

## 地球生命の普遍性 Understanding the generality of terrestrial life

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We only know the life on the Earth. In this presentation I am going to evaluate the system especially genetic system of terrestrial life. Water is needed for life to solubilize the molecules and especially important to maintain the structure of protein. Protein is needed to almost all activity of life, especially catalytic activity that is carried by the protein called enzyme. All terrestrial living organism consists of (a) cell(s), surrounded by membrane. Membrane is maintained by the hydrophobic interaction driven by the hydrogen-bonding network between water molecules. Genetic information is used to form the structure of enzymes to induce catalytic activity, forming the arrangement of amino acid residues. What are the necessities and what are the coincidences? I will present some clues to the questions. These can be useful for searching for life in the Universe.

キーワード: 細胞, 有機化合物, 細胞膜, 遺伝物質  
Keywords: Cell, Organic compounds, Cell membrane, Genetic material

## Extremophiles under pressure: Integrating experimental and field studies at deep-sea hydrothermal vent sites

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In the great depths of the Earth's interior, forces capable of moving continents sculpt the seafloor and form volcanoes transferring materials and energy to the ocean. Seawater circulation within these magmatic provinces results in the development of deep-sea hydrothermal vents that are often considered to resemble the conditions on early Earth. It is under these extreme conditions that, by a synergy of chemistry and biology, life thrives in the absence of light and sparse nutrients. Notably, anaerobic chemolithoautotrophic bacteria that inhabit these extreme environments tend to branch deeply in the tree of life, probably retaining relics of early metabolic pathways.

Here, we present data from shipboard continuous-culturing incubations of hydrothermal vent fluids conducted during an R/V Atlantis-ROV Jason/Medea expedition to the deep-sea vents sites (2500 m) at 9°50'N East Pacific Rise (January of 2014). This was accomplished through a multi-disciplinary and multi-institutional collaborative effort to collect; transfer and culture vent fluids from the diffuse flow sites, onboard the vessel under seafloor pressure conditions (250 atm). Experiments were designed to study the cycling of N through the metabolic processes of denitrification and dissimilatory nitrate reduction to ammonia (DNRA) under *in-situ* deep-sea vent temperature and pressure conditions.

In detail, we studied the growth/metabolism of nitrate-reducing microorganisms at mesophilic (30 °C) and thermophilic (60 °C) conditions at pressures ranging from 5 to 250 atm. A high pressure bioreactor was employed onboard the ship to allow direct study of the biological functions of microorganisms collected from diffuse-flow vent fluids (Fig. 1). This experimental approach facilitates continuous culture of microorganisms at temperatures ranging from 25 to 120 °C and pressures up to 680 atm. The system allows incubating microbial communities in medium enriched with dissolved gases, under aerobic or anaerobic conditions, while permitting periodic sampling of the incubated organisms with minimal physical/chemical disturbance inside the reactor.

Experiments conducted simulate the subsurface biosphere environment and the continuous mixing of seawater and hydrothermal fluids in the oceanic crust. Vent fluids were delivered to the bioreactor under high pressure and homogeneously mixed with aqueous media solution enriched in dissolved nitrate, hydrogen, and <sup>13</sup>C-labeled bicarbonate to facilitate the growth of nitrate-reducing chemolithoautotrophic bacteria. Two distinct sets of experiments were carried out for 356 and 100 hours. During the course of the experiments we monitored the growth of deep-sea microbial communities by measuring cell density and the concentrations of dissolved aqueous species directly involved in nitrate based metabolism, such as NO<sub>3</sub><sup>-</sup>, NH<sub>4</sub><sup>+</sup>, H<sub>2(aq)</sub> and H<sub>2S(aq)</sub>. Subsamples were also collected for a number of shore based analyses to determine: i) the <sup>15</sup>N/<sup>14</sup>N isotope composition of NO<sub>3</sub><sup>-</sup>/NH<sub>4</sub><sup>+</sup> and constrain kinetic isotope effects associated with denitrification/DNRA; ii) to study the rates of autotrophic carbon fixation by NanoSIMS; iii) to perform single cell genomics on the microbial populations grown in the bioreactor and (iv) to isolate and characterize novel microorganisms from the communities established in these experiments. In short, experimental results constrain the function and metabolic rates of the native denitrifying microbial communities residing at moderate temperature conditions (30 °C), while DNRA metabolic pathways were identified for the populations residing at higher temperature diffuse flow fluids (60 °C).

キーワード: extremophiles, deep-sea hydrothermal vents, chemolithoautotrophic bacteria, high pressure, continuous culture, nitrate-based metabolism

Keywords: extremophiles, deep-sea hydrothermal vents, chemolithoautotrophic bacteria, high pressure, continuous culture, nitrate-based metabolism

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## 祖先生物超好熱菌説の確実さの検証 Robustness of the thermophilicity of ancient organisms

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All of the modern organisms are thought to have evolved from a single common ancestor named Commonote (1). In order to investigate the environmental temperatures of the ancient organisms, we resurrected amino acid sequences of ancestral nucleoside diphosphate kinases (NDKs) that might be hosted by the last common ancestors of Archaea and of Bacteria. The enzyme catalyzes the transfer of a phosphate from a nucleoside triphosphate to a nucleoside diphosphate. The ancestor of NDK family is thought to have been possessed by the ancient organisms because most extant cells, from bacteria to human, contain the gene(s) that encode a member of this family of proteins. More importantly, the denaturation temperature of a NDK correlates well with the optimal growth temperature of its host. Therefore, we can estimate the environmental temperature of the ancient organisms by reconstruction ancestral NDK's amino acid sequences and characterizing their thermal stabilities. In our previous study (2), the ancestral amino acid sequences of NDK were inferred from two phylogenetic trees with different topologies using a maximum likelihood program. The sequences were then reconstructed and characterized. From thermal denaturation experiments of the reconstructed enzymes, we estimated that the common ancestors of Archaea and of Bacteria lived at 81-97 °C and 80-94 °C, respectively. The Commonote was also likely to be a (hyper)thermophile that lived at a temperature above 75 °C. However, a criticism for our conclusion is that the ancestral sequences have been inferred with an assumption that the amino acid composition has been constant through evolutionary time. Gouy and coworkers (3) predicted the amino acid sequences of ancestral proteins using a Bayesian method that does not assume the constant evolutionary process through time. They estimated the optimal environmental temperature of the ancestral organisms from the amino acid composition of seven amino acid types: leucine, isoleucine, valine, tyrosine, tryptophan, arginine, and glutamate. Based on the analysis, they suggested that the archaeal and bacterial ancestors were thermophilic but the Commonote was not a thermophilic organism. In this study, we re-inferred ancestral NDK sequences using the same Bayesian program. The ancestral NDK sequences were inferred from two phylogenetic trees. One tree was built without constraints and the other with the constraint that Archaea and Bacteria each represent a monophyletic group. The gene encoding the ancestral NDK sequences were synthesized, expressed in *Escherichia coli*, and then the ancestral NDKs were purified. Thermal denaturation measurements showed that the newly inferred ancestral NDK sequences are also extremely thermally stable. Therefore, our conclusion of the (hyper)thermophilic ancestry is robust even if the ancestral amino acid sequences were inferred without the assumption that the amino acid composition has been constant over evolution.

(1) Yamagishi et al. In Thermophiles: the keys to molecular evolution and the origin of life? (1998), pp287-295.

(2) Akanuma et al. Proc. Natl. Acad. Sci. USA (2013)110, 11067-11072

(3) Boussau et al. Nature (2008)456, 942-947

キーワード: 祖先タンパク質復元, コモノット, ヌクレオシドニリン酸キナーゼ, 超好熱菌

Keywords: resurrection of ancestral proteins, Commonote, nucleoside diphosphate kinase, hyperthermophile

## アミノアシル tRNA 合成酵素の分子系統樹から見た真核生物の起源 Origin of Eukarya based on phylogenetic trees of aminoacyl-tRNA synthetase

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Woese ら (1990; PNAS 87:4576-4579) は、16S/18S rRNA に基づいた分子系統樹を作成し、全生物を3つのドメイン (真正細菌、古細菌、真核生物) に分類した。この3ドメイン間の系統関係、特に真核生物の系統学的位置については、真核生物が古細菌とは独立に進化したとする3ドメイン説と、古細菌から進化したとする2分岐説の間で議論されているが、結論は出てない。近年ではゲノムデータの増加に伴い、多くの遺伝子を同時に用いた全生物の系統解析が報告され、2分岐説を示す結果が多く得られている (Guy & Ettema 2011; Trends Microbiol. 19:580-587, Williams et al. 2012; Proc. Biol. Sci. 279:4870-4879, Williams et al. 2013; Nature 504:231-236, Williams & Martin Embley 2014; Genome Biol. Evol. 6:474-481)。しかしながら、真核生物と最も近縁な生物種については複数の可能性が示されている (Thiergart et al. 2012; Genome Biol. Evol. 4:466-485, Rochette et al. 2014; Mol. Biol. Evol. 31:832-845)。これらの結果から、真核生物起源の成立過程は複数提案されており、未だに議論が続いている。

本研究では、23種のアミノアシル tRNA 合成酵素 (ARS) の遺伝子の分子系統樹を作成し、それを比較することで全生物の系統関係を議論した。現存する生物は全て翻訳系をもっており、少なくとも全生物共通祖先以前にこのシステムが成立したと考えられることから、ARS の進化を調べる事は生命の初期進化の本質的理解に繋がる。真核生物は、細胞質で使用される ARS とミトコンドリアや葉緑体で使用される ARS を別々の遺伝子として持ち、それぞれが別の進化経路を辿っていることが知られている。今回は、真核生物の起源が持っていたと考えられる細胞質型の ARS の系統的位置と近縁な生物種に注目した。

まず、BLAST 検索を用いて23種の ARS のアミノ酸配列データ (118種:真正細菌 57:古細菌 23:真核生物 38) を収集し、23種のデータセットを構築した。それぞれのデータセットについてアライメントを行い、最尤法 (RAxML) とベイズ法 (PhyloBayes) を用いてそれぞれの遺伝子系統樹を作成した。また、近縁な ARS 同士を用いて複合系統樹を作成し、それぞれの遺伝子系統樹の根の位置を推定した。

解析の結果、23種の系統樹の内、13種の系統樹では真核生物の細胞質型 ARS が単系統であり、7種の系統樹では多系統であった。残り3種の系統樹のうち、2種は真核生物の細胞質型 ARS が存在せず、1種は細胞質型 ARS が真正細菌群と姉妹群であったため、考察から除外した。真核生物の細胞質型 ARS が単系統であった13種の系統樹の内、真核生物の系統学的位置は9種の系統樹で古細菌の内群となり、4種の系統樹で真正細菌の内群となった。多系統となった7種の系統樹でも、細胞質型 ARS は古細菌もしくは真正細菌の内群となった。これら20種の系統樹から2分岐説が支持された。

9種の系統樹の内3種では、細胞質型 ARS は TACK superphylum に属する古細菌と最も近縁であったが、別の3種では Euryarchaeota と近縁であった。これらの結果は、真核生物が TACK superphylum と Euryarchaeota の双方に由来することを示し、両者の起源が融合した生物が真核生物の起源であったのではないかとすることを提案する。また、真正細菌の内群となった4種の細胞質型 ARS は、全て別々の真正細菌と最も近縁だった。このことは、別々の真正細菌のゲノムから真核生物起源の核ゲノムへ独立した遺伝子水平伝播が起こり、伝播された遺伝子が真核生物起源の細胞質型に置き換わったことを示す。さらに、細胞質型 ARS が多系統になった7種の系統樹は、真核生物の進化の過程において古細菌もしくは真正細菌由来の独立した遺伝子水平伝播が細胞質型 ARS の置き換わりを起こしたということを示す。

以上を総括すると、真核生物の祖先は TACK superphylum の起源と Euryarchaeota の起源が融合した後に、様々な真正細菌由来の遺伝子水平伝播の影響を受け進化した生物であったと考えられる。

キーワード: 分子系統解析, アミノアシル tRNA 合成酵素, 初期進化, 真核生物の起源

Keywords: phylogenetic analysis, aminoacyl tRNA synthetase, early evolution, origin of Eukarya



## たんぽぽ計画における国際宇宙ステーションへの打ち上げ後初の報告 The First Report of the Tanpopo Mission after Its Arrival to the International Space Station

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To investigate the panspermia hypothesis and chemical evolution, The Tanpopo mission has been developed as Japan's first astrobiology-driven space experiments since 2007 (Yamagishi et al., 2009). This "Tanpopo" mission is launched this spring and it will be likely to start its first-year exposure on the ExHAM pallet onboard the Kibo Exposed Facility of International Space Station (ISS) by the time conference will be held.

The Tanpopo mission is composed of two main experimental apparatus: capture panels and exposure panels. Both will be prepared inside the Kibo module and exposed via airlock with its robot arm up to the maximum of 4 years. The capture panels are to intact capture micrometeoroids, space debris and possible terrestrial aerosols uplifted to the ISS orbit by the world's lowest density silica aerogels exposed to space. If the Tanpopo succeeds to capture terrestrial microbes embedded in the aerosol particles in the aerogel capture panels, it will push the upper limit of existing altitude for terrestrial microbes from the current record of 77 km to 400 km from the ground.

We also test both the survivability of some terrestrial microbes and the chemical alteration of astronomical analog organic compounds in the near Earth space environment. For the former, we emphasize on the importance of cell-aggregates, whose concept is known as "masapanspermia" (Kawaguchi et al., 2013), as the ark for interplanetary transfer of microbes

It is planned that the first samples of both panels will be retrieved back to the Earth in mid-2016, for post-flight analysis initially at ISAS and then at laboratories nationwide by the Tanpopo Team members.

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- Yamagishi et al., 2009, Trans. JSASS Space Tech. Japan, 7, ists26 (2009), pp. Tk 49-55.  
Kawaguchi et al., 2013, Origins of Life and Evolution in Biospheres, 43, 411-428.

Keywords: space experiment, ISS, panspermia hypothesis, chemical evolution

## 部分循環湖貝池の嫌気的水塊下でのリンと鉄の初期続成作用 Phosphorus and iron cycles during early diagenesis of sediments under anoxic water mass in a meromictic Lake Kai-ike

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鹿児島県上甕島貝池は、海洋と砂州で隔てられた部分循環湖である。砂州深部から浸入する海水と、低塩分の表層水との密度差によって湖水の経年的な成層が生じている。このため湖の深部は有機物分解により嫌気的な環境を呈する。水深4-5mに存在する湖水の酸化還元境界には、嫌気的な光合成を行う紅色硫黄細菌が生息している。堆積物表層には、主に緑色硫黄細菌によって構成されているマット状構造が見られる (Nakajima et al., 2003)。このような環境は、大気中の酸素濃度の急上昇前で還元的な環境が卓越していたとされる約24億年以前や、白亜紀 OAE のモデルと見なすことができ、過去に存在した海洋環境を理解する手がかりとなりうる (Oguri et al., 2003)。

本研究で着目したリンは生体必須元素であり、生物の一次生産の制限栄養元素 (limiting nutrient) でもある。また鉄は redox-sensitive element であり、溶解態の Fe(II) が酸化されると鉄酸化物が沈殿するが、その際にリンを吸着する。そのためリンも初期続成作用の過程で酸化還元状態の変化に敏感に影響を受け、海洋の還元化が進むと負のフィードバックを働かせる。すなわちリンの堆積物への埋没は大気中の酸素濃度と関連している可能性がある (Van Cappellen et al., 1996)。リンの初期続成作用に関する研究は、現代の酸化的海洋で多くなされており、本研究では嫌気的水塊下の貝池堆積物 (KAI4 コア; Yamaguchi et al., 2010) に着目した。リン及び鉄の存在形態別分析を行い、酸化的水塊下での地球化学的挙動との比較、OAE など過去の無酸素環境の復元への応用を目的とした。

堆積物試料中のリンは SEDEX 法 (Ruttenberg, 1992) を参考に、 $P_{abs}$  (吸着)、 $P_{Fe}$  (鉄結合態)、 $P_{auth}$  (自生)、 $P_{det}$  (砕屑性)、 $P_{org}$  (有機態) の5形態に、鉄については Poulton et al. (2005) を参考に、 $Fe_{HCl}$  (HCl 可溶)、 $Fe_{carb}$  (炭酸塩)、 $Fe_{ox}$  (酸化物)、 $Fe_{mag}$  (磁鉄鉱)、 $Fe_{resi}$  (残渣) の5形態にそれぞれ分画、定量した。

貝池最深部の11.5mから採取された KAI4 堆積物の表層において、全リン中の割合が最も多かったのは  $P_{org}$  であり、深さ約5cmで急激な減少が見られた。二番目に割合が多かった形態は  $P_{Fe}$  であったが、 $P_{Fe}$ 、 $Fe_{ox}$  はいずれも堆積物表層でピークは見られなかった。これは、鉄酸化物の自生の沈殿は生じていないことを示唆する。また、 $Fe_{py}$  は堆積物最表層では検出されず、深度を増すごとに存在量が増加した。

酸素が溶解する現在の海洋では、堆積物表層で生じるリンの鉄酸化物への吸着・埋没と、堆積物内部で生じる鉄酸化物の還元に伴うリンの間隙水への再放出、というリン-鉄サイクルにより、間隙水中のリン酸濃度は高く保たれ、自生アパタイトの沈殿が促進される (Slomp et al., 1996)。しかし、湖底に酸素が溶解しない貝池では堆積物表層の鉄酸化物の存在量が少ないため、間隙水中のリン濃度は自生アパタイトを形成する程高くなく、堆積物深度が増しても  $P_{auth}$  はほとんど増加しない。さらに、 $P_{Fe}/P_{org}$  比と  $P_{auth}$  の形成の度合いが正の相関を持つことから、 $P_{Fe}$  と  $P_{org}$  の量比がリンの埋没に深く関連していることが推測される。主に有機物分解から生じたリンは間隙水中に留まることなく水塊中に放出されていると考えられる。また、堆積物表層における鉄酸化物の沈殿は生じていないが、 $Fe_{py}$  の沈殿も見られなかった。その代わりに、 $Fe_{carb}$  の小さなピークが見られたことから、堆積物表層付近では  $Fe_{py}$  を生成するほどの  $H_2S$  は存在しないことが示唆される。 $Fe_{py}$  の存在量は深度を増すごとに増加し、それにしたがって過去の酸化還元状態を示す指標の DOP (degree of pyritization;  $Fe_{py}/(Fe_{py}+Fe_{HCl})$ ) や  $Fe_{HR}/Fe_{tot}$  の値も増加する。

貝池同様、過去の嫌気的環境で堆積したリンも大部分が水塊に戻り、結果として嫌気的水塊中に蓄積したリンは微生物活動や一次生産の強化、さらに酸化還元状態の変化のトリガーとなっていたことが示唆される。

キーワード: リン, 鉄, 初期続成作用, 嫌気的有光層, 嫌気的水塊

Keywords: phosphorus, iron, early diagenesis, photic zone anoxia, anoxic water mass

## 系外惑星探査によるアストロバイオロジーの展開 Development of Astrobiology with Exoplanet Explorations

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近年の系外惑星の研究の進展は目覚ましい。有力候補も入ると 5000 個以上の系外惑星候補が報告されている。すばる望遠鏡などでは木星型惑星の直接撮像観測も可能な時代になった。その結果、さまざまなタイプの主星のまわりに多様な惑星が存在することが明らかになった。とりわけ、NASA のケプラー衛星によるスペーストランジット観測や長期にわたる地上視線速度法観測により、スーパーアースや地球型惑星は恒星の型によらず多数存在することが明らかになった。しかし、ケプラー衛星で発見された惑星はいずれも遠方に位置し、数 10 光年以内の近傍の恒星のまわりのこれらの軽いハビタブル惑星は未開拓である。我々は、多様な環境における生命の普遍性に迫るべく、(1) 近傍の赤色矮星 (M 型星) のまわりの様々な惑星を検出するための専用施設を長期観測に向けた海外に建設し、多数のハビタブル惑星を検出すること、および、(2) とりわけ地球型惑星については、開発中のすばる望遠鏡用高精度分光器 IRD を用いた大規模サーベイを行う事を検討している。発見される惑星は、2022 年にファーストライトを迎える TMT30m 望遠鏡などによる、非地球型環境 (低光度・高活動性をもつ主星まわり) における生命のなりたちを研究する最適な対象となるだろう。

キーワード: 系外惑星, 赤外線, ハビタブル惑星, 赤色矮星  
Keywords: exoplanet, infrared, habitable planet, red dwarf



## 低質量星周りのハビタブル地球型惑星探索 Search for extrasolar Earth-like planets in the habitable zone using InfraRed Doppler and the Subaru

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Planetary systems around low-mass stars are attractive targets to search for Earth-mass planets in the habitable zone because Doppler signals caused by the planets are relatively large and the habitable zone of the low-mass stars is located at close-in orbits. For the advantages, we have a plan to conduct a planet search program of low-mass stars by the Doppler method using a new InfraRed Doppler (IRD) instrument to search for Earth-like planets. IRD to be mounted on the Subaru telescope in 2015 is composed of a very stable near-infrared high dispersion echelle spectrograph and a laser-frequency comb as a wavelength calibrator of the radial velocity measurements. The main goals of the program are to detect Earth-mass planets in the habitable zone and to understand statistical properties, formation and habitability of extrasolar Earth-mass planets around low-mass stars.

We performed a survey simulation of our planet search program using IRD and the Subaru telescope and estimate expected numbers of detectable planets around low-mass stars based on the results of theoretical population synthesis. In this simulation, we expect more than 50 planets including the more than 30 Earth-mass planets and 10 Earth-mass planets in the habitable zone on a suitable survey plan. And we would detect some transiting planets in the habitable zone, which can characterize planetary atmosphere and may discuss the habitability of the planets by making follow-up observations.

Keywords: Earth-mass planets, low-mass stars, habitable zone

## 太陽系外惑星の輻射環境にさらされた光捕集複合体の吸収効率 Absorption efficiencies of light-harvesting complexes exposed to the photoenvironment of extrasolar planets

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The detectable size of extrasolar planets, which are planets outside our solar system, is getting smaller. Recently, an Earth-size planet has already been discovered in the habitable zone, the region where a planet can hold liquid water on the surface. By obtaining spectra of exoplanets, a lot of information is derived. For instance, the surface type affects the spectral shape. If we detect the signal of vegetation on exoplanets, it will be a direct evidence of trace of life.

However, trace of vegetation on exoplanets is uncertain when the primal star is different from the Sun. As the first step before detecting trace of vegetation on the planets, it should be examined what kinds of photoenvironments are acceptable for photosynthetic organisms on the earth. Significant processes of photosynthesis, light absorption and excitation energy transfer (EET) processes, occur in light-harvesting complexes (LHCs) that contain photosynthetic pigments. Particularly, we modeled the two processes in the LHC in purple bacteria (LH2), which absorb longer radiation than that in plants, since planets around M dwarfs or M stars (cooler than the Sun) will be the observational targets. We investigated how efficiently the LH2 system absorbs light energies depending on stellar radiation using the quantum chemical calculations.

To begin with photosynthetic pigments, the absorption spectra are calculated to evaluate absorption efficiencies under seven stellar radiation spectra at the top of atmosphere (TOA) of the planets. The pigments and LHC have three main absorption bands: Soret, the Q<sub>x</sub> and the Q<sub>y</sub> in order of the wavelength. We found that, among the six major pigments, the efficiencies around higher temperature stars, the F, G and K type stars, vary depending on whether Soret bands are placed blueward or redward of 4000 Å break, which is a steep change due to the absorption by some metals in stars below 400 nm. Around the M stars, Soret bands do not contribute the efficiency anymore. Alternatively, Q<sub>y</sub> bands affect the efficiencies crucially.

Moreover, the EET process in the aggregation system of LH2 is investigated. The EET velocity becomes double when two pigments in the central antenna are exchanged to the pigments with low excitation energies (from 850 to 890 nm). We also found that the efficiencies using estimated spectrum of the 19 LH2 system are maximized offset from the solar effective temperature (5778 K). The Soret band still has a contribution to the efficiency because the band is just around 4000 Å break.

In order to estimate the efficiencies on planetary surfaces where the organisms inhabit, the planetary atmospheric effects are considered using simple radiation transfer calculations. The contribution of Q<sub>y</sub> region is affected due to absorption bands by water vapor. Atmospheric conditions, i.e. oxidizing earth-like or reducing, vary the efficiencies around M stars significantly than those around the Sun. This is particularly because of the spectral overlapping in the Q<sub>y</sub> region.

In order to examine conditions which would lead to effective light absorption around M stars, we evaluate the efficiencies with different conformations of the pigments and the LH2 and the solvent. The wavelength of absorption shifts about 120 nm longer in the 19 LH2 system whose central metals of the pigments are exchanged to Pd, compared to that without the metals.

In any conditions as considered the planetary atmospheres, Soret bands contribute the efficiencies due to being enough redward of 4000 Å break. Therefore, in the history of the Earth, there is a possibility for the organisms to have evolved the Soret band to absorb light energies effectively.

## 低地球周回軌道環境を利用した生体有機物の無生物的生成の検証 Verification of abiotic formation of bioorganic compounds by utilizing Low Earth orbital environment

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原始天体上での生命誕生に先立ち、アミノ酸、核酸などの生体関連分子が無生物的に生成したはずである。原始天体上での化学進化において、宇宙からの寄与（宇宙線や太陽紫外線など）の寄与が重要であったと考えられる。これまで、室内模擬実験においてそれぞれのエネルギーの寄与についての研究はあったが、実際の宇宙からのこれらのエネルギーフラックスにより有機物進化が可能かどうかは確認されていなかった。われわれは、国際宇宙ステーション曝露部環境を利用してその検証かどうかの検討を行った。その結果、たとえば、タイタン大気をモデルとしたメタン(5%)・窒素(95%)の混合気体を約30 mLの金属容器に封入したものを、国際宇宙ステーションのきぼう曝露部に1年以上曝露することによりアミノ酸前駆体の生成が期待できることがわかった。

キーワード: 惑星大気, 宇宙線, タイタン, 太陽紫外線, アミノ酸, 国際宇宙ステーション

Keywords: planetary atmospheres, cosmic rays, Titan, solar ultraviolet light, amino acids, international space station

## 初期地球における隕石衝突による核酸塩基とアミノ酸の生成 Formation of nucleobases and amino acids by meteorite impacts on early Earth

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Emergence of biologically important molecules on the prebiotic Earth was a critical step for the origins of life. Miller-Urey type synthesis was once demonstrated the formation of these molecules, such as amino acids and nucleobases. However, reduced atmospheres replicated in those experiments are not realistic considering hot accretion of primitive Earth and hence, this raised questions about how such biologically important molecules were formed. Impact-induced reaction is a potential process that provides these molecules on the early Earth. Formation of a few simple amino acids, amines, and carboxylic acids has been demonstrated in experimental simulation of impacts [1-3]. In this presentation, we report the formation of biologically important organic molecules in experiments simulating reactions induced by extraterrestrial objects impacting on the early oceans. The products contained cytosine and uracil, which are nucleobases found in both DNA and RNA. Proteinogenic amino acids, glycine, alanine, serine, aspartic acid, glutamic acid, valine, leucine, isoleucine, and proline, were also formed as well as non-proteinogenic of  $\beta$ -alanine, sarcosine,  $\alpha$ -amino-n-butyric acid, and  $\beta$ -aminoisobutyric acid. Furthermore, methylamine, ethylamine, propylamine, and butylamine were found in products. These organic molecules were formed from impact-induced reactions from iron, nickel, forsterite, water, and ammonium bicarbonate. The yields of produced organics were dependent on the amounts of both metallic iron and ammonium bicarbonate in the starting materials. Estimates based on the experimental results suggest that the formation rate of biologically relevant organics by impacts exceeded the rate supplied by carbonaceous chondrites and was comparable to the flux of interplanetary dust particles (IDPs), although the concentrations of such organics in IDPs remains unclear. These results significantly expand the availability of building blocks of life on the prebiotic Earth.

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キーワード: 生命の起源, アストロバイオロジー, アミノ酸, 隕石, 衝突, 有機物

Keywords: Origins of life, Astrobiology, Amino acid, Meteorite, Impact, Organic compounds



## 初期地球における有機物ヘイズの衝突成長と内部構造進化 Collisional growth and the evolution of the internal structure of Archean organic haze particles

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初期地球における暗い太陽のパラドックスに関して、様々な議論がなされてきた。恒星モデルによって太陽の光度が今より低いことが示されている一方、地質学的証拠によって水や原始生命の存在が示唆されており、この矛盾の解明が必要である。地球の表面温度に影響を与え得る様々な要因が存在するなか、アンモニアやメタンなどの温室効果ガスは大きく注目されてきた。温室効果ガスが温暖化にどの程度寄与していたかを知るには、当時の地球を覆っていたヘイズの遮蔽効果や冷却効果を調べることが必要不可欠である。

初期地球のヘイズはタイタンのヘイズと類似性がある。ヘイズを構成している粒子は、粒子の最小単位であるモノマーから始まり、大気中を落下しながら衝突成長し、内部に空隙があるフラクタルな粒子になる。しかし従来のシミュレーションではこの構造が無視され、内部がぎっしり詰まったコンパクトな粒子として単純化された仮定が用いられてきた。その後 Wolf and Toon (2010) がフラクタルな粒子を仮定した研究を行ったが、彼らの研究では粒子の圧縮過程が正確に考慮されていない。Wolf and Toon (2010) では圧縮の原因として Onischuk (2003) の実験結果を用いており、燃焼してつくられた煤アグリゲイトが帯電することを理由にしているが、初期地球のヘイズにこの実験結果を適用するのは不適切であると考えられる。

このような流れの中で、本研究では、初期地球を覆っていた有機物ヘイズの性質を力学過程にもとづいて正確に調べることを目的としている。本研究では、ヘイズが生成されてから地面に落下するまでの衝突成長過程と圧縮過程を力学計算をもとに再現し、粒子の内部構造進化を正確に考慮してシミュレーションを行った。圧縮過程としては、衝突合体時の衝撃によるもの（衝突圧縮）と、大気から受ける摩擦抵抗によるもの（静的圧縮）を考える。

その結果、初期地球ヘイズでは静的圧縮過程も衝突圧縮過程も起こり得ず、粒子がフラクタルな構造を保ったまま落下することがわかった。この結果を反映してシミュレーションを行った結果、この内部構造の違いによって各高度におけるヘイズの質量分布も変化することが明らかにされた。初期地球の有機物ヘイズ分布は、ヘイズの生成層付近の高い高度では光学的に薄く、生成層より下の高度で、光学的に厚いヘイズの滞留層が形成される。さらに、初期地球のヘイズは紫外線の光学的厚みが Wolf and Toon (2010) の仮定で出した値よりも高く、ヘイズがより紫外線をカットしていた可能性が高いことが示された。

効果的に紫外線がカットされることで、有機物の破壊がおさえられ、当時の大気がより還元的に保たれ原始生命にとって好ましい環境だったと考えられる。また、Wolf and Toon (2010) の研究結果により、可視光線に対しては光学的に薄く、光を通すことがわかっているため、効果的に地表面を温めながら紫外線をカットできるヘイズであった可能性が高い。また、ヘイズの生成層と滞留層が別の高度に分布していることが鍵となって、こうしたヘイズが持続的に生成され続け地球を温めていたシナリオも考えられる。メタンやアンモニアなどを暗い太陽のパラドックスの解決策として断定するには、まだ他にも解明が必要な点が存在するが、ヘイズが UV 遮蔽効果を持つこと、さらには冷却効果を持たないことは、温室効果ガスを候補として考える上で特に重要な役割を持つため、本研究結果は Wolf and Toon (2010) の議論を補強し、温室効果ガスの議論を前進させるという点で大きな意義を持っていると言える。

キーワード: 初期地球, ヘイズ, フラクタル粒子, 暗い太陽のパラドックス, 内部構造進化, 始生代

Keywords: the early Earth, haze, fractal particle, the faint young Sun paradox, the internal structure change, the Archean

## オリゴペプチドからのポリペプチドの生成 Polypeptide formation from oligopeptides

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ペプチドの非生物的生成については多くのシナリオが提案されてきたが、それらの研究結果はアミノから高分子量および多様性のあるポリペプチドの生成が困難であることを示してきた。水溶液中でアスパラギン、乾燥条件でのアスパラギン酸は加熱によりポリペプチドを生成するが、他のアミノ酸残基がペプチドの主鎖を占めることは困難であった。その理由は鎖状のジペプチドが容易に環化してジケトピペラジン (DKP) を生じることが挙げられる。本研究は特異な性質であるアスパラギンの残基をもつオリゴペプチドに焦点を当てている。ジペプチド (Gly-Asn, Ala-Asn) の水溶液を加熱して平均分子量が 3000 から 5000 程度のポチペプチドが生成した。アスパラギン残基をもつオリゴペプチドが原始地球環境下で生成したとすると、このオリゴペプチドはポリペプチドを生じたことが考えられる。

キーワード: オリゴペプチド, ポリペプチド, アスパラギン, 加熱

Keywords: oligopeptides, polypeptides, asparagine, heating

## A reinvestigation of ALH84001 magnetite using SQUID microscopy A reinvestigation of ALH84001 magnetite using SQUID microscopy

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The <sup>4</sup>Ga Martian meteorite ALH84001 has fine grained magnetite crystals embedded in carbonate blebs along its fracture surfaces (McKay, 1996). Some of these magnetites are strikingly similar (in grain size, morphology, and composition) to those made by magnetotactic bacteria on Earth (Thomas-Keprta et al. 2009). Great debate has raged concerning the origin of the putative biological magnetites. Until recently careful magnetic examination of the magnetite in the carbonate blebs was not possible due to a lack of instrument sensitivity. The ultra-high resolution scanning SQUID microscope (UHRSS) now allows us to study the magnetization of individual carbonate blebs that have been extracted from the meteorite. We are also able to visualize magnetization along fracture surfaces and within the bulk rock by scanning thin slices of the meteorite with the UHRSS.

Two leading hypotheses exist to explain the magnetites found within the carbonate blebs: high-temperature shock deformation leading to the decomposition of iron-bearing carbonate minerals to form magnetite (Treiman and Essene, 2011), and the sedimentary deposition of previously-formed, mature magnetite in an aqueous micro-environment as would be the case for a biogenic origin (Thomas-Keprta, 2009). A well-established paleomagnetic technique which can distinguish between these two hypotheses is the Fuller test of natural remanent magnetization (NRM) (Fuller et al. 1988) which probes the efficiency of the magnetization. If the magnetites grew in a solid state process inside the carbonates (like is suggested by Treiman and Essene (2011) they would be unable to physically rotate as they become stably magnetized and would have a highly efficient magnetization. If the magnetites were detrital (as would be expected from a biological origin scenario) the magnetization would be three orders of magnitude less efficient because the particles would be subject to Brownian motion as they are deposited. Additionally, the susceptibility of Anhyseretic Remanent Magnetization (ARM susceptibility) can be measured for the carbonate blebs. The ARM susceptibility measures the inverse of the effective r.m.s. field strength between magnetic particles (Cisowski 1981). We expect high ARM susceptibility for magnetites formed in situ because they would be evenly spaced as they form and therefore not highly interacting. However, magnetite particles falling through a water column will clump together as they fall (Kobayashi et al. 2006) and will have a low ARM susceptibility.

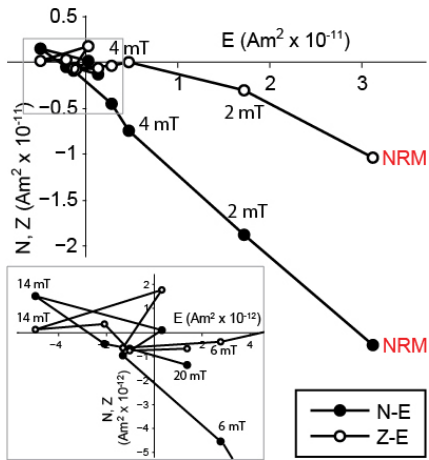
In order to conduct these paleomagnetic tests on the magnetites found within the carbonates and avoid interaction from other magnetic particles in the bulk rock, we extracted the carbonate blebs by carefully flaking them from the fracture surfaces using a non-magnetic needle. We then glued these blebs to magnetically clean microscope slides. We scanned the microscope slides with the UHRSS and were able to observe quantifiable magnetization from the individual blebs. The Fuller test of NRM requires demagnetization of the sample followed by application of an isothermal remanent magnetization (IRM). We have begun demagnetization of the sample. Thus far we observe a clear single magnetic component from NRM to 8 mT followed by chaotic changes in magnetic direction and approximately uniform strength (Figure 1). At this stage it is unclear whether multiple magnetization components will be recovered, our demagnetization is ongoing. Separately, we have measured slices of the ALH84001 bulk rock and observed heterogeneous magnetization, consistent with the work done by Weiss et al. (2000). We have also observed clustering of dipoles within the bulk rock, especially along fracture surfaces. Clustering of dipoles may indicate that multiple deposition or alteration events occurred or that portions of the meteorite have been fractured after emplacement/formation of the carbonates.

キーワード: Martian Life, ALH84001, Rock Magnetism, Paleomagnetism, Biogenic Magnetite, Meteorites  
Keywords: Martian Life, ALH84001, Rock Magnetism, Paleomagnetism, Biogenic Magnetite, Meteorites

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## 太古代枕状溶岩に微生物は住んでいたか？ Were Archean volcanic glasses habitats for microbial organisms?

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Submicron-tube structures have been found in quenched glasses of pillow lavas from Barberton (ca.3.4 Ga) and Abitibi (ca.2.7 Ga) Greenstone belts. These tubes are interpreted as products of bio-alteration (Furnes et al., 2003). However, abiotic processes could form the same structure, and some researchers are questioning biogenic origin of the tube structure (Grosch et al., 2014). Further examination of Archean volcanic glasses is important to constrain habitats of early life.

Here I examined pillow lavas from 2.7 Ga Abitibi Greenstone Belt in Canada. Pillow lavas have clear reaction rims, which were quenched and altered glasses before metamorphism. Typical mineral assemblages in reaction rims are paragonite, chlorite, actinolite, titanite, quartz, calcite, pyrite and epidote. Low metamorphic grade (lower greenschist facies) is suggested by those mineral assemblage. Mineral chemistries suggest that alkaline solutions was responsible for formation of primary minerals, implying alkaline 2.7 Ga ocean.

Titanite occurs in aggregates of fine crystals in chlorite matrix, and often accompanied by unclear “tubes.” Occurrence of titanite aggregates is identical to bio-alteration features found in other Archean pillow lavas. However, the length and density of “tubes” are much less compared to others. The examined samples in the present study were less metamorphosed compared to others (upper greenschist facies). Absence of clear “tubes” in less metamorphosed rocks suggest that “tubes” in Archean pillow lavas were not products of bio-alteration, but products of metamorphism.

キーワード: Archean, Pillow lava, microbes, Abitibi  
Keywords: Archean, pillow lava, microbes, Abitibi

## 約32億年前の縞状鉄鉱層中の希土類元素と酸素同位体組成から制約される海洋環境 Mesoarchean $pO_2$ and $pCO_2$ based on REE and oxygen isotope geochemistry of BIF from Barberton, South Africa

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A popular mechanism for BIF (Banded Iron Formation) deposition is that Fe-oxides were precipitated in deep-water setting by oxidation of dissolved  $Fe^{2+}$  supplied from submarine hydrothermal activity, by dissolved oxygen supplied from oxygenic photosynthesis in the surface ocean. When Fe-oxides precipitated, rare earth elements (REEs) were adsorbed on their surface. REE compositions of seawater have been recognized to reflect redox state of seawater and the extent of input from hydrothermal activity. In this study, we aimed to estimate Mesoarchean seawater chemistry and temperature based on REE signatures of 3.2 Ga old BIFs. These are directly related to  $pO_2$  and  $pCO_2$  in the Mesoarchean atmosphere.

Samples were collected from outcrops of the Mapepe Fm at the bottom of the Fig Tree Group and Msauli Member in the Onverwacht Group, both belonging to the Swaziland Supergroup. Powdered rock samples were analyzed for their major element, REE, and oxygen isotope compositions. Samples with  $<0.5$  wt.%  $Al_2O_3$  are considered to be pure chemical precipitates and thus used for further discussion.

Chondrite-normalized REE patterns of the Mapepe samples show positive Eu anomaly, elevated Y/Ho ratios, and  $LREE > HREE$ . Furthermore, there exist positive correlations among the extent of positive Eu anomaly,  $\sum Fe_2O_3$  contents, and Y/Ho ratios. The maximum Y/Ho ratios are surprisingly comparable to those of the modern ocean. These characteristics suggest a coherent story for BIF deposition;  $Fe^{2+}$  emanated from submarine hydrothermal activity was oxidized to  $Fe^{3+}$ , which, with enhanced particle reactivity, absorbed dissolved REEs and Y in the 3.2 Ga ocean, producing elevated near-modern Y/Ho ratios. The Msauli samples are mostly enriched in  $Al_2O_3$  and have clastics-dominated REE patterns, suggesting deposition at shallower, more proximal setting.

We also estimate temperature of seawater 3.2 Ga ago from which the BIF precipitated to be around 60-70 °C, based on their oxygen isotope compositions of silicate- and Fe-oxide phases and their binary mixing model. Although crustal heat flux at that time was most likely higher than today, the  $pCO_2$  in the Mesoarchean atmosphere should have been high enough to warm up the seawater under faint young Sun. The  $pO_2$  in the Mesoarchean atmosphere should have been high enough to oxidize dissolved  $Fe^{2+}$  supplied from submarine hydrothermal activity.

キーワード: 太古代, 縞状鉄鉱層, 希土類元素, 酸素同位体, 南アフリカ

Keywords: Archean, BIF, REE, Oxygen isotope, South Africa

## 冥王代における生命誕生場：間欠泉モデル Birth place of life on Hadean Earth: Geyser model

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Including us human being, life cannot survive with water only. The presence of water itself does not mean the emergence of life automatically. So what is life? Life is composed of three major big molecules, which is (1) carbon (sugar), big monster molecules, (2) metabolism which is the key to get energy. It does not work without P +K which is given from only landmass (provider of nutrients), and (3) self-replication, based on base pair. These 3 molecules are enclosed by membrane. That is life.

So where such molecules for life body are made on Hadean Earth. The most possible place for this process is geyser which locates below the ground. The reason why geyser is thought to be the most suitable site to synthesize building blocks for life body is (1) the ceiling of geyser located below the ground enable gases to be concentrated, such as CO, NH<sub>3</sub>, CH<sub>4</sub>, HCN, PO<sub>4</sub><sup>3-</sup> and so on. (2) Amino acid or peptide is possible to be synthesized as necessary material can be provided within cavity of geyser. (3) Periodicity is maintained due to the nature of geyser. (4) Heat source is secured due to the presence of uranium ore deposit which is the alternative heat source instead of solar energy.