stoichiometric matrix of the reaction network, generalizing the formalism used in the literature to describe the metabolisms of alive beings. The coupling of this description with kinetic and thermodynamic parameters allows the description of evolutionary chemical networks.

In this framework, homochirality doesn't appear as a strange event in the process of the origin of life, but is rather only one element that can be formed by the first emerging proto-metabolisms, potentially allowing further complexity. Such proto-metabolic patterns can be compared to Eigen's hypercycles [3]. They may have constituted the first replicator, not as template replicators of similar molecules, but allowing the replication of the hypercycles themselves as elementary objects, allowing bifurcation towards some, and extinction of others.

Such a description leads to a hierarchical view of the emergence of life, from synergy between simple reactions producing the emergence of proto-metabolisms, to synergy between proto-metabolism producing the emergence of metabolisms, evolving with increasing complexity towards replicative molecules.

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EVOLUTION OF BIOSPHERE AND CYCLIC CHANGES OF OIL CHEMICAL COMPOSITION IN PHANEROZOIC

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It is known that geotectonic processes impact on biosphere evolution. Geotectonic changes have cyclic character [1,2] related to galactic processes. In phanerozoic, there are three cycles of geotectonic changes periods of which are approximately equal to galactic year (about 180 Ma). They are Caledonian, Hercynian and Alpine cycles. Ronov [1] noted that global sea transgressions occur during the middle of tectonic cycles, and are accompanied by increased organic matter accumulation and consequently oil formation. Transitions from one cycle to each following one were accompanied by sea regressions and caused huge biogeological changes of biosphere and global ecological catastrophes. Large changes of biodiversity in paleobiosphere have been reflected in cyclic character of changes of amount of organic matter accumulation and oil resources. The purpose of this paper is a discussion of relationship between cyclic changes of chemical composition of oils and stages of biosphere evolution.

In this paper we summarize the results of recent investigation into variations of oil composition. These results use data in a worldwide database on petroleum chemistry created at the Institute of Petroleum Chemistry, Tomsk. The sulphur, resin, asphaltene and paraffin contents of some 16,500 Cenozoic, Mesozoic and Paleozoic oils were analysed statistically in terms of reservoir rock age. Results show cyclicity of oil chemical properties changes related to cyclicity of sea transgressions. Relationships between oil chemical composition, geotectonic cyclicity and stages of biosphere evolution are also discussed.

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TRANS HAMMERHEAD RIBOZYME: LIGATION VS. CLEAVAGE

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According to “RNA world” hypothesis, at early stages of prebiotic evolution both the genetic information and the catalytic activity were contained in RNA molecules. Among different RNA-catalyzed reactions, RNA ligation is one of the most important since it provides an extension of RNA molecules and complication of their structure. In the ligation reaction catalytic RNA plays two roles: a template that provides specific recognition and positioning of RNA substrates, and a catalyst necessary for the formation of phosphodiester bond. Hammerhead ribozyme can be considered as an example of ancient RNA catalyst because its catalytic motif was discovered in highly divergent organisms. A lot of artificial ribozymes capable of site-specific RNA cleavage were designed on the basis of hammerhead motif, but ligation activity of this ribozyme is studied rather poor.

We wonder if minimal changes of ribozyme structure could influence RNA ligation efficiency. To this aim, we have designed two variants of *trans* hammerhead ribozyme which could potentially possess an improved ligation activity. In the first variant of ribozyme, a semi-conservative U7 in catalytic core was replaced by cytidine, adenosine or guanosine. The second variant is represented by hammerhead ribozymes containing 7-nt bulge in one of substrate binding domains. The reaction of RNA ligation/cleavage by designed ribozymes and control non-modified ribozyme was investigated in water solutions and hydrated films simulated the conditions of pre-biotic RNA world. Both cleavage and ligation rates differed from those of control non-modified ribozyme in all cases. Kinetic parameters of ligation and cleavage reactions were determined. It was found that 7-nt bulge in stem III as well as U₇→C₇ substitution increases markedly the rate constants and yields of ligation (4 % and 2 %, correspondently, vs. 0.8 % for control ribozyme).

Thus, ligation activity of *trans* hammerhead ribozymes ligation activity of *trans* hammerhead ribozymes can be altered by changing the sequence of non-conservative regions of the ribozyme. However, equilibrium for the hammerhead reaction is still shifted towards cleavage.

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RESTRICTION – MODIFICATION (RM) SYSTEMS IN CLOSED BACTERIAL COMMUNITY ISOLATED FROM WOOLLY MAMMOTH BRAIN

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Head remains of woolly mammoths (*Mammuthus primigenius*) unearthed during excavation of ancient sediments usually consist only of skeletal material, due to postmortem decomposition of soft tissues by microorganisms. Recently a full head of the Yukagir mammoth was excavated in permafrost (Maxunuokha, Sakha Republic, Russia), that contained good stored organic masses, remnants of the brain. Radiocarbon examinations of the bones revealed assemblages of the material dated to approximately 18,000 years before the present.

We attempted to cultivate and identify bacteria from the brain contents using a variety of general and selective media. Only 7 bacterial morphotypes were cultivated, and 6 individual taxa were identified by fatty acid-methyl ester (FAME) profiles, and on the base of their biochemical characteristics. The taxonomic positions of the bacteria were also analyzed by 16S ribosomal DNA sequencing. Results indicate that the brain samples contain only bacterial taxa in which there are no predominant bacteria.

Each strain is characterized by unusual combination of biochemical characteristics. Determination of their systematic positions is complicated. We characterized the bacterial RM systems in order to find out if all the strains have the similar RM systems or one RM system is dominant for the strains.

Analysis of the RM systems revealed that 3 from 6 tested strains had restriction endonucleases recognizing and cutting the sequence 5'-CC*(A/T)GG -3', one strain had a restriction endonuclease with recognition site 5'-CC*TNAGG -3'. And two strains had restriction endonucleases with low activities (remain to be determined).

To our opinion, the RM systems help to construct new combinations of the strain features, and can play a considerable role in evolution of closed bacterial communities.

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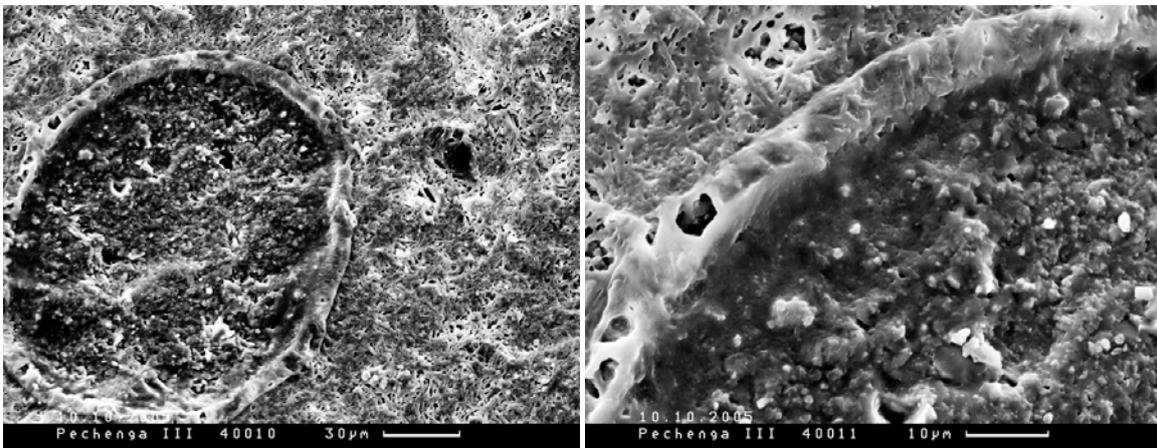
MICROFOSSILS IN THE EARLY PROTEROZOIC (2.0 GA) PHOSPHORITES FROM PECHENGA GREENSTONE BELT

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Till recent time phosphorites from Archaean and Early Proterozoic deposits were *practically* unknown. Now the appearance of ancient marine phosphorites is dated by 2.0 GA. These phosphorites occur as numerous rounded, soft-deformed, clasts in fine-pebble intra-formational conglomerates, forming two separate c. 200 m-thick turbidite fans within the 1000 m-thick OM- and sulphide-rich turbiditic greywackes of the Pilgujärvi Formation in the Pechenga Greenstone Belt, NW Russia. Carbonate-fluorapatite is the main mineral in the phosphorite clasts and OM, framboidal and micronodular pyrite, as well as inclusions of quartz and chlorite are additional components. Many clasts show micro-layering with a variable degree of soft-deformation, implying that they were derived from non-lithified, bedded phosphorites. They contain rich and diverse biogenic microstructures, among them newly found and described eucaryotic microstructure (*Pechengia melezhiki*, insertae sedis) and various microbial microstructures interpreted as cyanobacteria, represented by filamentous (1-3 μm in diameter, 20 μm in length), coccoidal (0.8-1.0 μm) and ellipsoidal or rod-shaped microfossils (0.8 μm in diameter, around 2 μm in length) which morphologically resemble modern *Microcoleus* and *Siphonophycus*, *Thiocapsa*, and *Rhabdoderma*, respectively, that have been reported from alkaline or saline environments.



Pechengia melezhiki – (eucaryot), Lower Proterozoic

No principle differences have been found between microfossils described from Cambrian and Phanerozoic and the 2004 Ma phosphorites. The very finding of eucaryots and phosphorites suggests the presence of high level of O₂ in atmosphere of that time.

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AGE OF LAKE BAIKAL'S PARASITE SYSTEMS

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According to current concepts, fishes appeared in Lake Baikal at different times (Pliocene-Holocene) (Rusinek, 2003, 2005). Baikal's faunal complex of fishes is the most ancient and had been shaping itself during a long time interval of isolation of Cottoidea; at present Lake Baikal is home also to other fishes with an evolution of several millions years (perch, pike, cyprinids, and sturgeon) but they colonized the lake considerably later. Fish introduction in Lake Baikal in the Pliocene-Holocene resulted in new cenotic connections. Cottoidei are included in the life cycles of cestodes, trematodes, nematodes, acanthocephales of new faunal complexes and play the role of parathenic, intermediate and definitive hosts. The great depth of Baikal was beneficial for the emergence of parasite systems similar to those from the sea and ocean water basins, with numerous intermediate, parathenic and definitive hosts (Rusinek, 1987). In Baikal it is the parasite system of cestoda *Diphyllbothrium dendriticum* (Pseudophyllidea). Forty-eight animal species form part of this parasite system (Rusinek, Fefelov, 2005). Fish-eating birds, predatory mammals, and humans are the main definitive hosts of *D. dendriticum*. The climate optimum of Holocene humidification developed main (powerful) migrations in Baikal, and there appeared numerous nesting groups of birds connected with water. Omul (2nd intermediate host of *D. dendriticum*) is also widespread in Baikal. The modern pelagic community shaped itself 11 ky ago, but it involves organisms with ancient evolution (Bezrukova et al., 1991; Granina et al., 1993; Grachev et al., 1998; Khursevich et al., 2001). Cottoidei incorporated in the life cycle of *D. dendriticum* at the climate optimum of Holocene moisture. *Phoca sibirica* (nerpa) is an abortive host of the parasite because this cestode is not mature in this animal organism. *D. dendriticum* causes intoxication in humans, especially in children. This fact is suggestive of the recent inclusion of humans in the life cycle of this parasite.

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VACUUM-UV DEGRADATION PATHWAYS OF PYRIMIDINE, PURINE, IMIDAZOLE AND BENZIMIDAZOLE IN THE 7 - 18 eV PHOTON ENERGY RANGE

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The vacuum ultraviolet (VUV) photophysics and photochemistry of pyrimidine, purine, imidazole, and benzimidazole is of considerable interest in view of the possible delivery of these molecules from space to the early Earth, and the role that they could have played in the origin and development of life on earth, and possibly on other planets or satellites. Purine and pyrimidine are building blocks of nucleic acid bases: adenine, guanine, cytosine, guanine, thymine and uracil, some of which we have studied recently [1]. Purine based nucleic acid bases have been observed in carbonaceous chondrites. Pyrimidines and purines have been reported in the data obtained during the flyby of comet Halley by the Soviet spacecraft VEGA 1. Upper limits of abundance in the interstellar medium have been established for pyrimidine [2] and imidazole [3]. In the present study, photoionization mass spectrometry (PIMS) was used to study the VUV degradation pathways of the four prebiotic species pyrimidine, purine, imidazole and benzimidazole in the 7-18 eV photon energy region. The ionization energies and ion appearance energies are reported, many for the first time, and are compared with results of electron impact and other studies. The measured ion appearance energies, in conjunction with existing thermochemical data, were used to clarify dissociative photoionization pathways. Astrophysical implications of these results concern the prospects for observation and survival of nucleic acid bases in the interstellar medium and in meteorites and these aspects will be discussed.

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PERMO-TRIASSIC TRANSITION IN RUSSIA, SOUTH AFRICA AND CHINA

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The most complete sections of the Permo-Triassic continental deposits and successions of the biotic assemblages are represented in Russia, South Africa and China. The stratigraphic succession at the Russian platform presents sixteen stages in the Late Permian, Early and Middle Triassic distinguished in the biotic history. They are very important for the reconstruction of the scenario of greatest global biotic crisis at Permo-Triassic boundary.

Paleozoic groups of vertebrates became extinct at this boundary and were replaced by Mesozoic ones. The last stage of the Permian biotic history was characterized earlier by gorgonopian-pareiasaurian-dicynodontian assemblage with carnivorous saber-tooth theromorphs – gorgonopians, herbivorous parareptiles – pareiasaurs and herbivorous theromorphs – dicynodontid dicynodonts (Sokolki assemblage or *Scutosaurus karpinskii* zone of Eastern Europe, *Dicynodon* zone of South Africa). After the mass extinction at Permo-Triassic boundary they were replaced by carnivorous thecodonts – proterosuchids and by herbivorous lystrosaurid dicynodonts respectively. These last groups formed a new, proterosuchian-lystrosaurian community at the beginning of Triassic throughout the world. The extinction of gorgonopians, pareiasaurs and dicynodontids and the appearance of proterosuchids and lystrosaurids are suggested as main characters marking the Permo-Triassic boundary on the continents.

The disappearance of pareiasaurs during the terminal Permian of South Africa and also the appearance of earliest lystrosaurids as well as their coexistence with dicynodontids in the terminal Permian of South Africa and China have been recognized recently. A unique and diverse Vyazniki biotic assemblage of the terminal Permian was discovered recently in Central Russia. Vyazniki assemblage includes the earliest world's proterosuchids (*Archosaurus*) and dicynodontids, excluding lystrosaurids.

Thus, the latest data demonstrate that Permo-Triassic biotic transition was more complicated and gradual than believed earlier. Endemic constraints of biotic evolution as well as abiotic environments might have caused the peculiarities of the East-European Vyazniki assemblage. This assemblage represented the last typical of only Eastern Europe stage of the global ecological crisis of the continental biota at the Permo-Triassic boundary.

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ATTACHMENTS OF THE VENDIAN ORGANISMS: SYMBIOTROPHIC STRUCTURES?

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Currently, modern symbiotic systems and those of the past are under careful consideration. There is no doubt that symbiosis was one of the key factors in development of the early biosphere, especially with regard to the origin and evolution of eukaryotes.

Recognition of new morphological features of the Vendian fossils previously interpreted as medusoid organisms completely changed their understanding and reconstructions. These forms are now reinterpreted as attachment disks of organisms, whose relationships are not yet understood (Gehling, 2000). This causes some questions on the nature of the attached species and their relations to substrate. The Vendian basal structures can be attributed to four main morphotypes:

- (1) discoid cyclic attachments, e.g. Ediacaria;
- (2) cone-like attachments bearing cyclic radial processes, e.g. Mawsonites;
- (3) cone-like attachments bearing radial processes rather randomly arranged, e.g. Hiemalora from Siberia;
- (4) composite forms showing a combination of some features of the above three morphotypes, e.g. Palaeophragmodictya.

These morphotypes seem to be ecological and ethological groups rather than true taxa. The diversity of the Vendian basal structures situated inside and above the sediments in life position appears to reflect the variety of attachment modes and substrate use. Widespread microbial mats on the ocean floor and minor bioturbation common for the Vendian environments were resulted in abrupt transition from oxygenic conditions in the bottom water to anoxic ones inside the sediments (Seilacher, 1999). The close association and likely symbiosis of these attachments present in the Vendian is noteworthy. Evidence supporting such an interpretation includes:

- (1) the considerable morphological diversity and complex structure of these basal structures,
- (2) the rapid cyclic isometric growth,
- (3) the absence of recognizable alimentary system,
- (4) the sedentary life-style,
- (5) large surface of attachments contacting with the substrate,
- (6) the preferential fossilization of the basal parts,
- (7) abrupt changes of fossil community with these sedimentary sequences,

- (8) the absence of apparent modern analogues,
- (9) indications of H₂S in sediments,
- (10) simultaneous extinction of many Vendian groups and abrupt decline of microbial substrates.

Taphonomic and morphological studies indicate that such Vendian attachments could be symbiotrophic structures. Bacterial symbiosis may indeed be the driver for morphological peculiarities of the Vendian attachments. This idea is supported by newly discovered symbiotic relationships between some living animals and sulphate-reducing, methanotrophic and photosynthesizing bacteria.

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PUTATIVE PREBIOTIC CARBOHYDRATE SYNTHESIS: COMBINED PHOTOCHEMICAL AND CATALYTIC OLIGOMERIZATION OF FORMALDEHYDE IN WATER SOLUTIONS

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Ribose and other monosaccharides can be generated from formaldehyde by the catalytic action of bases (the "formose" reaction). Unfortunately, in this synthesis a large array of straight-chain and branched oligomers of $(\text{CH}_2\text{O})_n$ is obtained with no selectivity ($n = 2-7$).

In the present work, we demonstrate the possibility of a preferable synthesis of some monosaccharides from a single substrate – formaldehyde - under plausible prebiotic conditions: in neutral aqueous medium and in the presence of natural minerals.

The first stage of the possible prebiotic synthesis of monosaccharides from formaldehyde is the synthesis of lower carbohydrates – glycolaldehyde and glyceraldehyde - under the action of UV-irradiation on aqueous formaldehyde solution [1].

We have tested insoluble (CaCO_3 , $\text{Ca}_5(\text{PO}_4)_3\text{OH}$, $\text{Ca}(\text{PO}_4)_3$, MgO , PbO , natural apatite and vivianite) and water-soluble (phosphate and borate buffers) substances available on prebiotic Earth as catalysts for aldolization of lower carbohydrates with each other or with formaldehyde. Vitally important ribose and fructose appear to be the products of aldolization of glycol and glyceraldehydes. The magnesium oxide which seemed to be prevailing on Protoearth appeared to be the best catalyst for this reaction. The interaction of glycolaldehyde and glyceraldehyde over MgO yields fructose (18 mol.%), sorbose (23 mol. %), ribose (10 mol.%) and arabinose (8 mol.%). Erythrulose and 3-pentulose are the major products of aldolization of formaldehyde with lower carbohydrates. Both water-soluble and insoluble phosphates are the best catalysts for this reaction.

The combination of photochemical synthesis of lower carbohydrates and their catalytic condensation with formaldehyde allowed us to synthesize 3-pentulose, erythrulose and ribulose from formaldehyde. The combined flow photochemical-catalytic installation which is able to imitate the day (UV-irradiation) – night (catalytic reaction) change have been created.

The combined photochemical-catalytic process can be supposed to be a probable prebiotic route to the monosaccharides synthesis, since the reactions do not require any complex substrates, extreme conditions, and proceed readily in neutral aqueous media.

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QUICK EVOLUTION AND ADAPTATION OF MICROBIAL LINKS IN ECOSYSTEMS OF DIFFERENT TYPES, INCLUDING ARTIFICIAL ONES

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Data on microbial populations development (evolution and adaptation) as microbial links of ecosystems of two types are discussed in the paper: artificial ecosystems (AES) for water purification and biological life support system (BLSS).

1. Microbial populations in artificial ecosystems (AES) for water purification are the most active transforming organisms and consumers of organic substances of wastes. In our experiments we observed different changes in Active Sludge (AS) structure and populations composition connected with changes in environmental factors and self-development of AS. As a rule in experiments, water purification ability of Active Sludge (AS) decreased after use of super-mutagenic substances. As a result of biological adaptations, microbial link practically recovered in 5–7 days, unutilized substrate concentration decreased in many cases. The exact structure of microbial community also changed, the biological diversity decreased. But, in all experiments, we observed certain increase of fluxes of energy utilized by the system.

2. The microflora of a BLSS (Biological Life Support System) can be divided into functional and associate. Functional microflora is introduced deliberately into a BLSS and performs a number of definite roles. For example, photosynthesizing microorganisms can be regenerators of the atmosphere; water bound consumers of human exometabolites and, depending on species, producers of partially edible biomass. Functional microflora is amenable to human control.

On the other hand, associate microflora is not cultivated specially, but inevitably accompanies humans and plants inside a closed habitat. Vital activity of associate microflora, which is an integral part of every component of the system, is an important environment-forming factor (formation of the atmosphere, closing the trophic connections in the microalgal cultivator and so on). The task of efficient management and control of microbial population's development in LSS highly depends on mission duration. As for short-term missions without recycling, the proper hygienic procedures are developed. For longer missions, the probability of transformation of the neutral forms into the harmful ones is becoming more dangerous. The problem of interaction between man and microorganisms in closed habitats is an inalienable part of the whole problem of co-existence between macro- and microorganisms. Artificial ecosystems of different types are the best models for macro- and microorganisms co-evolution studies.

**INVESTIGATION OF CYANOBACTERIAL STRAINS ISOLATED
FROM THERMAL SPRINGS OF THE BAIKAL RIFT ZONE:
MORPHOLOGICAL AND MOLECULAR APPROACH**

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The Baikal Rift Zone is rich in thermal springs, which are located both along the shore of Lake Baikal (Khakusy, Kotel'nikovskiy, Zmeiny, Sukhinsky, Goryachinsky springs) and in the Tunka Valley (Arshan, Zhemchug springs). Cyanobacteria represent the major component of thermal biotopes. However only a limited number of strains has been previously described for this region and there is no phylogenetic information available. We have obtained 16 strains from seven thermal springs in the framework of the BOE. We characterized the isolated strains using morphological and molecular methods in order to assign them to either previously known or new organisms. Molecular methods consisted of comparative and phylogenetic analyses of the partial 16S rRNA gene sequences.

Our results indicate that most of the strains belonged to the Oscillatoriales (12 strains). However there were also strains found belonging to Stigonematales (2 strains), Nostocales (1 strain) and Chroococcales (1 strain). Eight morphotypes of Oscillatoriales were distinguished and assigned to *Phormidium* sp., *Leptolyngbya laminosa*, *Leptolyngbya* sp., *Microcoleus* sp., *Pseudanabaena* sp., *Geitlerinema* sp., *Limnothrix redekei* and *Shizothrix* sp. Strains within the Stigonematales were assigned to *Fischerella* sp. The only Nostocales that was isolated was assigned to *Anabaena variabilis*, and Chroococcales was assigned to *Synechococcus bigranulatus*. Out of 16 strains characterized only about 40% were identifiable according to the available literature. On average, a good correlation was found between morphological and molecular characterization. Indeed, most of the strains that were found to be closely related at the 16S rRNA gene level belonged to the same morphotype with few exceptions (16 16S rRNA types / 11 morphotypes). Ecological characteristics of our strains also were differing; nine rRNA types exclusively affiliated with thermal springs. Geographical distribution of these cyanobacteria relatives was wide and included thermal springs of USA, Greenland, Italia, China, Thailand, Australia, New Zealand, Philippines and Japan.

Thus, polyphasic approach has allowed extending data about cyanobacteria from thermal springs of the Baikal Rift Zone.

BIOMINERALIC FORMS FROM LATE PROTEROZOIC DEPOSITS OF SOUTH OF THE SIBERIAN CRATON

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The organomineralic forms are well known among the microfossils of Late Proterozoic deposits of southern Siberian craton. The forms of various structures are typical for the sediments of different environmental settings of paleobasin. The first group of such forms is represented by iron bacteria, which look in microsections like chains and concourses of reddish-brown balls. They are typical for the sediments of shelf proximal zones. Probably, these forms participated in oxidation of iron before generation of intracellular ferrihydrite - amorphous iron oxide, moving over to hematite and other minerals during diagenesis. The *Bavlinella* Schep forms are example of some kind of "symbiosis" of the sulfide and anaerobic sulfur bacteria in stagnum zones. Framboid are formed as a result of interactions of biogenic sulphurs with iron in bacterial colony. The *Octoedryxium* are compared with benthos of sulfur bacteria, living in comparatively shallow, subaerial sediments, associating with stromatolithic carbonate. Is it presumed that sulphur accumulates and crystallizes in bacterial cells during oxidation. The shapes of these cells are controlled by outlines of the growing crystal. Under diagenesis the sulphur transforms in monoclinic modification and diffuses outside. Planktonic *Floris* Stan. have construction of spherical aggregation of crystals. They are compared with dinoflagellate and extracted from sedimentary-volcanic rock of the back-arc basin. It's presumed that intracellular crystallization of solution from captured biophile elements of volcanic origin occurred during growth of *Floris*. Planktonic *Dictyotidium minor* Stan. have a polygonal construction and are compared with colony of green algae. They complement homologous series of fulleren structures, uniting biogenic and mineral formations. It's presumed that the symbiotic relations of minerals and organisms reported above demonstrate a fragment of the mineral organobiosis evolution which probable could be responsible for origin of the life (Yushkin, 2004).

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HOW DID EXOTHERMIC CHEMICAL REACTIONS INFLUENCE THE CIRCUMSOLAR PROTOPLANET DISK DYNAMICS?

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According to astocatalysis hypothesis, abiogenic synthesis of organic substances most probably took place on protoplanet stage of evolution of the Solar System. Gas temperature is one of the key parameters affecting protoplanet disk stability and fragmentation. The work is aimed at study the thermal conditions in the circumsolar protoplanet disk on the stage of abiogenic synthesis of organic substances.

Heterogenic reactions of synthesis of organic substances have a great influence on protoplanet formation. But exothermic reactions (i.e. reaction of synthesis molecular hydrogen from atomic one and photochemical reaction of metastable helium) are worth considering first, as they can vary the temperature of gas in protoplanet disk and thus provide the favorable conditions for further fusion reactions.

Influence of exothermic reaction on disk dynamics was numerically investigated in the frame of multiphase self-gravitating protoplanet disk model.

Influence of temperature varying on the generation of non-linear wave structures in the circumsolar protoplanet disk was studied. It was found out that exothermic reactions extended the characteristic time of disk existence by improving stability properties of the system.

TRENDS OF DEVONIAN MIOSPORES AS REFLECTION OF EVOLUTION OF THE MOST ANCIENT TERRISTRIAL PLANTS

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Occurrence of the first terrestrial plants is the key in a geological history and reflects the largest biospheric process marked by many global events. The results of palynological analysis now bring significant corrective in understanding of flora's evolution laws (Tel'nova, 2005).

Trends of Early Paleozoic miospores reflect:

1 - progressing taxonomic biodiversity;

2 - transition of plants to terrestrial existence (Late Ordovician - Early Devonian), it had no one-stage character, and represented only one of stages of development in multistage process formation continental biota;

3 - testify to absence of spasmodic character of change of flora on borders of stratigraphic divisions and about continuity of evolutionary development in phylogenetic groups of Devonian plants;

4 - repeatability of attributes at different levels in complex biological systems.

The sporoderm ultrastructure in all plants, from the earliest terrestrial forms to the most developed extant angiosperms, displays a limited number of structural elements. During sporoderm evolution, these elements are repeated in different combinations (by way of analogy with the alphabet, a limited number of letters allows a great diversity of words to be formed).

Vegetative communities are considered as quickly evolving emergent systems described by a coordination of local and global processes and intensive interaction of different factors. In such condition the system possesses of the greatest lability and ability to evolutionary changes.

EFFECTS OF THE CHROMOSOMAL REARRANGEMENTS ON THE RECOMBINATION PATTERN IN THE COMMON SHREW

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Meiotic recombination generates genetic variation, decreases mutational load and ensures the genetic unity of species. Every chromosome arm has its own specific pattern of recombination, which is a complex function of its length, centromere and telomere effects, interference and sequence characteristics.

The aim of our study was to examine effects of chromosome rearrangements on the recombination patterns of individual chromosome arms of the common shrew (*Sorex araneus* L.). This species is characterized by spectacular autosomal variation of the Robertsonian type. The sites of recombination were mapped at pachytene chromosomes by immunolocalization of mismatch repair protein MLH1.

We showed that the recombination pattern of each individual chromosome arm varied substantially depending on whether it was an acrocentric chromosome or part of a metacentric chromosome and what arm it was fused with. We also found a substantial redistribution of the crossovers to more distal positions from the centromere in the metacentric homozygotes and heterozygotes in comparison with acrocentric homozygotes (Fig. 1). The suppression for genetic exchange in regions of the genome close to the centromere could promote greater genetic subdivision within races characterized by metacentric chromosomes than those characterized by acrocentrics.

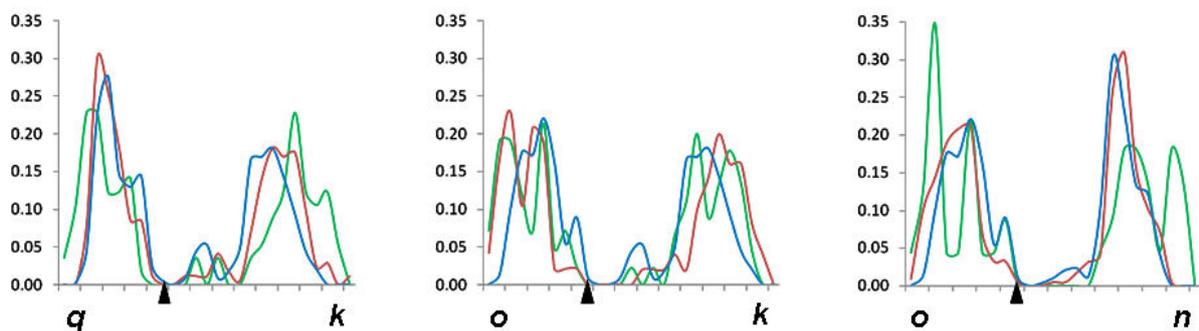


Fig.1. Distribution of MLH1 foci along the arms of the Robertsonian-variable chromosomes.

Letters indicate the chromosome arms, arrows show the centromere. The lines represent the overall frequency of MLH1 foci in each interval. The blue line shows the distribution in acrocentric homozygotes, green – metacentric homozygotes, red – heterozygotes.

THE PARTICIPATION OF MICROORGANISMS IN THE POST-MORTAL MINERALIZATION OF ORGANIC MATTER - THE MAIN FACTOR OF THE SOFT TISSUE PRESERVATION IN FOSSIL

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The knowledge about fossil microorganisms from the Archean provide a major source of information about early life on Earth. These data rest upon the studying of mineralized bacteriomorph structures, contained in oldest sediments. In the last decade it was shown that the preservation microorganisms bodies in fossil is the ordinary phenomenon. Our task was to understand in what rocks they are met most commonly, in what environments and in what a manner their fossilization occurs. Besides of fossil microorganisms in the Phanerozoic rocks remains of soft bodied fossils of Metazoa (epithelial tissue, cellular details of soft-tissue, muscles, eggs, larva, etc) are found (Martill, 1988; Briggs, Bottrell, Raiswell, 1991; et other).

In the many science collectives series of laboratory experiments were realized to simulate the cause of microorganisms and Metazoa mineralization. Similar experiments took place in our collective as well (Bacterial paleontology, 2002). In addition the studying of fossils from Lower Cambrian Lagerstätten (Siberian platform, river Lena), the research of the structure of the small Cambrian brachiopods with phosphate shells have helped to understand the main causes of organic matter mineralization in the past (Ponomarenko, ed., 2005). All these investigations show that there is only one way to stop the decay of organic matter after death of organisms (both Protozoa and Metazoa), it is early mineralization. In all times the basis of early mineralization, it trigger, is activity of bacteria. Another important conditions for preservation of soft-bodied are rapid burial and anoxia, both they are reduce the rate of decay, but are not halt it. Bacteria in the course of the metabolism change chemical medium around decay organisms, modulate (in the different direction) pH , as well as the concentration of a variety of organic and inorganic solutions. Sometimes these induce the precipitation of authigenic minerals as thin films around organic bodies or replace them. In many cases bacteria bodies and extracted by them EPS were ineralized too. The common known types of organic matter mineralization are phosphatization, silicification, carbonatization and piritization.

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MIDDLE PALAEOOLITHIC HUMAN REMAINS FROM CENTRAL ASIA AND SIBERIA – NEANDERTHALS OR MODERN HUMANS?

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Central Asia only played a marginal role until now in the discussions about modern human origins, even though the area is a crossroads for human migration between Europe/Western Asia and Southeast and East Asia. In the last 20 years, Middle Palaeolithic human remains were discovered at several sites in the region, including Obi-Rakhmat and Anghilak in Usbekistan, and Okladnikov, Strashnaya and Denisova Caves in the Altai. The affinity of most of these remains is disputed, some are claimed to be morphologically similar to Neanderthals (e.g Turner, 1990), and some show derived traits of anatomically modern humans (e.g. Shpakova and Derevianko, 2000). Until now, no synthetic treatment of these remains was attempted, even though they are of great importance.

We will discuss the morphology and chronological position of these remains, and discuss their implications for the question of the origin of modern humans.

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ROLE OF VOLCANISM IN FORMATION AND EVOLUTION OF THE BIOSPHERE

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About half a century ago one of the authors has formulated conclusions that “the geological evolution of sedimentary, water and air Earth’s outer shells, as well as the origin and development of life is a transformation basically of a volcanic material in due course. During a geological history volatile components of volcanic products have undergone especially complicated evolution: from carbonic gas through various sorts of carbonaceous compounds up to an organic basis of life and from volcanic vapors through sea water up to the blood circulating in vessels of highly organized alive creatures” (Markhinin, 1967).

In 1973, during the Tyatya volcano eruption a discovery has been made: abiogenically formed complex organic compounds have been found in juvenile ashes from this eruption. This has demonstrated that “volcanic eruptions were a first step which was made by the nature in a way from non-alive matter to alive. Volcanoes were those huge chemical reactors in which prebiological compounds were formed. Chemical evolution has created the first alive organisms from them” (Markhinin, 1980).

Since 1998, the problems of connection of volcanism, setting up and evolution of the biosphere are regularly discussed at the International Conferences entitled “Volcanism, Biosphere and Environmental Problems” in Tuapse (Russia).

Four conferences were held during 1998, 2000, 2003 and 2006, the fifth conference is scheduled for 2009. The above-stated concepts and other points of view were presented at these conferences, including setting up of the biosphere at a late stage of evolution of magma oceans of the Earth and other planets (Kuznetsov, 2006); necessity for the origin of life of a stage of mass occurrence of fullerenes in superficial parts of planets as a result of space bodies impact (Cherkasov, 2006); the data on procarote traces in coaly chondrites (Gerasimenko et al., 2003) etc.

In a number of reports the authors prove multi-rank cyclicity of geological processes, including volcanism and biocenotic crises: mass extinction of alive and the origin of new forms of life and their evolution (Volkodav, 1998, 2006; Epifanov, 2006).

INFLUENCE OF GAMMA-RADIATION ON NATIVE MICROBIAL COMMUNITIES IN ANCIENT PERMAFROST

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Revealing of living cells in deep ancient rocks and permafrost, deep sea sediments, salt crystals, evaporates etc. goods a new look on cell's life longevity and microbial life strategy. These data as well as new knowledge in relevance to high stability of microorganisms under hard stress enables to discuss new hypotheses of origin of life and its spreading in the Universe.

Dormant cells in deep ancient polar permafrost possibly have received very high doses of background and cosmic radiation during geological time. The limits of life and radiation stability of microorganisms in natural ecosystems are still unclear. Deep ancient permafrost and contemporary soils represent two model ecosystems of different genesis for investigation of microbial communities' stability to stress.

Microbial communities in permafrost sediments and soils survive and save biodiversity after irradiation in situ in doses up to 15 Mrad. The species composition of microbial communities has been investigated by chromatography-mass spectrometric analysis of chemical signature markers and by conventional cultural techniques as well. After irradiation communities underwent reconstruction: some populations have been activated, and others inhibited. Nevertheless, Cyanobacteria and Acetobacter predominated in situ before and after irradiation. Soils and sediments after irradiation saved metabolic potency, and many populations were enabled to proliferate. Bacteria isolated from irradiated samples revealed cytomorfological features of cells' damage or other signs of irradiation but some of them were stable to stress in cultures, namely could grow in wide range of temperatures, and displayed stability to salts and irradiation.

BACTERIAL MORFOLITOGENES IN HOLLOW OF BAIKAL RIFT ZONE

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It is established, that bacterial communities play the main part in formation of some positive relief micro- and nanoforms in depressing structures of the Baikal rift zone. Relief forming activity of bacterial biocenoses is directly connected with the processes of gas and mud volcanism, which have provided favorable conditions for microorganisms existence and rough growth of their number.

Structurally self-organizing bacterial organo-mineral systems forme positive micro- and nanoforms of relief in two conditions of morfolitogenes: arid-vale-mound and lake-marsh. In arid-vale-mound is formed stalagmito-similar type of microrelief, in lake-marsh conditions the microorganisms form dome and tussocks types of a microrelief. All stages of formation of these microforms of relief - from domes covered with bacterial mats up to intensively, overgrown hillocks and tussocks, track out by us in shallow half waterlogged lake (area 70x40 m), located on outskirts of a resort Baunt, arisen in caldera mud of a volcano.

The growth of domic-tussock microstructures occurs on sandbank of reservoirs. The size of them reaches 1-2 meters in diameter, height - 20-30 centimeters and more. The initial dome form of these microstructures is defined by activity of microgryphon, around of which are formed hillocks of sand. The last become covered by black silt sated with microorganisms, and then with partially mineralized tzeanodacterial mats. At the last stage of growth of microdomes, above water bacterial-mineral-uliginous substratum is transformed to the top soil-vegetative layer, due to which bacterial hillocks are transformed to usual marsh tussocks.

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MICROBIAL COMMUNITY DEVELOPING DURING CULTIVATION OF A FRESHWATER DIATOM *SYNEDRA ACUS* FROM LAKE BAIKAL

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Interaction via metabolites is one of the forms of biotic relations between algae and bacteria during their life cycle. Bacteria influence diatoms in different ways: on the one hand, these are favourable relations with an associated population of microorganisms; on the other hand, influence of microorganisms that causes destruction of diatoms. The participation of bacteria in silicon cycle and dissolution of silica *in situ* during diatom growth was discussed (Bidle, Azam, 1999; Bidle *et al.*, 2003; Kang *et al.*, 2005; Terekhova *et al.*, 2006).

The culture of a diatom microalga *Synedra acus* was isolated from the natural population at the site of Listvenichny Bay (Lake Baikal). The total abundance of bacteria associated with *Synedra acus* varied from 1.5×10^5 to 3.0×10^6 . We applied a unique technique of bacteria cultivation on the extract of the studied alga for analyzing maximal diversity of microorganisms. The abundance of cultivated microorganisms made up between 8.0×10^2 and 3.0×10^5 . As a result of amplification and sequencing, a nucleotide sequence of 16S rRNA gene was determined for 12 strains with different morphological characteristics. The analysis of sequences of 16S rRNA gene showed that studied isolates were represented by specific phylogenetic groups: α -, γ -*Proteobacteria* and *Cytophaga-Flavobacterim-Bacteroides (CFB)*. These data are in agreement with the previous studies of microorganisms colonizing marine diatoms (Bidle, Azam, 2001; Nicolas *et al.*, 2003; Sapp *et al.*, 2006). Bacterial strains revealed high homology (97-100%) with sequences of the following species: *Pseudomonas putida*, *Brevundimonas alba*, and *Variovorax paradoxus*. Two strains were close to microorganisms of Glacial ice bacterium.

TEM and SEM studies showed that bacteria were localized in the polysaccharide diatom mucus. Intensive development of bacteria at the beginning of the observation did not influence the growth and viability of algae. However, during longer observations it was noticed that in some cases valves of *Synedra acus* were destroyed.

The study was in part financially supported by the Program of the Presidium of the Russian Academy of Sciences (project # 18.4) and Scientific School 4738.2006.4.

COMPUTER SIMULATION OF THE SUGAR SYNTHESIS OF BUTLEROV REACTION IN A CIRCUMSTELLAR DISK

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It is supposed, that the abiogenous synthesis of organic compounds, as a stage of forming of earth-life, happened on the stage of forming circumstellar protoplanetary disk. Our problem was to estimate the quantity of organic compounds synthesized at the stage of collapse of molecular gas cloud. For getting such estimate, we built the numerical model of dynamics of gravitating gas taking into account the transformation of chemical compounds according to Butlerov reaction.

We used data of changes of organic compounds when in use condensation of glycolaldehyde, glyceraldehydes and dihydroxyacetone with each other, obtained in vitro. The system describing kinetics of Butlerov reaction was built by using the program package *ChemPack*. This reaction was described as a combination of reversible, parallel and successive reactions, in all 44 reactions. Velocity constants of the kinetic model of splitting of Butlerov reaction were obtained by solving direct problems. The kinetic model of the transformation of chemical compounds according to Butlerov reaction was included into numerical method of solving of equations of gravitational gas dynamics according to splitting-up method.

As a result we solved the problem of gravitational gas dynamics with chemical reactions. For modeling we chose the collapse in the presence of a protostar. As a consequence we calculated quantities of separate components of organic compounds, such as ribose, allose, aldose and others, incipient at the stage of forming circumplanetary accretional disk. It was shown that xylulose, erythrose and dendroketose were generated in maximum quantities (~0.6, 0.4 and 0.2%, correspondingly). And such compounds as ribose are generated in quantity ~0.01-0.02% of total amount of gas. Is obtained quantities of ribose satisfied for a posterior abiogenous synthesis of prebiotic compounds?

THE STRUCTURAL PECULIARITIES OF AMORPHOUS SILICA OF VEGETABLE ORIGIN

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It is known that in the process of evolution the silicon-containing plants arose. In this work we studied the structure peculiarities of the amorphous silica obtained from the plants (rice, buckwheat, oats, needles of pine, fir-tree, larch) by different physicochemical methods. The content of silica in the samples fluctuated in the range 67–99.99%. The max water content was equal to 15%. The calcination of the amorphous silica at the 1000 °C during 1 hour resulted in the obtaining of different crystal forms or did not change the amorphous state depending on the admixture cations and on the sample origin. The form and dimensions of the amorphous silica were various and dependent on the precursor nature. The IR spectra of amorphous silica samples were studied in the range 400–4000 cm⁻¹. The signals of silicium 2p-electrons of the amorphous silica samples were investigated by the photoelectron spectroscopy method. It was shown that in the husk rice samples these spectra had two lines of different intensities Si1: Si2 = 1 : 3. The weak component with low bond energy observed up to 350 °C may be ascribed to the silicium atoms bonded to organic fragments. The NMR cryo-porometry method has been used to estimate the pore size distributions in different porous solids. Previously we studied the pore size distribution in the samples of the husk rice and their amorphous silica. Now there are the results of the study of the investigation of the pore size in the samples of the pine and fir-tree needles and in the samples of the amorphous silica obtained from the different needles. It was shown that one can observe a difference even between various sorts of the same species of the plants.

MICROBIAL COMMUNITIES IN LAKE BAIKAL BOTTOM SEDIMENTS FROM SUB-AQUATIC SEEPS

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During the last decades, studies carried out at the bottom of Lake Baikal have revealed numerous zones with seeps where a flow of more mineralized gas-and-oil saturated fluids occurs (Crain et al., 1991; De Batist et al., 2002; Klerkx et al., 2003). In these zones an abundance of benthic animals and microorganisms utilizing the energy of inorganic reconstructed compounds for their vital activity has been recorded (Grachev et al., 1994; Namsaraev et al., 1994).

The microbial communities sampled in the zones of sub-aquatic seeps have been studied with molecular methods. They have been obtained from different layers of the mud volcano "Malenki", from the underwater hydrothermal vent in Frolikha Bay and the shallow area in Posolskaya Bank.

In the aerobic zone of the Holocene sediments, we have found representatives of alpha-, beta- and gamma-proteobacteria, *Nitrospirae*, *Actinobacteria*, *Verrucomicrobia*, *CFB*, *Acidobacteria*, *Planctomycetes*, *Chloroflexi*, *Synechococcus*, *Clostridium*, *Euryarchaeota*, and *Crenarchaeota*, while in the anaerobic zone those of alpha-, beta- and gamma-proteobacteria, *Planctomycetes*, grampositive, *Euryarchaeota*, and *Crenarchaeota*. Colourless sulfur bacteria of the genus *Thioploca*, which represent the base of the communities, have been recorded in the hydrothermal vent of Frolikha Bay. Besides eubacteria, in the regions of mud volcanoes we have detected *Archaea* from the kingdom *Euryarchaeota* belonging to the order *Methanosarcinales*. Those sediments formed in the Pleistocene during the glacials have a poor species composition of microorganisms. It should be noted a low percentage of similarity of Baikal sequences with the known structures (85-94%). They form singular clusters in phylogenetic trees. The combination of molecular and biological data allows to confirm that the majority of Baikal microorganisms are endemic as they do not have similar analogs in the world database. This may be resulted from the fact that Lake Baikal is a unique freshwater body which has existed for, at least, eight million years, and it has never dried and changed significantly its salinity. Thus, Lake Baikal might have been and is probably continuing to be a potential reservoir for microorganisms that are able to conquer new habitats.

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FUNCTIONAL CONSERVATION OF THE MC DOMAINS IN TRANSLATION TERMINATION FACTOR eRF3

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Eukaryotic translation termination employs two protein factors, eRF1 and eRF3, which form a complex both in vivo and in vitro. In yeast *Saccharomyces cerevisiae*, these factors are encoded by the SUP45 and SUP35 essential genes, respectively. Mutations of these genes reduce the efficiency of translation termination, act as omnipotent nonsense suppressors (1).

Proteins of the eRF3 family each consist of three domains. The N and M domains vary in different species, while the C domains are highly homologous. Mammals have two homologous eRF3 proteins, eRF3a (GSPT1) and eRF3b (GSPT2). While eRF3 proteins of higher eukaryotes have similar structure they differ significantly by their functioning: only full-size mGSPT2 can functionally substitute yeast Sup35 in vivo (2). In this work, we demonstrated that deletion of the N domain enables hGSPT1 (*Homo sapiens*), XSup35 (*Xenopus laevis*), and mGSPT1 (*Mus musculus*) to function in yeast cells.

The MC domains of *H. sapiens* eRF3a (hGSPT1), *X. laevis* eRF3 (XSup35), and *M. musculus* eRF3a (mGSPT1) and eRF3b (mGSPT2) compensate for the sup35-21 thermosensitive mutation and lethal disruption of the SUP35 gene in yeast *S. cerevisiae*. At the same time, strains containing the MC domains of the eRF3 proteins from different species differed in growth rate and the efficiency of translation termination. The lowest growth rate was characteristic of the transformants that carried MC domains of mGSPT1 and hGSPT1. The growth rates of transformants carrying the MC-mGSPT2 and MC-XSup35 were comparable with growth rate in the presence of the full-length yeast SUP35 gene. The lowest extent of suppression was observed for MC-mGSPT2. Despite the structural similarity of the C domains in mGSPT2 and mGSPT1, MC-mGSPT1 displayed a higher level of suppression of all three stop codons. MC domains of eRF3 proteins, in contrast to variable N domains, are evolutionary conserved in their structure and functioning in translation termination.

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TEMPOS AND MODES OF THE EVOLUTION OF PROCARYOTIC GENOMES

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Gene orders were compared in more than 40 procaryotic genomes with the use of original measures of similarity elaborated by us. The results of computer simulation of the evolution of genomes upon occurrence of various rearrangements were compared with the values of similarity among genomes of different groups of prokaryotes.

Relative frequencies of large and small genome rearrangements (inversions and transpositions) on the evolution of prokaryotic genomes have been evaluated for twenty pairs of closely related species belonging to different groups of bacteria archaea. The pairs examined strongly differed in the relative frequency of large and small rearrangements. However, computer simulation showed that the total variation can be reproduced with the same input parameters of the model. This means that the differences observed can be stochastic and can be interpreted without assuming different mechanisms and factors of genome rearrangements for different groups of prokaryotes. Relative frequencies of large and small rearrangements displayed no noticeable correlations with taxonomic position, total rate of rearrangement fixation, habitation conditions, and the abundance of transposons and repetitive sequences.

The rate of evolutionary changes in the gene order widely varied in different evolutionary lineages of alfa-proteobacteria. The highest rate (40 – 60 genome rearrangements per 100 Myr) was characteristic of the intercellular parasite *Wolbachia* (Rickettsiales).

ECOLOGICAL SPECIALIZATION OF MICROBIOTAS IN THE VENDIAN EVOLUTION OF THE BIOSPHERE

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Vendian evolution of the biosphere is marked by the appearance of macroscopic organisms and co-evolutionary transformations in microbial communities. Vendian sedimentary sequences of the East European Craton contain a vertical succession of fossil microbiotas: the Lower Vendian Pertatataka-type microbiota of large acanthomorphic acritarchs (Weiss *et al.* 2006) followed by the peculiar Middle Vendian Redkino-type microbiota, which is succeeded by the Late Vendian Kotlin-type microbiota of filamentous organisms. This succession has traditionally been regarded as the three major stages in the Vendian evolution of microbiota.

Middle Vendian siliciclastic deposits of the Nepa Regional Stage (eastern and western flanks of the Nepa-Botuoba anticline, inner parts of the Siberian Craton) have an established record of four disparate, albeit stratigraphically coeval, microfossil assemblages, each restricted to a certain depositional paleoenvironment:

1. Microbiota of the open basin settings (the Kursovsky Fm, eastern flank of the Nepa-Botuoba anticline). Comprises diverse large acanthomorphic acritarchs including *Tanarium*, *Cavaspina*, *Appendisphaera*, *Micrhystridium*, *Paracrassosphaera* (Moczydlowska *et al.* 1992). It is similar to the Lower Vendian Pertatataka-type microbiota.
2. Microbiota of the semi-isolated basin settings of the rising marine transgression (middle part of the Vanavara Fm, western flank of Nepa-Botuoba anticline). Comprises filamentous, including spiral cyanobacterial remains; banded filaments; random-sized *Leiosphaeridia*; a filamentous vaucherian *Jacutianema*; large compressed spheroidal and piriform vesicles; *Germinosphaera* sp.; *Pulvinosphaeridium*; *Polygonium*; vesicles with arcuate, occasionally conical outgrowths.
3. Microbiota of the isolated basin of the waning marine transgression (middle part of the Vanavara Fm). Consists of filamentous forms with sporangia-like structures *Vanavarataenia insolata*, complexly branched filamentous remains, vesicles with arcuate outgrowths, *Omalophyma solida*, filamentous cyanobacteria and small *Leiosphaeridia*. It is similar to the Upper Vendian Kotlin-type biota in the south of the East European Platform.

4. Microbiota of the vast shallow-marine basin at the maximum flooding of the craton (upper part of the Vanavara Fm). Comprises taxonomically poor communities of filamentous cyanobacteria, small spheroidal acritarchs, filamentous *Omalophyma solida*, as well as *Pomorja rhomboidales* which is a characteristic taxon of the Kotlin-type microbiota in the north-east of the East European Platform.

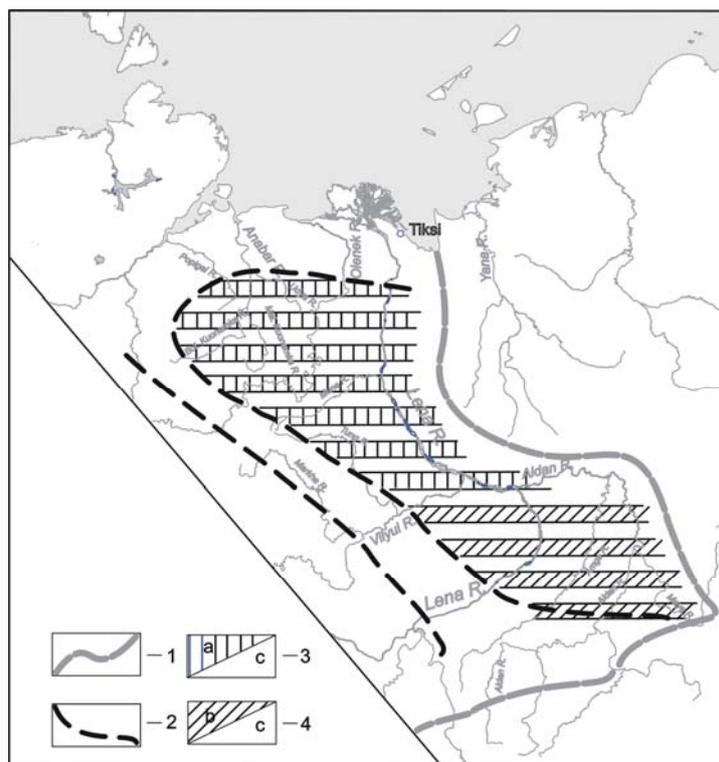
Although a significant stratigraphic importance has been placed on the Pertatataka- and Kotlin-type microbiotas in the Vendian of the East European Craton, these two assemblages appear to be coeval in the inner parts of the Siberian Craton. The Pertatataka- and Kotlin-type microfossil assemblages represent two different ecologically specialized microbiotas each restricted to a certain lithofacies within a single depositional system. This conclusion has important implications for reconstruction of the Vendian evolutionary trends of microbiota.

MICROBIOTA OF MARINE BASINS IN THE KUONAMKA TIME (EASTERN SIBERIAN PLATFORM)

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The Kuonamka time is the time of accumulation of carbonaceous deposits in the Botomian, Toyonian, Amgaian (Lower and Middle Cambrian). The diversity of microbiota in sea of this time was determined from biochemical parameters – from variations of the content and distribution of biomarkers. Three microbiocenosis were distinguished. Also, it is established that the content of the total organic carbon (TOC) and biomarker compositions are connected. The TOC distribution in the Kuonamka complex of deposits has been studied by analytical and published dates. Thus, the occurrence of different microbiocenosis in the Cambrian marine basins was reconstructed based on the TOC and biomarker compositions of studied rocks. The first generalized sketch map of diversity and occurrence of the Kuonamka microbiota is showed in the figure.



1 – boundaries of Siberian platform, 2 – limits of reef complex, 3 – northern microbiota, 4 – southern microbiota (a – predominance of planktonic-algal microbiocenosis, b – predominance of bacterial community, c – planktonic-bacterial microbiocenosis).

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THE MEDIEVAL PALEOENVIRONMENTS IN THE NORTHERN CENTRAL RUSSIA AND THEIR RESPONSE TO THE MAN ACTIVITY

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We have studied pollen spectra in 8 sediment sequences from two archeological sites located in the areas which played an important role for the economical and cultural advance of the ancient Russia. The sites are (1) Minino settlement at the Kubenskoye Lake in Vologda Region, and (2) Rurik Gorodishche fortified settlement at the Ilmen Lake in Novgorod Region. The data comparison revealed both different and common features in a development of the vegetation in the areas of study.

The vegetation changes exhibited an influence of the climate as well as man activity. The latter started by the end of VIII century on the Rurik Gorodishche, and by the end of X century on Minino settlement. The population of the Rurik Gorodishche has an advantage as there were more open, not forested space in the Ilmen Lake area being suitable for the house building, and for farming. However, the active expansion of the Rurik fortified settlement consumed the high volumes of the wood, so that the primary conifers were replaced by the secondary birch forests. Such a replacement was the most expressed on both settlements in the middle of XI century, and at the end of XII century.

Together with the forests' replacement, a general decrease of the forests, and increase of the farm fields and grasslands occurred. At the end of XII century around Minino settlement, the squares of the farm fields and grasslands were approximately equal, and the forests were significantly reduced. At the end of XIII century around Rurik Gorodishche, the landscapes became practically deforested.

As for the natural changes in the vegetation, we may make two conclusions. The first one: the warming in the middle XI century allowed an increased contribution of the broad-leaved trees to the forests around both settlements. The second one: it have been detected several events of cooling and the associated higher humidity at the boundary of X and XI centuries, XI and XII centuries, and at the end of XIII century. The former cooling event was one of the possible causes to decrease a status of Rurik fortified settlement. The latter cooling event, probably, promoted a degradation of Minino settlement.

DEEP GAP BETWEEN ABIOGENIC SYNTHESIS AND RNA-WORLD

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The RNA macromolecules is widely considered as an exclusive candidate to perform a key role in the pre-biology because of their ability to both the template-directed self-assembly and the specific catalytic activity. In this connection, it is important to understand if the RNA is a very peculiar macromolecule for abio-genous conditions. When answering this question positively, one usually means the property of homochirality [1]. Let us leave this important feature aside and address the question to peculiarity of nucleotide sequences in the RNA.

It is recognized that these sequences, as well as nucleotide sequences in the DNA and amino acid sequences in proteins, clearly demonstrate scale-free correlations inherent in the "Levy-flight" stochastic processes [2]. Template-directed assembling does not need peculiar sequences (except homochirality). However, given "purely random" sequences, a probability to re-fold of the PNA into the same structure is vanishingly small [3]. Indeed the very peculiar (Levy-flight) sequences are necessary to fold RNA-chains into the structures possess specific catalytic activity. At the same time, a part q of the Levy-flight-sequences among all possible sequences of the length N is estimated as $q \sim 4^{-\left(N-N^{2/3}\right)}$ [4]. This value becomes vanishingly small even for short RNA-chains. For example, if $N = 150$, $q \approx 4^{-123} \approx 10^{-74}$. Thus, the RNA functional (catalytic) specificity is closely coupled with such peculiarity of the RNA which was not occurred "by chance" at the abio-genous condition. With this in mind, one might suggest that early RNAs were originally made up of "purely random" sequences of bases. Then, as it may be thought, they were evolved due to abio-genous matrix replication, while the Levy-flight-sequences were selected already later. However, such pre-biotic scenario can not be accepted as well, mostly because selection of any peculiar sequences, e.g. the Levy-flight sequences, strongly limited under abio-genous conditions due to the error catastrophe [1,5]. By this reasons, a popular idea about that the RNA could constitute an "all-sufficient" pre-biotic world seems rather insubstantial. In fact, the RNA-world is actually "all-sufficient" only within a vanishingly small part of the sequence space, just as the valuable biological world, and in this sense it is by no means "simpler" than the earliest life. How could this problem be overcome? General aspects of this question are discussed.

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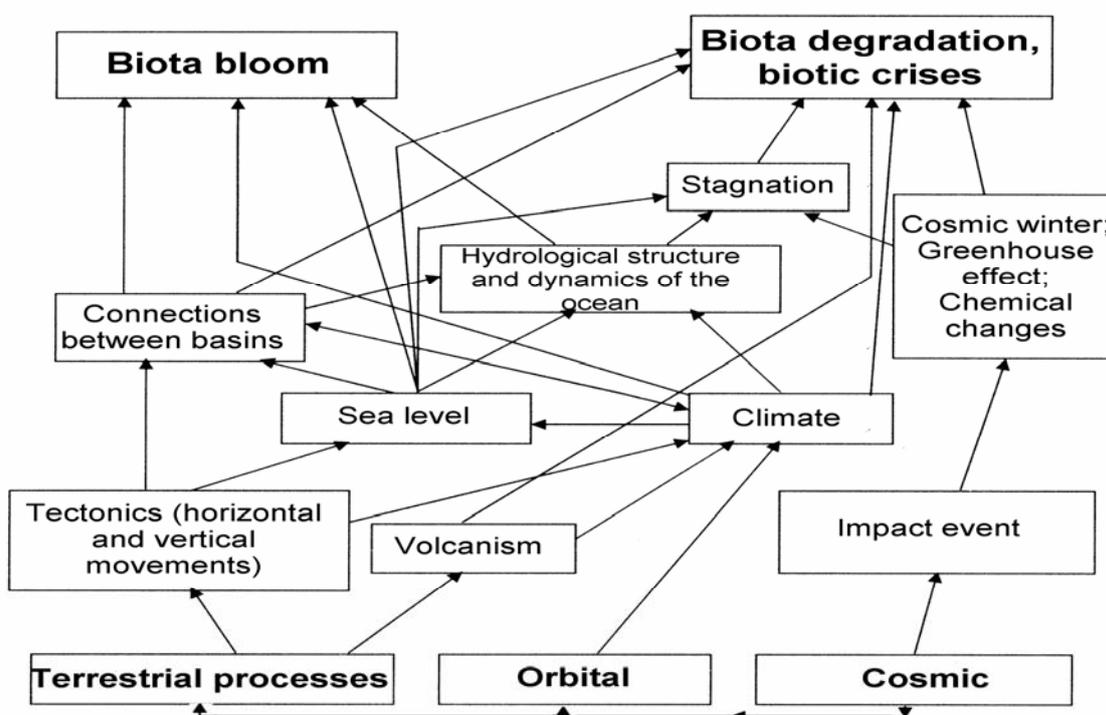
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DEVELOPMENT OF MARINE BIOTA IN THE PHANEROZOIC IN RESPONSE TO ABIOTIC FACTORS

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An analysis of the biota development in response to the changing of abiotic factors shows that long relatively stable periods of transgression, high-energy hydrodynamics, and diverse ecological niches are favorable for a growth of biodiversity and the abundance of organisms. Biota reduction is determined by sharp environmental changes, particularly by multiple alteration of opposite development trends (transgression-regression, warming-cooling, and others). In addition, events harmful for the development of organisms such as global anoxia in the oceans, powerful eruptions of trapp basalts and volcanism, and collision of the Earth with extraterrestrial bodies negatively influence the biota evolution. The impact of different factors is particularly notable during biotic crises. The abiotic factors influencing the biota development are determined by three fundamental causes: terrestrial, orbital, and extraterrestrial. Frequently, these causes and relevant factors were synchronous or almost synchronous in terms of geological time. Inasmuch as there is no cause-effect relationship between them, we can assume that large-scale environmental changes are determined by general extraterrestrial factors originating beyond the Solar system.



Causes and factors responsible for marine biota bloom and degradation

COMPUTER SIMULATION OF EVOLUTION OF PHASE-SEPARATED AUTOCATALYTIC SYSTEM IN EXPERIMENTAL MODELS OF CHEMOSPHERE, THE PROTOTYPE OF EARLIER BIOSPHERE

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Theoretical models that have been used for mathematical simulation of evolutionary processes on the earlier biosphere, exactly, into chemosphere, since living cells didn't exist yet, are based on the scheme of experimental facility (Fig.1).

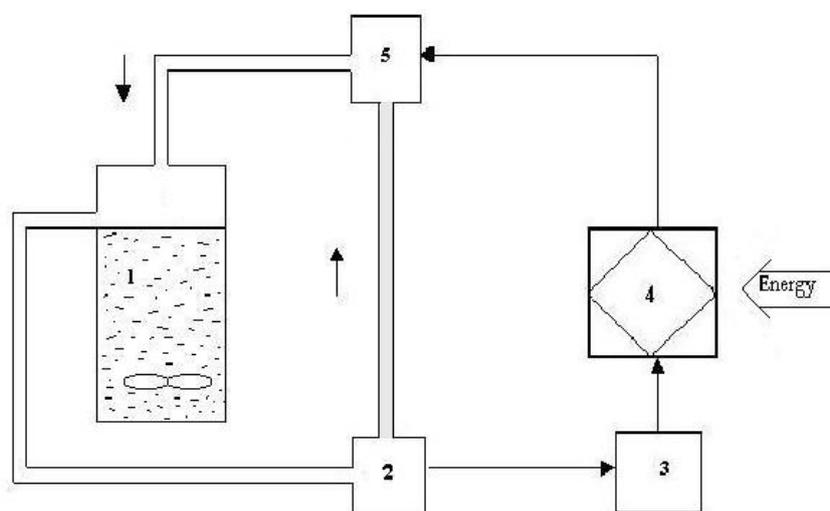


Fig. 1. Simplified scheme of experimental facility including closed cycle of matter turnover for simulation of initial stages of chemosphere evolution. 1. Flow reactor of ideal mixing simulating liquid environment where PSAS develops. 2. Separator, separating water from other substances in the reactor. 3. Depot of all substances that comes from the reactor. 4. Physicochemical block of substances regeneration. It is used for obtaining substances required for preparing reaction medium. 5. Device for preparing reaction medium.

Reagents necessary for origin and existing phase-separated autocatalytic system (PSAS) are feed into the flow reactor of ideal mixing with controllable rate. PSAS that have been formed in the reactor are evolving in the flow due to competition for reagents necessary for existing. Content of the reactor, which is taken from it, is separated on the clean water and other substances including “chemo-mass”, goes into depot, and then regenerates in physicochemical block. Water returns back into the reactor after adding required substances from the regeneration block.

It's assumed self-formation of PSAS in the reactor and their modifications occur with some small probabilities. Due to the competition on flow natural Darwinian selection takes place, and properties of evolvable PSAS change in certain directions.

Essentially more complex behavior is observed after origin of different types of PSAS in the reactor due to interactions among them. In this paper parasitical and symbiotic interactions are considered. There are plans to use the simulation results for purposeful laboratory experiments.

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THE COMPLEX INVESTIGATION OF DENTAL AND SALIVARY CALCULI AND MECHANISM OF THEIR FORMATION

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The collection of 120 dental and 13 salivary calculi was investigated by X-Ray diffraction, IR-spectroscopy. All analyzed stones have carbonate-hydroxyapatite as the basic mineral component, and whitlockite prevails only in one apatite-whitlockite sample of salivary calculi. The comparative analysis of mineral composition of pathological (dental and salivary calculus) and biological hard tissues (teeth) showed that the mechanisms of their formation are quite similar.

The wide spectrum of trace elements of dental stones is determined by synchrotron X-Ray fluorescence spectrometry. The method of optical emission spectrometry with inductively coupled plasma was used for determination of element composition of saliva. It was established, that content of such elements as K, Zn, Ba, Zr, Rb, Mn, Fe, Cu, Ni, V is maximum in analyzed samples of dental stones. Similar element distribution is observed in body fluids (saliva) of Omsk region inhabitants, which is caused by ecological situation in Omsk region. The incorporation of foreign ions in calcifications is associated with peculiarities of hydroxyapatite isomorphism, which mechanism is not well understood even today.

Also the amino acid composition of dental and salivary calculi and saliva was analyzed by reversed-phase high-performance liquid chromatography. The mass content (wt%) of amino acids varies from 5.23 to 7.69% depending on the stone type. The obtained results were processed by methods of cluster and dispersion (ANOVA) analysis. We can point out that qualitative and quantitative amino acids compositions varies in different stone types: 5.23 ± 1.49 % - dental calculi, 7.69 ± 3.20 % - salivary calculi. It is possible to assume that the protein substances play important role in process of calculi genesis.

Influence of some medicines on dental stone formation is investigated. It is shown, that acceptance of cardiological medicines leads to increase in concentration of potassium and sodium. As the result the structural properties of a saliva change and formation of dental stones is observed.

THE «GENE – PROGENE» QUASICYCLE AND EVOLUTION

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The theoretical approach in evolutionary biology is gaining wider. Recent genetical research has allowed to come close to the definition of the «life» concept. The problem of evolution may be now considered within the framework of the deductive approach. The interpretation for the fundamental concepts of the «gene» and the «progene» and their relationship model (*quasicycle*) are given in this report. The quasicycle model allows to define the essence of the living and to treat the evolution of the living as one of its manifestations.

The «gene» and the «progene» concepts. It is suggested to consider a DNA molecule region as «*progene*». «*Genes*» are the informational mobile products formed on DNA. This renaming allows to formalize the gene- progene relationship.

The «gene» – «progene» quasicycle. The activation of a progene by a gene, which in turn produces another gene, has been termed the quasicycle. The term *cycle* is used because it starts with a gene and ends up with a gene, and tern *quasicycle* (almost cycle) because the genes at the start and end are different. Ontogeny is composed of a set of consecutive quasicycles. Quasicycle passes also through the event of the conception of new organism. Quasicycle is an energy consuming process. *The process of undampening absorbtion and storage of free energy in the cyclic reaction is the essence of the process called life.* The specificity of the genes and progenes makes possible the processes to enfold in a definite sequence (to be programmed). The program is a cycle consisting with quasicycles. The cycle acquires a «*target*» as a definite quasicycle in the cycle.

Programmed development (ontogeny) and development as change in the program itself (*epigenesis*). The amount of energy in circulating form depends on the number of components in a cycle and on the number of interrelated cycles. The living organism is a complex of cycles. Living organisms are united into higher order cycles, including the biosphere cycle. Development according to a once arisen developmental program can proceed infinitely without change, entirely serving its designation (energy adsorption in the circulation mode). A cycle composed of quasicycles may be expanded by the incorporation of a new member, a cycle can also become a member of a higher ranking cycle. This results from mutational changes in progenes (*epigenesis*). Epigenesis is the base of biological evolution.

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Genetic model of quasicycle and evolution. The model in its generalized form describes real genetic events and can be, at the same time, the basis for the development of living matter problems. In terms of quasicycle, problems concerning life emergence, chemical evolution, conception and development of the genetic code, reproduction and expansion of the living, speciation, biocenosis, biosphere can be broadly considered. Traditional problems of evolutionary biology can be examined in a new light. These include the role of orthogenesis and selection in evolution, goal-orientation in living nature, the role of the environment in the evolutionary process.

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NANNOPLANKTON DEVELOPMENT IN THE PALEOGENE SOUTHERN OCEAN

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Two large periods in the development of the Paleogene Southern Ocean Nannoflora were distinguished: Paleocene-Eocene (I) period and Oligocene (II) period. They drop into 9 smaller stages:

1. Beginning of the Paleocene. The Cenozoic Nannoflora appeared on the Cretaceous flora background;
2. Early Paleocene. The new genera and species were formed. Up to the middle of the epoch the diversity exceeded 90 species;
3. Late Paleocene. The fast nannoflora development continued;
4. Early Eocene stage was marked by the high generation rates of the species;
5. Middle Eocene. Species diversity was at maximum (up to 140 species). The first cooling symptoms influenced the associations composition;

The active positive evolution took place during the above stages. The appearance of the new Cenozoic nannoflora was faster than its extinction;

6. Late Eocene differed with some elimination of the nannoflora species diversity, especially for the Antarctica close surroundings. Some Paleocene and Eocene species went out, and new species appeared, including ones with smaller coccoliths.
7. Beginning of the Oligocene is marked by the sharp temperature drop of the surface waters. The nannoplankton diversity momentum (about 110 species) kept tonus until the middle of this epoch, with no abrupt decline of the diversity upon the most of the Southern Ocean.
8. Late Oligocene was the time for sharp decline of the common abundance and the number of species. Association composition changed significantly. Some species began dominating. Species extinction prevailed.
9. Close End of the Oligocene. Associations contracted to 1-6 species due to extinction and retreat to the north. Some of the species dominated sharply. No new species appeared during all of the Late Oligocene.

Essential nannoplankton crisis in the Southern Ocean was related to the surface water temperature reduction, water stratification, and amplification of the hydrological processes. This was a replica to the start of the Antarctica criosphaera development, and establishing of the powerful deep Antarctic Circumpolar current.

**SPECIES COMPOSITION AND DISTRIBUTION OF FORAMINIFERS
IN THE BASIN WITH COLD BARITE/METHANE SEEPS
(SEA OF OKHOTSK)**

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Analysis of the composition and quantitative distribution of foraminifers in bathyal sediments collected at 14 stations in the Derugin Basin and at 11 stations in other regions of the Sea of Okhotsk, Sea of Japan, and North Pacific demonstrated specific foraminifer complex in the basin at depths from 1650 to 1800 m associated with cold barite/methane seeps. Poor community with prevailing agglutinated foraminifers and *Saccorhiza ramosa* as the dominant was shown to develop in these zones.

URBOGEOECOSYSTEMS AND THEIR POSITION IN ORGANIZATION OF BIOSPHERE

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Problems of ecological safety of urbanized parts of lithosphere, one of the largest ecosystems of the Earth, can not be effectively solved without modernization of theoretic-methodological base of geoecology, without taking in the account:

- a) the objective natural laws;
- b) structurally-and-hierarchical organization of biosphere as a phenomenon of geological nature and the major ecosystem on the planet;
- c) functions of its subecosystems.

In the report a new theoretical and methodological approaches to study the natural and anthropogenic ecosystems of the urbanized space of ecosphere and lithosphere as their ecological subsystems are presented. For denotation of urbanized ecosystems, which are limited de bene esse by the space of lithosphere, in accordance with offered approaches a concept of «urbogeoecosystem» is suggested.

The place of urbogeoecosystem at lower level of structurally-and-hierarchical organization of biosphere is determined.

NEW METHOD OF DATING OF OSTEAL FOSSILIZED MATERIAL

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The new elaboration of authors is directed on the research of the materials by methods of Nuclear Magnetic Resonance (NMR). In contrast to radiocarbon and thermal dating methods of the organic part (collagen) the new method suggested is based on analysis of both organic (carbon-13) and inorganic (phosphorus-31) components of the osteal stuffs.

This dating method is embodied in investigation of isotopes of both C-13 and P-31 in native state and solutions. The important merit of the NMR-spectroscopy is fundamental opportunity of the achievement of such experimental conditions, under which integral intensities of the signals is in direct to proportion to content of the nucleuses, responsible for these signals, the quantity of the nucleuses depends on age of the investigated material. The opportunity of gaining of the exact quantitative information about the content of nucleuses in different fragments of the object under investigation is realized. The high resolution NMR-spectroscopy for investigation of the objects is the exclusive method because of following important features:

1) All elements which are included in organic and inorganic parts of the osteal material possess magnetic active isotopes which may be registered on reaching the appropriate sensitivity level of the NMR-spectrometer.

2) Integral intensities of signals in NMR-spectrum under quantity experimental conditions are in direct proportion to the content of the appropriate atoms.

3) The chemical shifts of the NMR-signals of the different molecular fragments is observed in characteristic regions which permit to realize differentiate determination of them.

4) The applicability of the NMR-method for the quantitative fragmental and component analyze of the osteal material is not confine oneself to characteristics of they aggregative state, elemental composition and others.

5) The information about the molecular structure of osteal material forms in base of the data file according to the fragment composition.

Thus, the new methods which have been elaborating at present give an opportunity to forecast chronological chain of archaeological structure in base of the research of the osteal materials of wide chronological range.

MOLECULAR IMPRINTING OF TERPENOIDS AND NUCLEIC ACIDS IN INORGANIC MATRIXES AS A POSSIBLE PRE-BIOTIC STAGE

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Affinity plays an important role in transport and catalysis of biometabolites and in storage and duplication of genetic information. We propose the hypothesis for importance of organic-inorganic affinity on the same background as the traditional organic-organic affinity has. In our previous papers we have shown a highly specific enzyme-like action of some aluminosilicate nano-organized media. Particularly, the increase of particular product's selectivity or even formation of unusual products was observed. In order to prepare the affinic materials towards some important chiral biometabolites we carried out molecular imprinting of them in inorganic matrixes of aluminosilicate and aluminophosphate composition. To demonstrate the universality of the developed approach two extremely different metabolite classes were taken. The first class was presented by hydrophobic terpenoids: abietinic, dehydroabietinic and lambertianic resin acids, which are structurally similar to cell membrane components. The second class was presented by hydrophilic deoxyribonucleotides and deoxyribonucleosides, which are components of DNA and akin to those of RNA. By HPLC the prepared materials were found to be specific to selection of the used organic substance for imprinting (templates) from the mixture of the group of related compounds. The synthetic approach, sensitive to the chemical nature of the imprinted substance, allowed for the first time to prepare crystalline inorganic matrix specific to organics with anionic functional group. Owing to the specificity to the templates, the synthesized materials may act not only as collector of template's monomeric molecules but can polymerize them due to inherent acidity of aluminosilicate(phosphate) materials. Combination of collecting and catalytic properties may result in formation of chemical components of living cell as well as in their organization and encapsulation – the basic pre-biotic stage of the life evolution model.

BIOMINERALIZATION AS THE MAJOR STAGE OF DEVELOPMENT OF THE LIFE ON EARTH

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Biom mineralization is the major stage of evolution of the Earth - biospheres and alive highly organized organisms. Such interrelation (coevolution) has provided a variety of existing vital forms and geological abiotic environments of a planet.

The apatites of biogenic and abiogenous origins act as the major source of the information. The apatites mineral organisms open geochemical features of deposits, a biogeochemical cycle of phosphorus in the nature. Bioapatites, being the main component of a bone, reveal the laws of occurrence and evolution of mineral skeletonization of alive organisms, the mechanism of genesis of various bone gies. For what it is necessary to study the life of a bone: its modelling and remodelling, participation in the maintenance of a homeostasis of the internal environment on a physiological level, a "response" to the metabolic failures.

Our research is directed at studying the features of a bone fabric of the person at its pathological condition - deforming koxarthros, which is the defeat of structure of a hyaline cartilage of a hip joint that leads to its deformation. Such "lifeless" joint is replaced with an artificial limb.

Epiphyses of the femurs of the inhabitants of Omsk region removed at total prosthetic replacement at stage III of the disease (at the age of 40-70 years old) as object of research act. By means of modern physical and chemical methods of the analysis, it is established that crystal structure of a bone fabric is made up of non-stoichiometric carbonhydroxyapatatite of low degree of crystallization that is obviously connected with the presence of amorphous components. The technique of division of mineral and organic components of a bone was used in the research. The complex analysis of its components is being conducted. It is found that in pathogeny of the examined disease a change of the structure of a bone fabric of an articulate head takes place. The most part of phosphatic ions is replaced by the carbonate-ions, the reduction of the maintenance of an albuminous component is stated. The understanding of the laws of the interaction of mineral and biological components during the evolution of biosphere and on its present stage (noosphere) is important for the diagnostics of diseases of bone.

STUDY AND REVEALING LAWS OF NUCLEATION CALCIUM OXALATE IN AQUEOUS SOLUTION

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Biological mineralization is an important biological process in living organism. It can be a normal phenomenon such as the formation of bone and teeth or a pathological process such as the formation of renal stones (urolithiasis). However, kidney stone is a pathological manifestation of the phenomenon, exhibiting features typical of uncontrolled biomineralization.

The studies of physical and chemical properties of urinary stones are important to understand their formation. By the methods of X-ray diffraction, infrared spectroscopy and other it was established, that 22.5% calculi corresponded to calcium oxalate (calcium oxalate monohydrate, calcium oxalate dehydrate), 9.7% calcium phosphate (hydroxyapatite, struvite, brushite), 6.7% uric acid calculi, 47.3 % calcium oxalate/phosphate mixed calculi and 10.8% calcium oxalate/uric acid mixed calculi.

Development of thermodynamic and mathematical models of crystallization of some urinary stones constituents is one of the methods of study and understanding the specificity of this processes. Special attention on solubility of substances was paid to conditions of formation of crystals in urinary system: pH, temperature and ionic strength of urine. It was established, that in a hypothetical solution with mineral composition similar to composition of urine of healthy man, the formation of some crystal substances is possible such as: calcium oxalate, hydroxyapatite, struvite, brushite and uric acid. Results obtained on determination of composition of urinary stones have shown, that the most popular mineral is calcium oxalate, therefore first we developed the mathematical model of nucleation.

The given models reflect specificity of process crystallization in ideal conditions, however urine is a complex solution, which contain both inorganic ions and organic substances in particular proteins and amino acids. By the method of Ion-Exchange Chromatographer with spectrophotometerical detector we determined 14 amino acids in the composition of most popular types of urinary stones. The results obtained in the experiments permit us to assume that presence of albumin, Glycine and Glutamine acid in aqueous solutions decreased the general reaction order, nucleation time and rate constant of nucleation COM and inhibited growth and aggregation rates of its crystals.

Work is executed at partial financial support of the Russian fund of basic researches (grant № 06-05-65165).

MONOTHEIC RETICULOFENESTRA PSEUDOUMBILICA ASSEMBLAGE FROM THE KONKIAN SEDIMENTS OF THE TAMANSKII PENINSULA AND WESTERN CISCAUCASIA

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Nannoplankton from the Konka sediments of Taman peninsula and Pshekha River section (Western Ciscaucasia) were studied. The obtained results allow characterizing cycles of basin's development, studying of assemblages of nannoplankton in time and their reaction to the change of hydrologic parameters of the basin. A thorough study of nanofossils in the relatively deep-water sediments permitted the elucidation of faunal peculiarities important for the refinement of the regional stage boundaries. The impoverished, compared to the oceanic assemblages, nannoplankton complex lacks zonal species. The most diverse assemblage including 10 to 12 species occurs in the thin interval, then it rapidly becomes impoverished and is replaced by the monothetic *Reticulofenestra pseudoumbilica* assemblage. The number of *Reticulofenestra* coccoliths is so great that they become the rock-forming and make up a 1-m-thick marker bed obtained from the Konkian sediments of the Tamanskii Peninsula and Western Ciscaucasia.

The coccolith abundance and preservation are striking; the mass occurrence of whole, perfectly preserved coccospheres is observed in light and scanning electron microscopes. Almost all the *Reticulofenestra pseudoumbilica* coccoliths retained a tracery thinnest lattice on the proximal side. A thorough examination of samples from the marker bed showed that though *Reticulofenestra pseudoumbilica* composes the main body of the assemblage, the extremely scarce specific *Rhabdosphaera* sp. also occurs there. The flourishing of the monospecific assemblage is observed only within the marker bed. The nannoplankton suggest a rapid decrease of salinity in the basin. The flourishing of *Reticulofenestra pseudoumbilica* was most likely associated with the frontal contact zone of the river and marine waters or with the upwelling zone. Therefore, in the studied region the Konkian stage terminated with peculiar bionomic conditions. This work was supported by the Russian Foundation for Basic Research, project no. 06-05-60424.

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THE RADIOWAVE AS A SOURCE OF FREE ENERGY FOR THE SYNTHESIS OF ORGANIC MOLECULES INTO THE DROPLETS OF THUNDERSTORM CLOUD

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This paper advances the hypothesis stating that low-molecular-weight organic compounds, precursors of living cell components, may be synthesized from inorganic oxides in the presence of alternating electromagnetic field as an energy source. This synthesis can be implemented in the water droplets hovering in a thunderstorm cloud of the Earth or another planet prebiotic atmosphere. A stroke of lightning is known to excite a broad spectrum of electromagnetic waves. These, in turn, can excite the Langmuir vibrations of protons in water droplets. The molecular mechanism of this process has been described in detail [1, 2].

For the convenience of simulation, we will consider the ideal case, namely, that the Langmuir proton vibrations possess, on average, a spherical symmetry. This idealization does not contradict the physics of the process: since the object is spherically symmetrical, the geometry of stationary vibration processes taking place in this object should also possess a spherical symmetry. We will assume that the form of the Langmuir vibrations is represented by periodic thickening and thinning of protons in the central area of the droplet. We will discuss processes in droplets whose radius $R_0=5\times 10^{-5}$ cm, which corresponds to the average microbe size.

The activation energies of most homogeneous chemical reactions fall in the 1-3 eV range; therefore, in the central area with the radius $R=R_0/2$, the energy of protons is sufficient both for activating the reactions and for the synthesis itself to proceed. The calculations carried out in [1, 2] allow one to estimate the required amplitude ($E\approx 700$ V/m) and frequency ($\nu\approx 6\times 10^9$ Hz) for an electromagnetic wave able to excite the Langmuir vibrations of protons with an energy of about 3 eV.

The time spent for the whole process of synthesis of primary organic matter is much shorter than geological periods; under conditions formulated above, this time is only 1 s. An advantage of this model is the possibility of its real-time verification. As to my mine, the described processes can take place on the Earth at the nowadays.

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PRECAMBRIAN TRILOBOZOA: PREDECESSORS OF COELENTERATA?

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The Ediacaran (Vendian) Period is traditionally regarded as the time of Coelenterate radiation because of reconstruction of “cyclic” and “pinnate” fossils as medusoids or pennatularians. Indeed, these forms dominate in the Ediacaran communities, and in some fossil localities only these forms are preserved. Radial symmetry, medusoid appearance of “cyclic” forms and pinnatularian appearance of the frond-like ones are the main evidence supporting such an interpretation, but it does not seem to be the necessary and sufficient criterion for Coelenterate grade. An absence of some characters casts doubts in the assignment of Ediacaran “polyps” and “jellyfishes” to Coelenterata: there are no signs of tentacles, neither mouth nor coelenteron. Recognition of new morphological features of the Vendian fossils previously interpreted as medusoid organisms has completely changed their reconstructions. Many of “cyclic” forms are now reinterpreted as attachment disks of organisms, whose relationships are not yet understood (Gehling, 2000). Coelenterate organisms that can be directly compared to Phanerozoic members appear to have still been absent in the Vendian.

Ediacaran organisms are characterized by different kinds of radial symmetry including threefold organization, which is not typical of modern non-colonial Metazoa. All the Vendian and Early Cambrian organisms with triradial body plan were classified as Trilobozoa (Fedonkin, 1985). These fossil organisms can be attributed to four main life-forms: (1) sedentary frond-like organisms with basal anchoring bulb (triradial attachment disks); (2) sedentary hemispherical organisms (*Tribrachidium*, *Albumares*, *Anfesta*); (3) ovoid pelagic organisms (*Ventogyrus* and some other *Petalonamae*); (4) sedentary forms with tubular conic exoskeleton (*Vendoconularia* and some *Angustiochreida*). We could expect medusae-like planktonic Trilobozoa to be found. Thus, trilobozoan living-forms appear to have been simulated the living-forms of coelenterates (including ctenophores).

Being the closest relatives of the Vendian bilaterians, true Cnidaria are to be expected not early than Cambrian that is consistent with the data on comparative anatomy, embryology and molecular biology; namely metameric organisms with alternating left and right segments might be considered among possible ancestors of Cnidaria (Malakhov, 2004). Ovoid pelagic metameric trilobozoans, which developed a gastral cavity, settled on the sea bottom and could become the ancestral forms of metameric organisms mentioned above. This assumption can be the explanation for obvious parallelism between the life forms of Trilobozoa and Coelenterata: evolutionary trends in both Palaeozoic Coelenterata and their Precambrian ancestors might be uniform. This work is supported by RFBR 05-05-64825 and NSH-2899.2006.5.

CRYSTALLIZATION FEATURES OF MONOHYDRATE CALCIUM OXALATE

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Among the mineral phases which are making nephroliths, the spherulites of hydrated calcium oxalates ($\text{CaC}_2\text{O}_4 \cdot \text{H}_2\text{O}$) are most widespread. These are the crystallization products of high supersaturation, such processes are taking place in kidneys. It is important to find the influence of organic as well as of inorganic impurities (which are an integral part of a physiological solutions) on the monohydrate calcium oxalate during studies of its crystallization mechanisms.

The purpose of given work is to find out the regularity of the monohydrate calcium oxalate crystallization over an organic and inorganic makeweights in conditions, approached to the physiological solution parameters.

The results of XRD analysis and IR–spectroscopy of the sediments, which were obtained over an organic and inorganic makeweights with the different pH meanings, shows that in all experiments only monohydrate calcium oxalate were grown.

With the help of conductometric and dispersion analysis it was found that amino acids inhibit the growth of monohydrate calcium oxalate, reducing the average size of the crystals. The inhibiting effect of amino acids depends on its structure and increases with the extension of carboxyl groups and concentration of acid.

As the result of dispersion analysis:

1. The magnesium ions can also cause the inhibiting effect on the monohydrate calcium oxalate crystallization, increasing the critical supersaturation of the beginning of crystallization up to $\gamma = 20$, if the concentration of ions will correspond to a physiological solution (urea).
2. The ionic force ($I = 0.3$) of the biological fluid is a factor of stable supersaturated solution of calcium oxalate.
3. The presence of crystals of the hydroxylapatite in the solution causes the calcium oxalate crystallization processes.

The obtained results set the direction for researches aimed at the detection of a true role of fibers and hydroxylapatites in a formation of nephroliths and potential development of a synthetic peptides for use in urolithiasis therapy.

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ASYMMETRIC CATALYSIS IN PREBIOTIC CONDITIONS AS A POSSIBLE STEP ON THE WAY FROM CHEMICAL TO BIOLOGICAL STAGE OF EVOLUTION

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In the complex of contemporary conception of the origin of life in Earth one of the key problems that allow determining the conditions of transition from chemical to biochemical stage of evolution is the investigation of the possibility of enantiomerically enriched media formation without bioorganic catalysts. One of the decisive conditions required for the building of homochiral biopolymer having the capability for chirality transfer and multiplication in the absence of biological environment is the availability of at least enantiomerically enriched monomer substrate giving the opportunity for stereoselective polymerization. Asymmetric catalysis can be regarded as one of the prebiotic mechanisms for enantiodifferentiation, where the low-molecular organic compounds play the role of chiral inductors. At that, these compounds act as both organocatalysts and ligands in metallocomplexes.

Natural optically active compounds are the convenient models for the study as chiral inductors in catalytic asymmetric reactions. In our earlier work we developed procedures of synthesis of chiral P-, N-containing ligands starting from phytogetic tricyclic diterpenes [1]. As a result of our further investigations we designed the new synthetic routes to a number of optically active nitrogen derivatives of natural terpenoids. These amines, ureas, thioureas, and azomethines are able to serve as ligands for metallocomplex catalysts and as organocatalysts in a variety of most possible prebiotic reactions resulting in the formation of amino acids, amino- and hydroxycarbonyl compounds representing chiral building blocks for biopolymers.

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MID-INFRARED SEMICONDUCTOR WGM LASERS

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Whispering gallery modes (WGM) are universal linear excitations of circular and annular resonators. They have been first observed in 1910 in the form of sound wave travelling along the outer wall of a walk way in the circular dome of St. Paul's Cathedral in London and were investigated by Lord Rayleigh. Referring to the acoustic phenomenon the name "whispering gallery modes" was also coined for electromagnetic eigenmodes of circular resonators. Dielectric rings, disks or spheres can be used as passive or optically pumped active resonators with integrated active media. This paper is devoted to the development of electrically pumped WGM semiconductor lasers for the mid-infrared waverange.

The spectral range of 3-5 μm is extremely important for applications based on molecular spectroscopy. This range corresponds to a window of atmospheric transparency and, on the other hand, it contains strong absorption lines of hazardous or explosive gases. Spectroscopic systems based on tunable semiconductor lasers can be used for high accuracy and selective monitoring of these substances and in trace concentrations.

At present, there are no semiconductor lasers exhibiting high performance in the 3-5 μm range near room temperature, which makes difficult the development of corresponding systems for gas analysis. There are several types of semiconductor lasers able to operate in this spectral region such as type I double heterostructure or quantum well lasers, type II "W" lasers, interband cascade lasers or quantum cascade lasers. For different reasons all these lasers exhibit low gain decreasing with temperature and, consequently, require low loss waveguides to achieve high temperature operation. The Q-factor of the micro-disk resonator can exceed the factor of 10^6 . Thus, it is possible to obtain laser emission from the structures with relatively small optical gain. The use of the WGM resonators makes it possible to reduce lasing thresholds and consequently to increase operating temperatures of mid-infrared semiconductor lasers.

InAs based interband WGM lasers emitting in the 3-4 μm range have been reported by the Ioffe Institute and the Lancaster University. This investigation was awarded as the best work of the Ioffe Institute for 2005 year. These devices exhibit higher operation temperature than Fabry-Perot lasers fabricated from the same material but room temperature operation has not yet been achieved.

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Many particular tasks were solved:

- The mathematical modeling of the processes in the active region was performed including the processes of the radiative and non-radiative recombination, current distribution, optical gain-loss and optical mode distribution in the disk resonator for particular resonator geometries;
- MBE and MOVPE growth of above mentioned heterostructures for WGM lasers was developed;
- Post-growth processing was developed for all types of active media;
- Ring laser structures with various diameter of the active area, and with different deformation degree, was fabricated and studied;
- Extraction of output emission from WGM resonators was studied;
- Optimized design of mid-IR WGM lasers was proposed;

Conclusion: We have obtained laser emission in the mid-IR at 3 μm from a ring resonator DH diode fabricated by LPE. Coherent emission was observed at temperatures up to 125 K and was thought to originate from a whispering gallery mode. The results obtained earlier will be combined to realise room temperature mid-infrared WGM lasers.

We wish to thank Russian Foundation for Basic Research and FASIE for support of this work.

HUMAN IMPACT OVER NATURAL ENVIRONMENT IN THE SAMBIAN PENINSULA REGION DURING LAST TWO MILLENNIA

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In the course of the investigations conducted at the complex of archaeological sites in the Aleika River basin in the Sambian Peninsula (Kaliningrad Region, Russia) pollen studies were carried out. The obtained materials help to shape an idea on the character of changes in the natural vegetation cover within the territory in question, starting from the Iron Age. It was impossible to reconstruct environmental processes and separate events, not taking into account man-caused changes in natural geosystems. Human impact over the environment was related, first of all, to the character of land development (including forest clearing, arranging reservoirs, drainage of boggy plots, stock pasture, land tillage).

Main stages of evolution of vegetation cover during the last two millennia were determined for the territory of the Sambian Peninsula, as well as the role climatic and man-caused factors played in these transformations. Judging from the data of the pollen analysis combined with the information provided by the archaeological materials, a series of stages and regularities were singled out in the process of development of the investigated territory, starting from the Iron Age till the Modern Time. Only on the initial stages of opening up the territory in the Iron Age, pollen spectra show the characteristic conditions of forest landscape zone; by the early Roman period forests occupy separate plots only, while the share of meadows and arable lands increases substantially. It is in the Modern Time only (the 19th – 20th cc.), that forests' role increases again to a certain extent, owing to pine spreading.

According to the pollen data, the beginnings of agriculture in the investigated settlements' environs date as early as the late Iron Age, while the period of its flourish falls within the Middle Ages. Evidently, in this period the agricultural development of the region might be characterized as industrial-scale grain production. When analyzing the patterns of land development on different stages of settling the Sambian Peninsula starting from the Iron Age, it should be pointed out that man had to led permanent struggle with increased soil moisture and even temporal flooding low lands.

BIOLOGICAL INFORMATION SYSTEM FOR RESEARCHES OF CELL EVOLUTION

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The work is dedicated to the original method of biological information system (BIS) allows describing cell with any degree of accuracy that is available at the moment. The information n-dimensional model of live system for pre-biogenic synthesis and embryology researches is being developed. It is a number of dots in a closed space of the cell [1]. Each dot the geometric model consists of the set of the numerical indexes. These numerical indexes reflect the definite structural, energetic and histological areas. The scientific significance of BIS is connected with the development of a universal approach to creating a unified virtual informational imitation models for prospective research of biosphere origin and evolution. The application of BIS-modeling in mathematical morphology, embryology, ecological physiology, medicine computer diagnostic for stem cell therapy, bioinformatics, biomathematics, cell biophysics and clinical radiology practice gives encouraging results [2].

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COSMIC HIGH-ENERGY IMPACTS IN PREBIOTIC SYNTHESIS OF POLYPEPTIDES ASSOCIATED WITH ICY MATRIX

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Diverse carbon-containing compounds – from methane down to fullerenes – possessing a complex three-dimensional structure were discovered in different regions of interstellar space. They are thought to be originating on particles of interstellar dust clouds under the effect of cosmic radiation. Such molecules could have been synthesized long before the birth of life on our planet and even before it, the Planet Earth, came into being. Radioastronomical observations and studies of the «celestial» matter landing on our planet confirmed the presence of carbonaceous compounds in outer space. Terrestrial origin of organics must have been accompanied by substantial delivery of biological molecules from outside, thus making period of chemical evolution surprisingly short in geological scale. Since the primordial Earth had no atmosphere, the natural carriers, i.e. meteorites and cosmic dust particles, could get freely onto its surface and thus raise the concentration of organic molecules. In the interstellar medium the most probable source of organic molecules could be non-equilibrium processes driven by photons, cosmic rays, shock waves and solid bodies' collisions. Cosmic galaxy radiation originates from outside our solar system possessing the important constituent of 12% alpha particles (helium nuclei), 1.3% heavy ions (fully ionized ions of all elements from protons to uranium with $Z \leq 92$), 1% electrons. The dense cold phase of ISM host icy dust grains – important chemical catalyst during its life cycle. Such particles consist of mineral core composed by silicate or olivine admixed with metal sulfides and oxides, with the water-icy envelope containing organic molecules. Organic molecules in the ISM evolve and become later incorporated in solar system material (comets and meteorites). The formation of polypeptides from single aminoacids was traced in simulation experiments representing the inner structure of icy dust grains. Experimental chamber was irradiated at subzero temperatures at the dosage of 2.54 kRad/min. Solid frozen solutions of Gly and Phe were taken as the experimental samples inserted into the metal tube kept at subzero temperatures in the presence of liquid nitrogen. Formation of di- and tri-peptides was demonstrated after applying mass-spectrometry and HPLC techniques. Having polypeptides within the icy matrix, dust grains with ice mantles are transported to warm, dense, and active protostellar regions, where ultraviolet irradiation may become important and alter the grain composition. Furthermore UVC radiation may contribute to the formation of additional amounts of polypeptides, since short-wave photons are totally adsorbed by a thin outer layer. This presumption coincides with our previous investigations concerning UV impact on prebiotic formation of the main biological molecules. Combining of two irradiation types in different stages of interstellar flight could compensate the effects of low reagents concentration and temperature.

GEOLOGICAL CONDITIONS OF ORIGIN OF ENDEMIC FAUNA IN EIFELIAN TIME OF THE POLAR URAL MOUNTAINS

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The Eifelian Age in the European North-East was characterized by a stabilization of the sea basin after the Late Emsian transgression, which led to a strong differentiation of sedimentary conditions. The taxonomic diversity of tabulates in the region in this time was caused by qualitative changes in the genus-level composition. Representatives of Favosites and Squameofavosites have almost disappeared, whereas Alveolites, Crassialveolites, and Syringopora became widespread. Communities of tabulate corals now included more polyprovincial species. However, the facies differentiation of the sedimentary basin resulted in a partial isolation of some biotopes with a subsequent emergence of endemic forms there. One of these fossil biotopes has been found in the basin of the Syv'yu River, the left tributary of the Kozhym River (Polar Urals).

Deposits of the Eifelian Stage in the middle reaches of the Syv'yu River are composed by gray hummocky-bedded clay limestones alternating with organogenic detrital and clay limestones, and with thin interlayers of calcareous argillites. Limestones contain a rich fauna of stromatoporoids, tabulates, rugoses, brachiopods, and bivalves. The most representative in this biota is the fauna of tabulates, which together with stromatoporoids and rugoses compose small bioherms. Massive colonies of tabulates typically have a spherical or discoid shape; they normally occur in a lifetime position, but some coralla are overturned. It is assumable that this community occupied the littoral zone of the sea.

The tabulate assemblage in the section at the Syv'yu River contains 12 species of the genera Gracilopora, Alveolites, Crassialveolites, Caliapora, Scoliopora, Syringopora, Armalites, and Tetraporinus. Most corals are represented by colonies of syringoporids. The important feature of the Syv'yu assemblage is the co-occurrence of the globally distributed genus *Siryngopora* with genera Tetraporinus and Armalites. Species of Tetraporinus are not numerous and have a rather limited range. They are so far known only from the Lower Carboniferous of China and occur in the Silurian and Lower Carboniferous deposits of the Arctic areas of Russia. Forms of this genus have not been found in the Devonian deposits yet. Few species of the genus Armalites were found in the upper part of the Lower and in the lower part of the Middle Devonian of Kuzbass, and two species were established in the lower Devonian of Gornyi Altai.

THE NONENZYMATIC RECOMBINATION OF RNA OLIGONUCLEOTIDES CATALYZED WITH MAGNESIUM IONS

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RNA ligation reaction could be a powerful driving force for increasing of the complexity in the RNA world. Nonenzymatic ligation of RNA fragments could proceed in the oligonucleotides with 2', 3'-cyclophosphate end group that are generated in transesterification reaction of RNA molecules. We investigated nonenzymatic combined cleavage/ligation reaction of two RNA oligonucleotides in the presence of magnesium ions. Oligonucleotides CUCUCCUCCUGAAAA and GAGAGCGGAA were chosen to form the concatemeric double-stranded complex with dangling tetraadenilate tails, not involved in Watson-Crick base pairing and protruded out of the double helix. Though the low stability of the complex, the length of the double-stranded region and of the expected ligation products are not restricted.

This complex was incubated at 25–37 °C for 3-5 days in the presence of 5 mM magnesium ions at pH 9.0. The formation of dimer and trimer ligation products was shown. Products contain the novel sequence motifs, non-existing in the parent oligonucleotides. The yield of the ligation products reached 6%.

Analysis of the isolated dimer product demonstrated that at least 5% of the formed linkages were 3', 5'-phosphodiester (natural) bonds, the others are 2',5'.

Described cleavage/ligation reactions, catalyzed with different ubiquitous metal ions, could proceed in various complexes of RNA molecules, including pseudo-knots, bulges and loops. The emergence of RNA molecules with novel sequences and extended lengths demonstrates the possible contribution of the cleavage/ligation reaction to the development of the RNA world, representing a mechanism for the increase of the diversity of RNA sequences.

This work was supported by grants from FCSTP (RI012/001/254), RAS programs "Origin of life and evolution of the biosphere" and "Molecular and cellular biology".

**APPEARANCE AND DISAPPEARANCE OF RADIOLARIAN SPECIES
IN THE SEA OF OKHOTSK DURING THE LAST MILLION YEARS**

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The radiolarians were studied in the long sediment core IMAGES MD01-2415 from the Sea of Okhotsk. The number of radiolarian datum events (17 all in all) for the last million years is much higher compared to the previous data on different microfossils from the North Pacific.

Datum events mark the levels of the serious paleoceanographic changes during the Quaternary ice cycles, and the Mid-Pleistocene Climatic Revolution. There is a coherence between the paleoclimatic events and a specific down-core distribution of the extinct species. Radiolarians, disappeared during the warm stages or on the transitions to the latter, were abundant during the glacials or out of the interglacial optima. Radiolarians, disappeared during the glacials, were typical for the interglacials. A concurrency of the species' appearance and paleoclimatic changes is not so obvious.

The work was supported by RFBR.

**MACRO-KINETIC POPULATION DYNAMICS, BIOSPHERIC
EVOLUTION AND DEMOGRAPHY**

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New mathematical theory of population dynamics and demography is presented. Physico-chemical analogies of population dynamics are revealed and discussed. Broad range of nonlinear dynamics attributes in the evolution and stability of complex systems such as biosphere is applied.

BACTERIAL MARKERS IN PRE-CAMBRIAN OIL OF SIVA OIL FIELD

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The producing well N.1 of Siva oil field have stripped oil pool in sediments of bavlin age at depth of 2788-2800 m. Oil was of naphthenic-aromatic type and depleted in $\delta^{13}\text{C}$ (-3,05 ‰), it density was 0,9549 g/sm³.

According to GC-MS analysis of high-temperature oil fractions, hydrocarbons of sesquiterpene, triterpene, and hopane series were found. Polycyclic naphthenic hydrocarbons of hopane series could represent the fossils of *archea* membrane lipids which have kept their initial structure.

GENERALIZED HYDRATE HYPOTHESIS OF SIMPLEST LIVING MATTER ORIGINATION UNDER EARTH'S CONDITIONS

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This paper develops the original Life Origin Hydrate Hypothesis (LOH-hypothesis) assuming repeated simplest-living-matter formation from methane (or other methane hydrocarbon), niter, and phosphate under the Earth's surface or seabed within honeycomb structures of hydrocarbon-hydrates in the following sequence: niter diffusion into hydrate structure → formation of N-bases and riboses within structural cavities → phosphate diffusion from outside into structural cavities → formation of DNA- (RNA-) like molecules through polymerization → melting of the system and water-organic-soup formation → formation of amino-acids and simplest organelles in the soup → self-replication of nucleic acids and concentrating of the soup → formation of cells etc. LOH-hypothesis is supplemented with the sub-hypothesis of formation of deposits of hydrocarbon-hydrates. Life origination is considered as a phenomenon thermodynamically caused and necessary for the atomistic world subjected with a definite natural conditions. The mechanisms for each step are proposed. LOH-hypothesis is initiated by results of calorimetric studies of sorption-desorption processes in systems water – biologically-active substances, by surprising coincidence between the sizes of hydrate structural cavities and N-bases, riboses, and phosphates, and by analysis of available works. Extended thermodynamic calculations and observed natural phenomena proving the feasibility of the supposed processes are presented and discussed. A new possibility for understanding the mysterious homochirality of nucleic acids, a PC experiment for examination of this supposition, and the principal scheme and conditions for a laboratory experiment capable of testing the LOH-hypothesis are also proposed. If the LOH-hypothesis is proved, it will give the clue for the most intriguing riddle of Nature and show that living matter had originated repeatedly and, possibly, originates presently in the regions where deposits of necessary chemical substances are located under appropriate conditions.

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TITAN AND ASTROBIOLOGY

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Ever since the close encounter with Titan by the Voyager 1 Spacecraft in 1980, there has been intense speculation about the possible relevance of current chemical reactions on Titan to pre-biological chemical evolution on Earth and Mars. This talk will review the latest findings of the Cassini- Huygens Mission to the Saturn system in this context. The lakes and rivers of liquid hydrocarbons, the dunes of deposited organic aerosols, the active ion-molecule reactions and photochemistry in Titan's atmosphere all offer intriguing subjects for future investigations. Models for the origin of the atmosphere itself seem to support the now classical Miller-Urey model for the early Earth, possibly offering one of the most relevant aspects of Titan for astrobiology.

THE CULTURE-SPHERE OF THE EARTH

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Till now, - at least in the Russian science, - the opinion dominates, that the mankind exists inside relationships which were installed in biosphere. Breaking of these relationships leads a planet to eco-catastrophe and loss of life. Supporters of the concept of a noosphere (Le Roy E., 1927, Vernadsky V.I., 1945) though stand apart of this opinion, but essentially do not separate conditions of the Earth state before and after occurrence of Homo sapiens. For these scientists the noosphere is biosphere modified by human mind. But the concept "intellect " hardly has terminological meaning accepted by all. If to start from the definition of culture, as a set of the fixed emotional-rational activity results of the person (Pchelenko S.P., 2005) it is possible to reach more certain understanding, that the mankind transforms world around all set of those emotional-rational displays of its vital functions which are fixed by it as elements of culture.

I think, that synthesis of the concepts mentioned in the first paragraph, allows to make a following step. The moment of occurrence Homo sapiens on the Earth it not only the moment of occurrence of new superbiogenetic state of a matter (*superorganic* according to Kroeber A., 1917) – human culture. But also the moment of occurrence of new sphere of the Earth – sphere of existence of human culture. By analogy to biosphere (*the sphere of existence of a life* according to V.I. Vernadsky, 1926) there are all reasons to termed it as *culture-sphere*.

Considering the culture-genesis at a level of its most complex formations – occurrence of more and more complex national, and then super-national civilizations - it is necessary to assume the globalization of culture-sphere of the Earth from the most complex civilization formation, instead of occurrence of the inter-civilizations formation coordinating culture-genesis, to be the most probable way of increasing the mankind controlled factor of influence on a course of culture-genesis,.

ANTIBIOTIC RESISTANCE OF BACTERIA FROM PERMAFROST SEDIMENTS AND ITS SIMILARITY TO THAT OF PRESENT BACTERIA

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According to current view, before the wide spread use of antibiotics, resistant bacterial strains were a small fraction of the microorganism ecosystem. It is suggested that environmental bacteria provide a natural reservoir of antibiotic resistance genes which can then be transferred to clinically relevant bacteria (D'Costa et al., 2006). Certain advantages for investigation of antibiotic resistance among environmental bacteria may have the isolates from subsoil sediments, especially from permafrost that represents the biotopes of the preantibiotic epoch. Bacterial strains from more than 50 samples of Arctic permafrost subsoil sediments dated from 5 thousands to 3 millions years were examined for the capacity to reinstate viability on nutrient media supplemented with different antibiotics (streptomycin, kanamycin, tetracycline, gentamycin, chloramphenicol). The collection of antibiotic resistant strains of ancient bacteria including Gram-positive (Firmicutes, Arthrobacter) and Gram-negative bacteria (Bacteroidetes, γ -Proteobacteria, α -Proteobacteria) was created. The strains resistant to two and three different antibiotics were isolated. Among strains resistant to streptomycin the ones with strA- strB genes coding for aminoglycoside phosphotransferases closely related to those of present-day bacteria and the strains with aadA genes determining aminoglycoside acetyltransferases were revealed. Genes closely related to catA gene was detected in the chloramphenicol resistant strains and gene closely related to tetC gene was determined in "permafrost" strain resistant to tetracycline.

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LUMINESCENCE OF STABLE DENSELY PACKED STACKING AGGREGATES OF NITRIC BASES AND MODELING OF FIRST STAGES OF CHEMICAL EVOLUTION

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Stable stacking aggregates of adenine, adenosine and cytidine have been revealed in water solutions at concentrations of 10^{-2} – 10^{-4} M by the fluorescence and its excitation spectra methods [1]. At 10^{-4} M spectra coincide with the same spectra of corresponding dinucleotides [2]. Revealed stacking aggregates do not dissociate at 85 °C whereas the usual stacking aggregates in adenylic dinucleoside monophosphate dissociate at 27 °C (data of UV and CD spectroscopy). The excitation spectra of fluorescent stable stacking aggregates have exciton splitting about 3500 cm^{-1} that gives the unusually small interplane distance $\sim 3.0\text{ \AA}$ (dense packing). This small distance may be the cause of stability of aggregates. We suppose that the stability may also be caused by the water and cation bridges between the nitrogen atoms of the different molecules in the aggregate. These bridges play the role of sugar-phosphate chain in RNA molecules.

The stability of the fluorescent stacking aggregates of nitric bases allows us to interpret them as precursors of RNA molecules in chemical evolution (proto-RNA).

The replication mechanism of stable stacking aggregates without any ferments based on consecutive rises and falls of temperature (1–20 °C) is proposed. The mechanism is partially confirmed experimentally for mixed Ade+Thy and Ade+Ura water solutions. We think the “world of stable densely packed stacking aggregates of nitric bases” had preceded to “RNA world”.

A new definition of the first life phenomena is also proposed and the variants of first life in systems without nitric bases are discussed. The role of attractors in chemical evolution is discussed also.

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ENVIRONMENT OF ANCIENT MAN AT NORTHWESTERN AND CENTRAL ALTAI IN THE PLEISTOCENE

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The results of the study the small mammals fauna from the five cave sites: Ust-Kan cave, Charyshskii naves (Central Altai); Strashnaya cave, Hyena den cave (North-Western Altai) in the 1999-2006 seasons are provided. The stone tools of ancient man were disclosed in the each cave excepting Hyena den cave. The accumulation of osteological material in this came without human participation. In others caves human participation took place. The sites have different ages. The oldest deposits are in the Ust-Kan cave. It contains a characteristic of Early and Middle Pleistocene association of voles. The age of the others caves is Late Pleistocene-Holocene.

As a result of studying the fauna of small mammals from Paleolithic sites I suppose, that open landscapes were widespread in Pleistocene and Holocene at Altai. There were steppes, semideserts and nival areas. Our investigation also shows that there is a dependence between structure of fauna of small mammals and geological age, geographical location and of the height above the sea level. The mosaic landscapes were expressed greatly. Especially this fact is noticeable on the Altai North-Western sites, which are situated below 1000 m at the sea level (fig. 1). The climate in Pleistocene was more soft and humid, than nowadays, that is important for human migrations.

Age, location Height above the sea level (m)	Late Pleistocene		Holocene	
	Central Altai	North-Western Altai	Central Altai	North-Western Altai
Over 1000				
Below 1000				

Designations:



Fig. 1. Dominate biotopes at the Altai region in Pleistocene and Holocene.

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THE BALANCE OF ORGANIC SYNTHESIS AND DESTRUCTION IN THE EVOLUTION OF BIOSPHERE

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Biosphere is a global ecosystem which develops according to the laws of ecological succession. The balance of synthesis and destruction is the most important ecosystem developmental quotient. The analysis of literature data makes it possible to come to conclusion that the mass of living material has been increasing throughout the evolution of biosphere. The most plentiful growth took place at the initial development stages, especially when the ozone layer appeared. The colonization of dry lands resulted in further growth of the biomass which continued even after the full colonization of space. The growth of the living material and photosynthetic index of the biosphere took place until the period of neogene. The prevalency of synthesis over destruction facilitated the accumulation of the mortmass. It is a well-known fact that before the neogene there was a constant formation of coal, oil and gas fields. Even nowadays in sedimentary deposits and swampy ecosystems of the Variable Zone the enormous amounts of organic carbon are stored every year. All the above mentioned facts make it possible to come to conclusion that the growth and development of the global ecosystem continues.

In the modern era the global processes are being shifted towards destruction because of the man's interference. This is primarily connected with the fossil fuel firing, with extermination of the living vegetation on the land and in the ocean, with desertification. The consequences of these distortions are as follows: the biota is unable to maintain the natural dynamic balance between synthesis and destruction. This is manifested first of all in the constant growth of carbon dioxide concentration in the atmosphere. From the point of view of the global ecosystem, equally dangerous is the accumulation of recalcitrant organic wastes of anthropogenic origin which upsets this balance. But we know that in the evolution of biosphere there was a good few periods of destabilization caused by external factors. One can assume that the involvement of enormous mortmass's amounts into the active processes is quite regular because it encourages the activation and further development of the global system. Perhaps, the current destabilization of the biosphere has a naturally temporary character. The examination of past periods shows that the destabilized biosphere does not lose its functions. While dealing with the problem of the global ecological crisis special attention should be paid to the utilization of recalcitrant organic wastes.

**DEVELOPMENT OF PHYTOCENOSES IN ENVIRONMENTS
CONTACT AREA**

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Introduction

Under the condition of natural and anthropogenic transformation of the environment, it is very important to study the vegetation structure in contrast territories both in interzonal and of intrazonal environmental systems. Thus, the main task is to find out the regularities determining the peculiarities of biocenotic interplays within a system providing its functional importance at any level. The phytocenoses of transitional territories have a specific structure. They differ functionally from the cenoses of zonal vegetation or of altitudinal belt and determine the continuity of a biocenotic cover. The elevated activity of ecological processes at contrast territories reflects the evolutionary adaptation of phytocenosis resulting in formation of a vegetation of a spatially and genetically particular type. The cenoses of environments contact can reflect spontaneous dynamics of environments at local, regional or global level.

Discussion

As under the condition of environments contact a complicate spatial diversity of vegetation with the evolution of cenoses in a particular time occurs, we have to mean here probably a paragenesis in vegetation development. There are different opinions on paragenesis phenomena in formation of concrete environments [1-3]. In our opinion, the formation of phytocenoses having vegetation with features of other environmental zones (or altitudinal belts) with extrazonality effect can be considered as a paragenesis phenomenon. The availability of cenoses diverse cenotically and dynamically, the species composition of which consists of plant species of different morphology, ecology and areology just manifests paragenesis in the tendencies of vegetation development in environments contact areas.

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THREE-DIMENSIONAL NUMERICAL SIMULATION OF DUST IN CIRCUMSTELLAR DISKS

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Study of circumstellar disk dynamics and protoplanets formation is an important problem of astrocatalysis, since it gives an idea what processes have an influence on distribution of certain elements over a circumstellar disk, which are essential for organic synthesis. At the same time dust component of disk has a strong impact on the behaviour of the whole system.

Investigation of dynamics of dust disk is a problem of collisionless gravitational physics. To solve this problem there was created 3D numerical model, based on numerical solving of collisionless Vlasov equation and Poisson equation using particle-in-cells method. With the help of this model we performed series of numerical experiments, aimed at study of processes which lead to protoplanets formation.

It was found that under a certain ratio of radial and azimuth dispersions of velocities in dust disk with massive protostar there were radial flows of matter appeared due to the intersections of Keplerian orbits of individual particles, similar to the Saturn's rings. These flows were able to drive evolution of azimuth instabilities in two-components (gas and dust) disk.

Obtained results of numerical experiments have a close intersection with another important problem of circumstellar disk simulation. There is no approved knowledge what initial conditions should be taken, and what is the initial distribution function of matter in circumstellar disk. This function is known only for later stages of disks, when all planets have been already formed. Use of density profiles like exponential or power may introduce uncontrolled modifications of simulation results. For solving this problem we developed approach, based on tracing evolution of dust disk to its final stationary state. This state, combined with some known perturbations, is considered as initial one. Since model of circumstellar disk has a big number of various parameters, we obtain an opportunity to understand what is an impact of each of them on the dynamics of the whole system.

TO THE SKELETON ORIGIN OF STROMATOLITES

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The application of concept skeleton historically is connected with existence of solid parts in eukaryotic organisms. Mineral macroformations of prokaryotic nature – stromatolites – are known more than 150 years and primarily were considered as skeletons of stromatoporates and sponges, though they possess a sufficient structural analogy with skeleton of primitive metazoan eucaryotes. Recently the prokaryotic nature of stromatolite formations was stated and skeleton nature of stromatolite was denied because prokaryotic macrobodies were unknown.

On the basis of the reversible differentiation in the recent communities of filamentous cyanodacteria as an organismic state of community integrity (Sumina, 2006) the stromatolite may be regarded as a particular case of differentiation with formation of supporting mineral body as a skeleton in view of its origin, structure and function.

Macroskeleton origin of stromatolite appears as co-ordination of its structure features for different hierarchical levels – type of building and structure of its individual parts and microstructure. Co-ordination appears also in the time-varyence of stromatolites features. The type of building is also controlled biologically and appears both in case of column top division (branching) and in absence of accretion for the approaching columns (Raaben, 1964).

Microscopically a form transition from inductive-type biomineralization (banded type of low riphean stromatolites microstructure) to a matricated or some analogue type (condensed type of microstructure for upper riphean forms) was observed.

Matrix-type biomineralization structures are known for recent cyanobacteria and appear sufficient analogy to skeleton eukaryotic structures (Lowenstam, 1984). The time-depending type change for skeleton biomineralization observed also for eukaryotes (Barskov, 1984).

Accordingly, presence of the inductive type for biomineralization has no contradictions with the skeleton origin of mineral formations.

MEGAPHYLOGENESIS: FROM PROBIONTS TO EUKARYOTES

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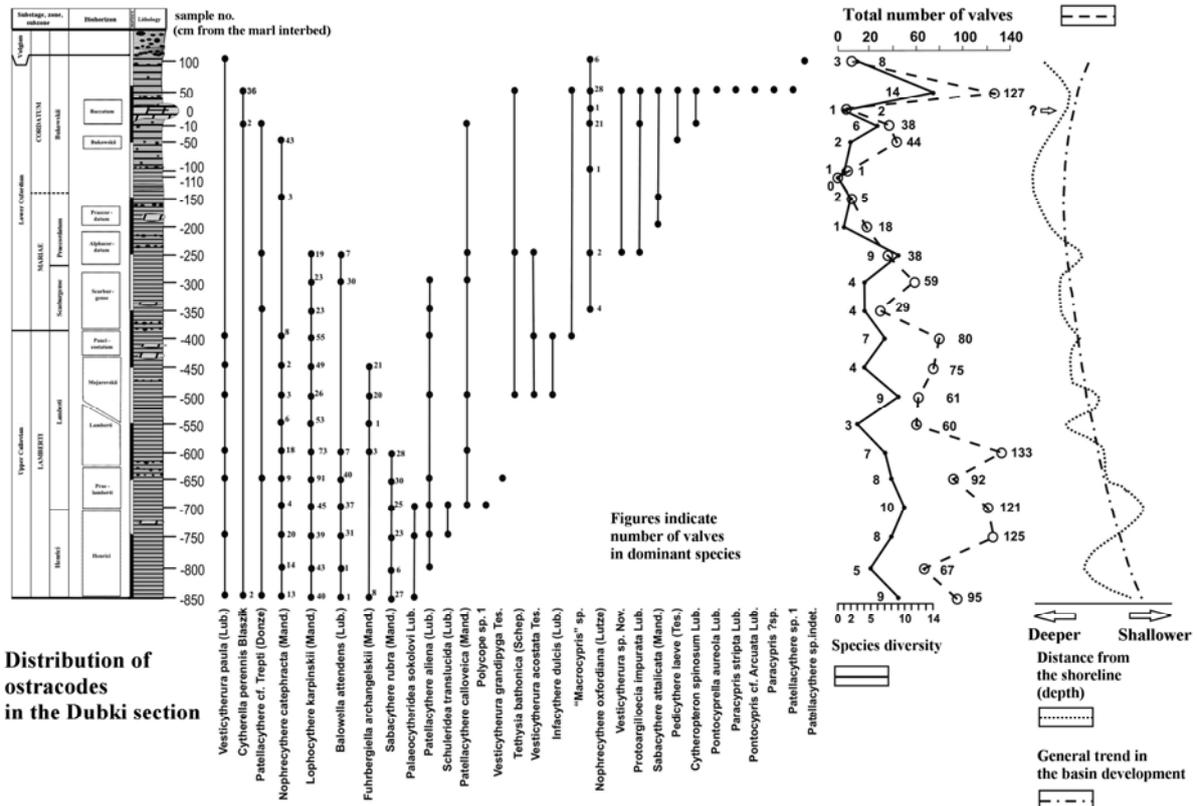
An effort has been made to treat phylogenesis processes by and large in the context of a non-canonical theory of heredity, according to which a necessary condition for hereditary information to be stored, encoded, transmitted and realized lies with the organization of genes into governing gene and epigene networks. It has been shown that epigenes and epigene systems straighten out general hereditary variability and thus canalize the evolutionary process to some extent. Moreover, these systems provide the means of realizing *Non-Darwinian evolution strategy*. The notion of a *virtual canal of heredity* has been introduced, that binds an arbitrary species, via chain of parents and offsprings, to all its ancestors starting with the first probionts. A procedure has been put forward to reconstruct the oldest phylogenetic history of an arbitrary representative of any taxon using a law which is the reverse of the Haeckel-Muller biogenetic law, thus enabling to obtain a number of contentions about initial stages of phylogenesis. Also, a hierarchy of phylogenetic processes has been established by their speed; these are macro-, micro- and megaphylogenesis. Characteristic time periods of macro-, micro- and megaphylogenesis processes differ respectively at least by three orders. The introduction of temporal hierarchy for phylogenetic processes when mathematically described allow in a number of cases to substitute sets of algebraic equations for those of differential equations that essentially simplifies the study of phylogenetic processes.

POPULATION ANALYSIS OF OSTRACODE COMMUNITIES OF THE LATE CALLOVIAN-EARLY OXFORDIAN OF THE DUBKI SECTION (THE VOLGA REGION NEAR SARATOV)

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Diverse (30 species) and abundant associations of ostracodes from the transitional Callovian-Oxfordian deposits of the Dubki section (the Volga Region near Saratov) have been studied (fig.). Taphonomic features of these associations indicate an autochthonous burial of all assemblages. As inferred from a rather rough, costate-cellular or spiny sculpture of most forms, the presence of several dominant species in paleocommunities, and frequent changes of structure and density of populations, caused by instability of environment with fluctuations of salinity, temperature, and ground types, the studied ostracodes represent a shallow-water off-shore association of a marginal shelf zone. The comparison of change dynamics in the structure of ostracode communities (variations of species diversity, changes of dominants) with variations in ostracode numbers in the section allow to assume some transgressive-regressive cycles in the Late Callovian and Early Oxfordian with their amplitude gradually decreasing near the boundary. Taking into account the Late Jurassic marine water stratification with the cold water mass at the bottom of the basin and the warm



one near the surface (Tesakova, Rogov, 2005), the intervals with the maximal diversity of ostracodes probably corresponded to regressive events.

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GROWTH OF MICROORGANISMS AT MARTIAN SUBSURFACE CONDITIONS: LABORATORY MODELING

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Modern environmental conditions on Mars prohibit liquid water existence in surface layer of martian soil because of extremely low atmospheric pressure. But according to observational data large amount of water ice presents in subsurface layers of Mars. In this case ice is able to intensive sublimation if the surface is heated enough by sunlight. According to TES data temperature of some areas of martian surface can be heated up to 300 K at daytime. Under such conditions vapors diffuse through the porous surface layer. As a result the “wet layer” appears under sand’s surface. In our experiment we used special vacuum chamber for modeling process of ice sublimation and vapor diffusion while heating. In order to model it we used water ice sample covered by several centimeters of sand with weight fraction of organic matter (glucose) $\sim 10^{-5}$ – 10^{-4} . Ice sublimation was provided by radiation heating of sand’s surface. We studied possibility of growth of microorganisms in the “wet layer” under three different temperatures: 280 K, 300 K and 200 K. Bacteria *Vibrio* sp. X were added to the sand. We carried on several three days experimental runs of the intensive sublimation of ice. As a result, we have discovered the increase of bacterial population in the “wet layer” after each run at 280 K and 300 K. These results confirm that shallow ground ice and a few hours of heating per day could provide sufficient conditions for growth of bacterial population under martian surface. Environments of some areas of modern Mars are close to that we have modeled in our experiments.

BIOMIMETIC SYNTHESIS OF THE COMPLEX HETEROCYCLIC SYSTEMS INVOLVING CYANOACETYLENE – A COMPONENT OF INTERSTELLAR PROTO-SUBSTANCE

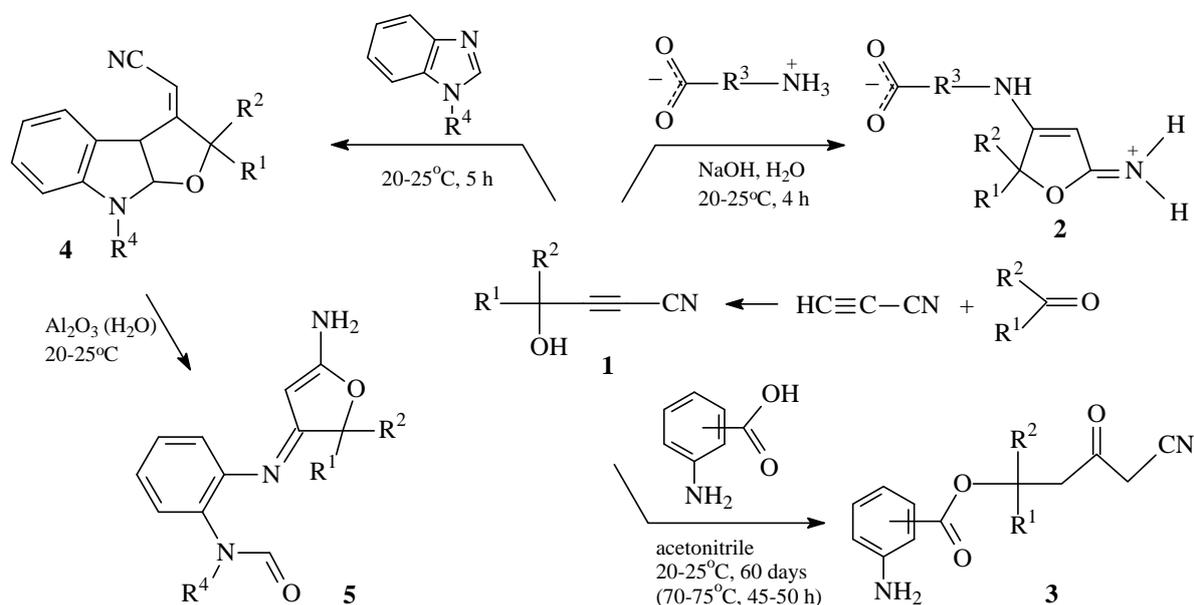
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The role of cyanoacetylene and its derivatives (found in interstellar space), in particular hydroxycyanoacetylenes **1** in a self-assembling process (abiogenic synthesis) of the complex heterocyclic compounds has been evaluated.

It has been found that the hydroxycyanoacetylenes **1** act as “active building blocks” in the reactions with aliphatic and aromatic amino acids as well as with 1-substituted benzimidazoles. The reactions proceed under biomimetic conditions to afford functionally substituted amino acids **2**, cyanoaminobenzcarboxylates **3**, condensed heterocyclic systems – 1,3-oxazolidinodihydrobenzimidazoles **4** and aminophenylformamides **5**, which are likely to be involved in the protobionts formation.



$R^1 = R^2 = \text{Me}$; $R^1 = \text{Me}$, $R^2 = \text{Et}$; $R^1 - R^2 = (\text{CH}_2)_n$ ($n = 4, 5$);

$R^3 = (\text{CH}_2)_n$ ($n = 1-3, 5$), Me_2CHCH , $\text{Me}_2\text{CCHCH}_2\text{CH}$; $R^4 = \text{Me}$, Et , $\text{HC}=\text{CH}_2$, $\text{H}_2\text{C}-\text{CH}=\text{CH}_2$

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