Japan Geoscience Union Meeting 2013
(May 19-24 2013 at Makuhari, Chiba, Japan)

BAO01-01 会場:301A 時間:5月21日 09:00-09:30

グリシン前駆体 CH_3NH_2 の推定存在量
Estimated Abundances of a Precursor of Glycine, CH_3NH_2

大石 雅寿 [1]*
Masatoshi Ohishi[1]*

[1] 国立天文台
[1]National Astronomical Observatory of Japan

In is widely accepted that prebiotic chemical evolution from small to large and complex molecules would have resulted in the Origin of Life. On the other hands there have been conflicting two views regarding where inorganic formation of organic molecules (hereafter OMs) occurred in the early Earth, in the Earth or out of the Earth. Ehrenfreund et al. (2002) indicated that exogenous delivery of OMs to the early Earth could be larger than their terrestrial formation by three orders of magnitude. If amino acids are formed in interstellar clouds, significant amount of them may be delivered by comets and/or asteroids to (extra-solar) planets. Detection of amino acids would accelerate the discussion concerning the universality of “life”.

So far, many trials to detect simplest amino acid, glycine (CH_2NH_2COOH), were made towards Sgr B2 and other high-mass forming regions, but none of them were successful due to insufficient sensitivities and spatial resolution of telescopes. This is the background that detection of amino acids and other prebiotic in the Universe is one of the key science targets for ALMA. However we need to have carefully selected good candidate sources for amino acids before conducting searches for amino acids by ALMA since lines could be contaminated by other molecular lines. One idea would be to survey precursors of amino acids; higher abundances sources of precursors would be amino acid rich sources.

Although the chemical evolution of interstellar N-bearing OMs is poorly known, methylamine (CH_3NH_2) is proposed as a precursor to glycine; theoretical and laboratory studies have indicated that glycine is formed on icy grain surface from methylamine and CO_2 through UV irradiation (Holtom et al. ApJ, 626, 940 (2005), Kim and Kaiser et al., ApJ, 729:68 (2011)). These studies also suggest that methylamine can be formed from abundant species, CH_4 and NH_3, on icy dust surface. Although CO_2 is widely known in molecular clouds, distribution of methylamine is poorly known. Further methylene imine (CH_2NH) would be related to CH_3NH_2. These species are thought to be formed through hydrogenation (addition of hydrogen) to HCN on dust surface (Dickens et al., 1997, Kim and Kaiser et al. 2011): HCN -> CH_2NH -> CH_3NH_2. This is similar to the hydrogenation of CO to form CH_3OH: CO -> H_2CO -> CH_3OH.

The first detection of methylamine was made by Kaifu et al. (1974). But even now, CH_3NH_2 is known toward two objects (Orion KL and Sgr B2) only. CH_2NH has been reported only in Sgr B2, W51, Orion KL, and G34.3 (Dickens et al.1997).

Therefore it would be crucial to estimate abundances of CH_3NH_2 and CH_2NH by using a chemical reaction network, which may be compared with observations. In this paper we present preliminary results of estimated abundances of these species, which would provide good guidance in finding good glycine sources and in understanding poorly known chemistry of N-bearing organic molecules in the Universe.

キーワード: 宇宙有機分子, 化学進化, 惑星形成
Keywords: Organic Molecules in Space, Chemical Evolution, Planetary Formation

Japan Geoscience Union Meeting 2013
(May 19-24 2013 at Makuhari, Chiba, Japan)

BAO01-02 会場:301A 時間:5 月 21 日 09:30-09:45

NGC 6334-V の近赤外円偏光撮像:アストロバイオロジーへの示唆
Near-Infrared Circular Polarization Images of NGC 6334-V: Implication for Astrobiology

權 静美 [1]*, 田村　元秀 [1]
Jungmi Kwon[1]*, Motohide Tamura[1]

[1] 総合研究大学院大学／国立天文台
[1]The Graduate University for Advanced Studies, National Astronomical Observatory of Japan

We present results from deep imaging linear and circular polarimetry of the massive star-forming region NGC 6334-V. These observations show high degrees of circular polarization (CP), as much as 22% in the Ks band, in the infrared nebula associated with the outflow. The CP has an asymmetric positive/negative pattern and is very extended (~80” or 0.65 pc). Both the high CP and its extended size are larger than those seen in the Orion CP region. Three-dimensional Monte Carlo light-scattering models are used to show that the high CP may be produced by scattering from the infrared nebula followed by dichroic extinction by an optically thick foreground cloud containing aligned dust grains. Our results show not only the magnetic field orientation of around young stellar objects, but also the structure of circumstellar matter such as outflow regions and their parent molecular cloud along the line of sight. This is the second case to support the large CP in scattering protostellar nebulae as a possible explanation for the extraterrestrial origin of homochirality of life on Earth.

Japan Geoscience Union Meeting 2013
(May 19-24 2013 at Makuhari, Chiba, Japan)

BAO01-03 会場:301A 時間:5月21日 09:45-10:00

太陽系外惑星バイオマーカー検出に向けた光捕集機構のエネルギー転移計算
The energy transfer calculation of light harvesting systems for detecting biomarker on extrasolar planets

小松 勇[1*], 梅村 雅之[1], 庄司 光男[1], 矢花 一浩[1], 白石 賢二[1], 神谷 克政[1], 栢沼 愛[1], 田口 真彦[1], 佐藤 皓允[1]
Yu Komatsu[1*], Masayuki Umemura[1], Mitsuo Shoji[1], Kazuhiro Yabana[1], Kenji Shiraishi[1], Katsumasa Kamiya[1], Megumi Kayanuma[1], Masahiko Taguchi[1], Akimasa Sato[1]

[1] 筑波大学
[1]University of Tsukuba

A large number of extrasolar planet candidates have been detected by Kepler. Moreover the planets in habitable zone have already been detected, and ELP (Earth-like planet) is expected to be discovered. As detecting signs of life from the spectrum of ELPs in future, several indicators called as biomarkers or biosignatures were proposed [1]: (1) molecule absorption line, such as O_2, CH_4, and (2) red edge, which is a strong contrast in NIR (˜700-750 nm) that derives from plant's feature. Red edge comes from absorption in visible by the chlorophyll, which is one of the photosynthetic pigments, and reflectance in NIR due to the structural features such as cell wall, air space of leaf and so on. The spectrum considered as red edge is observed by remote sensing or earthshine [2].

However, it is not guaranteed that red edge on extrasolar planets is detected as same wavelength on Earth. In fact, the photosynthetic organisms on Earth harvest light according to the surrounding environments to efficiently use light having a variety of wavelength that reaches, and of course their spectrum varies. In case of photosynthesis in extrasolar planets, photosynthetic organisms should evolve as optimized to utilize their principal star. We focus on the fundamental light harvesting mechanism and aim to propose how to detect the spectrum of the planet orbiting the different spectrum types of star otherwise Sun. At first, we adopted our models to photosynthetic organisms on Earth and compared with the experimental data. The light harvesting antenna in these organisms differs from kinds of pigments and their conformations.

We investigated the mechanism how the organisms harvest light by quantum mechanical calculation. However, because of the cost difficulty, we introduced an approximation instead of calculating all the electrons in the system. First, we calculated the excitation energies and the transition moments from the ground state to the excited states in the pigments by TDDFT (time-dependent density functional theory) [3]. Then, by introducing the transition moments of each pigment to the antenna, which consists of several kinds of pigments (other environment: proteins, solvent,...), we assume as an approximation that one pigment has the excited energy and interacts with the other pigments by the dipole-dipole interaction. When the light, as it seems to be considered as traveled from a star to a surface of an extrasolar planet, induces the system, we traced the time evolution of the energy transfer by solving Liouvile equation. We dealt the light with an external potential. By this method, we can calculate the spectral intensity and energy efficiency.

In certain types of bacteria, the contrast like red edge can be detected, although the contrast is weaker than that of plants. In purple bacteria, red edge is not detected or emerges in longer wavelength (˜1013-1025 nm). In addition, its structure of the antenna is simple so that we adopted easily our model to the bacteria. The calculated spectrum has a good agreement with the experimental result from purple bacteria. We will extend our model to the other species. By comparing the light harvesting mechanisms showing red edge and no red edge, we can examine how red edge emerges in photosynthetic organisms. For the other inducing light condition, we will survey the light harvesting mechanism optimized to extrasolar planets.

[1] N. Y. Kiang et al., Astrobiology, 7 (1), 252, 2007
[2] L. Arnold et al., A&A, 392, 231, 2002
[3] M. A. L. Marques and E. K. U. Gross, Annu. Rev. Phys. Chem., 55, 427, 2004

Keywords: extrasolar planet, biomarker, quantum mechanical calculation

BAO01-04 会場:301A 時間:5月21日 10:00-10:15

惑星間塵中の有機物とその生命起源との関連
Organic compounds in interplanetary dust particles and their relevance to origins of life

小林 憲正[1*], 川本 幸徳[1], 岡部 拓人[1], 金子 竹男[1], 大林 由美子[1], 神田 一浩[2], 三田 肇[3], 薮田 ひかる[4], 中川 和道[5], 奥平 恭子[6], 矢野 創[7], 橋本 博文[7], 横堀 伸一[8], 山岸 明彦[8]
Kensei Kobayashi[1*], Yukinori Kawamoto[1], Takuto Okabe[1], Takeo Kaneko[1], Yumiko Obayashi[1], Kazuhiro Kanda[2], Hajime Mita[3], Hikaru Yabuta[4], Kazumichi Nakagawa[5], Kyoko Okudaira[6], Hajime Yano[7], Hirofumi Hashimoto[7], Shin-ichi Yokobori[8], Akihiko Yamagishi[8]

[1] 横浜国立大学, [2] 兵庫県立大学, [3] 福岡工業大学, [4] 大阪大学, [5] 神戸大学, [6] 会津大学, [7]JAXA 宇宙科学研究所, [8] 東京薬科大学
[1]Yokohama National University, [2]University of Hyogo, [3]Fukuoka Institute of Technology, [4]Osaka University, [5]Kobe University, [6]Aizu University, [7]JAXA/ISAS, [8]Tokyo University of Pharmacy and Life Science

原始および現在の太陽系環境下での惑星間塵中の有機物（アミノ酸・核酸塩基を含む）の安定性や変成に関して，シンクロトロン放射光等を用いた模擬実験を行った。その結果をもとに地球上での生命起源との関連を議論する。

キーワード: 惑星間塵, アミノ酸, 生命の起源, 複雑有機物, 軟X線, たんぽぽ計画
Keywords: interplanetary dust particles, amino acids, origins of life, complex organic compounds, soft X-rays, the Tanpopo Mission

Japan Geoscience Union Meeting 2013
(May 19-24 2013 at Makuhari, Chiba, Japan)

BAO01-05 会場:301A 時間:5 月 21 日 11:00-11:30

Interdisciplinary Perspectives on Abiogenesis
Interdisciplinary Perspectives on Abiogenesis

Hut Piet[1*]
Piet Hut[1*]

[1] プリンストン高等研究所，地球生命研究所
[1]Institute for Advanced Study, Earth-Life Science Institute, Tokyo, Japan

I will report on new interdisciplinary activities at the Institute for Advanced Study, in Princeton, NJ, USA, focused on the origins of life. We have recently started a series of weekly meetings, involving mathematicians, physicists, chemists, biologists, astrophysicists and others. Our discussions range from important technical details to more general meta-level discussions concerning the flow of information through biological networks and the characteristics of life in general, on Earth and possibly elsewhere in the Universe. We include scholars in humanities and linguistics, since there are interesting parallels between the origins of culture and the origins of life, and in general with the origins of ”systems”, where unreliable parts are used to create reliable systems.
My work is inspired by my affiliation with ELSI, the new Earth-Life Science Institute at Tokyo Tech, under the WPI program of MEXT.

キーワード: 生命の起源, 情報の流れ, 生物学的ネットワーク, 生命の特徴, システム
Keywords: origins of life, flow of information, biological networks, characteristics of life, systems

Japan Geoscience Union Meeting 2013
(May 19-24 2013 at Makuhari, Chiba, Japan)

BAO01-06 会場:301A 時間:5月21日 11:30-11:45

たんぽぽ計画における有機物曝露実験
Exposure experiments of organic compounds in space environments in the TANPOPO mission

三田 肇[1*], 横堀伸一[2], 橋本博文[3], 東出真澄[4], 今井栄一[5], 河口優子[2], 河合秀幸[6], 川本幸徳[7], 神田一浩[8], 小林憲正[7], 中川和道[9], 鳴海一成[10], 奥平恭子[11], 田端誠[3], 薮田ひかる[12], 山下雅道[3], 矢野創[3], 吉田聡[13], 山岸明彦[2], たんぽぽ WG[3]
Hajime Mita[1*], Shin-ichi Yokobori[2], Hirofumi Hashimoto[3], Masumi Higashide[4], Eiichi Imai[5], Yuko Kawaguchi[2], Hideyuki Kawai[6], Yukinori Kawamoto[7], Kazuhiro Knada[8], Kensei Kobayashi[7], Kazumichi Nakagawa[9], Issay Narumi[10], Kyoko Okudaira[11], Makoto Tabata[3], Hikaru Yabuta[12], Masamichi Yamashita[3], Hajime Yano[3], Satoshi Yoshida[13], Akihiko Yamagishi[2], Tanpopo WG[3]

[1]福岡工大・工, [2]東京薬大・生命科学, [3]JAXA/ISAS, [4]JAXA・未踏技術研究セ, [5]長岡技大・生物, [6]千葉大・院理, [7]横浜国大・院工, [8]兵庫県立大・LASTI, [9]神戸大・院人間発達環境, [10]原子力機構・量子ビーム, [11]会津大, [12]阪大・院理, [13]放医研
[1]Fukuoka Inst. Technol., [2]Sch. Life Sci., Tokyo Univ. Pharm. Life Sci., [3]JAXA/ISAS, [4]Innovative Tech. Res. Cen., JAXA, [5]Nagaoka Univ. Tech., [6]Grad. Sch. Sci., Chiba Univ., [7]Grad. Sch. Eng., Yokohama Natl. Univ., [8]LASTI, Univ. Hyogo, [9]Grad. Sch. Human Develop. Environ., Kobe Univ., [10]Quantum Beam, JAEA, [11]Univ. Aizu, [12]Grad. Sch. Sci., Osaka Univ., [13]NIRS

The Tanpopo mission is a Japanese astrobiological experiment which will be conducted on the Japanese Experiment Module (JEM) of the International Space Station (ISS). The Tanpopo mission consists of six subthemes: 1) capture of microbes in space, 2) exposure of microbes in space, 3) exposure of organic compounds in space, 4) capture of organic compounds (in micrometeoroids) in space, 5) evaluation of ultra low-density aerogel developed for the Tanpopo mission, and 6) capture of space debris at the ISS orbit (approximately 400 km altitude).

Here, we overview the exposure experiment of organic compound in space environment. Since many kinds of organic compounds, especially, amino acids which are ones of most important organic compounds in living organisms, are found from extraterrestrial materials, extraterrestrial and outer-solar environments are thought as the place for the prebiotic organic compound synthesis. Then, it is proposed that the first organisms on the earth was born from the prebiotic organic compounds delivered into the early earth on meteorites, micrometeorites and/or comets. In order to discuss the possibility of the hypothesis, alteration of prebiotic compounds in space environments should be clear. Therefore, we will expose some prebiotic organic compounds on the exposure facility at ISS-JEM.

Glycine, isovaline, hydantoin, ethylmethylhydantoin and complex organics (CAW) are chosen for the exposure. Hydantoin and ethylmethylhydantoin are plausible low molecular weight precursors for glycine and isovaline, respectively. CAW which is a simulated material of interstellar medium prepared by proton radiation into mixture of CO, NH_3 and H_2O is a different type of plausible precursors for amino acids. In the space environments, uv-light and cosmic rays (heavy ions and gamma-rays) will cause the alteration of organic compounds. Therefore, simulation experiments were studied using Xe-excimer lamp (uv 172 nm), synchrotron radiation at NewSUBARU BL06 (uv $>$ 130 nm), 60Co gamma-ray radiation (JAEA Takasaki) and carbon ion beams (290MeV, NIRS). gamma-Ray and heavy ion beam irradiation with dose of ISS environment for one year induced little decomposition of organic compounds. However, uv irradiation was critical for organic compounds. Although almost all glycine and isovaline were decomposed, remains of hydantoin and ehtylmethyl hydantoin were approximately 29% and 72%, respectively, with uv dose of ISS environment for one year. Furthermore, CAW was more stable than hydantoins. Amino acids precursors, especially, complex organics were more stable than free amino acids. Therefore, extraterrestrial amino acids precursors would be effective source for origins of life on the earth. We will demonstrate this conclusion on the ISS-JEM.

In addition, Nakagawa and his colleagues were found that dialanine was formed from alanine films by uv-irradiation. We will demonstrate a peptide synthesis with uv-irradiation in the space environment. Furthermore, piece of meteorite will be also exposed in order to examine the weathering effect in the ISS environment.

キーワード: たんぽぽ, 有機物曝露, 国際宇宙ステーション, アミノ酸
Keywords: Tanpopo, exposure of organics, ISS, amino acids

Japan Geoscience Union Meeting 2013
(May 19-24 2013 at Makuhari, Chiba, Japan)

BAO01-07 会場:301A 時間:5 月 21 日 11:45-12:00

リボースの安定性に対するホウ酸の影響
Effects of borate on the stability of ribose

古川 善博 [1*], 堀内 真愛 [1], 掛川 武 [1]
Yoshihiro Furukawa[1*], Mana Horiuchi[1], Takeshi Kakegawa[1]

[1] 東北大学理学研究科
[1]Graduate School of Science, Tohoku University

RNA is considered an important biomolecule for the origin of life, with its abilities as the carrier of genetic information and catalysts for biological reactions. RNA is composed of phosphoric acid, nucleic acid bases, and ribose. Among them, ribose is the most unstable component. Therefore, accumulation of ribose on the early Earth is an important step for the origin of RNA. Ribose as well as other aldopentoses can be abiotically synthesized by formose reaction in which formaldehyde oligomerize under alkaline conditions. Previous studies showed a stabilization of pentoses in the formose reaction by borate. In this study, we have investigated the effects of borate on the stability of aldopentoses.

Incubation experiments of each four aldopentoses were conducted at approximately 45 degree C with sodium tetraborate decahydrate of three concentrations. The pH of the experimental solution was buffered with calcium hydroxide. The experimental solution was collected at a fixed interval and analyzed with liquid chromatography-mass spectrometry.

In the borate-free experiments, all aldopentoses showed high decrease rates. In borate-containing experiments, formations of pentose-borate complexes were observed. The decrease rates for all aldopentoses were reduced with the concentration of borate. These results indicate that borate can stabilize all aldopentoses. Therefore, borate might have stabilized aldopentoses including ribose and contributed to the formation of primordial RNA on the early Earth.

キーワード: リボース, ホウ酸, RNA, 生命の起源
Keywords: ribose, RNA, borate, origin of life

BAO01-08 会場:301A 時間:5 月 21 日 12:00-12:15

オリゴペプチドによるホモキラリティー濃縮の経路
A Possible Pathway of Homochirality Accumulation by Oligopeptides

胸組 虎胤 [1]*
Toratane Munegumi[1]*

[1] 鳴門教育大学大学院自然系コース（理科）
[1]Department of Science Education, Naruto University of Education

多くの仮説が生体物質の片手構造を説明するために提案されてきたが、その多くはアミノ酸や単糖のような単量体の片手構造に関するものであった。しかしながら、単量体の片手構造は必ずしも、多量体中での片手構造を保証するものではない。なぜならば、原始地球および地球外には単量体を分解するような様々なエネルギー源が存在するからである。

本研究はオリゴペプチドによるポリペプチド中での片手構造の濃縮に焦点を当てている。ラセミ体のアミノ酸が２量化するとジアステレオマーが生成する。それがたとえば、アラニンであれば、鎖状、環状合わせて７種類のジアステレオマーが生じる。これらの化合物は化学構造ばかりでなく、疎水性、反応性、エピ化速度も異なる。一般に、ヘテロキラルペプチドはホモキラルペプチドよりも疎水性が高い。

発表では、オリゴペプチドによるポリペプチド中での片手構造の濃縮のスキームを、ジアステレオマーの分別、分解、立体特異的縮合に関連づけて示す。

キーワード: ホモキラリティー, 縮合反応, オリゴペプチド
Keywords: homochirality, condensation, oligopeptides

BAO01-09 会場:301A 時間:5 月 21 日 12:15-12:30

GADV peptide/aggregate synthesis using a hydrothermal simulator at elevated temperature

GADV peptide/aggregate synthesis using a hydrothermal simulator at elevated temperature

Kuhan Chandru[1]*
Kuhan Chandru[1]*

[1]Faculty / Graduate School of Engineering Yokohama National University
[1]Faculty / Graduate School of Engineering Yokohama National University

GADV peptide/aggregate synthesis using a hydrothermal simulator at elevated temperature

Kuhan Chandru, Eiichi Imai, Yumiko Obayashi, Takeo Kaneko and Kensei Kobayashi

GAVD peptide hypothesis was proposed by Ikehara (2009) as a possible alternative that precedes the RNA world hypothesis (Gilbert, 1986) due to many limitations. The hypothesis suggest a very plausible explanation, but has only been experimentally tested by Oba and co workers (2012), in terms of possible peptide formation using heat-drying cycles and their catalytic activities. We would want to examine the formation of GADV aggregates (or peptides) in an simulated hydrothermal system to represent a more realistic prebiotic environment. We have used Gly, L-Asp, L-Asp and L-Val into our Supercritical Water Flow Reactor (SCWFR) at a temperature range of 100-300 Celsius . Our initial results suggest that no visible aggregates (bigger than 0.2micrometer) were seen after the heating of 2 min in the mentioned temperature range. Initial MALDI-TOF-MS are also suggesting that we only obtained a small peaks about m/z 410 within the spectrum lesser what Oba et al (2012) which was 525, 539, 657. Although many hydrothermal simulation experiments has shown the recovery of amino acids (Islam et al 2002; Kohara et al; Kobayashi et al, 1997) and the formation of oligomers (Imai, 1999; Goto et al , 2005) we only believe, that only small aggregation occur and cannot promote bigger oligomers or polymers due to heat and pressure stress. Hence, based on our initial findings, we are very uncertain about the formation of GADV aggregates or peptides in a hydrothermal system if we use free-form amino acids. It would be of interest to investigate the hypothesis by using bound amino acids or amino acid precursors.

References

Ikehara, K. (2009). Pseudo-Replication of [GADV]-Proteins and Origin of Life. International Journal of Molecular Sciences, 10(4), 1525?1537. doi:10.3390/ijms10041525

Gilbert, W (1986) The RNA world. Nature 319, 618

Oba, T., Fukushima, J., Maruyama, M., Iwamoto, R., & Ikehara, K. (2005). Catalytic activities of [GADV]-peptides. Origins of Life and Evolution of the Biosphere : the Journal of the International Society for the Study of the Origin of Life, 35(5), 447?460.

Kohara, M., Gamo, T., Yanagawa, H., & Kobayashi, K. (2003). Stability of amino acids in simulated hydrothermal vent environments. Chemistry Letters, 1?2.

Islam, M. N., Kaneko, T., & Kobayashi, K. (2003). Reaction of Amino Acids in a Supercritical Water-Flow Reactor Simulating Submarine Hydrothermal Systems. Bulletin of the Chemical Society of Japan, 76(6), 1171?1178. doi:10.1246/bcsj.76.1171

Kobayashi, K.,Kohara., Dokiya, M and Yanagawa, H (1997) Formation and stability of amino acids in simulated hydrothermal vent environments. Viva Origino 25, 167 - 176

Imai, E.-I., Honda, H., Hatori, K., Brack, A and Matsuno, K (1999) Elongation of Oligopeptides in a Simulated Submarine Hydrothermal System. Science, 283(5403), 831?833. doi:10.1126/science.283.5403.831

Goto, T., Futamura, Y., Yamaguchi, Y., & Yamamoto, K. (2005). Condensation reactions of
amino acids under hydrothermal conditions with adiabatic expansion cooling. Journal of
Chemical Engineering of Japan, 38(4), 295?299.

キーワード: GADV, Hydrothermal, prebiotic
Keywords: GADV, Hydrothermal, prebiotic

Japan Geoscience Union Meeting 2013
(May 19-24 2013 at Makuhari, Chiba, Japan)

BAO01-10 会場:301A 時間:5 月 21 日 14:15-14:30

数理モデルによる全球凍結直後の酸素濃度上昇過程の復元：マンガン及び鉄鉱床形成への示唆
Modeling the rise of oxygen after the Snowball earth: implications for the Paleoproterozoic manganese and iron formation

原田 真理子 1*, 田近 英一 2, 関根 康人 2, 尾崎 和海 3
Mariko Harada1*, Eiichi Tajika2, Yasuhito Sekine2, Kazumi Ozaki3

1 東京大学大学院地球惑星科学専攻, 2 東京大学大学院複雑理工学専攻, 3 東京大学大気海洋研究所
1Dept. of Earth and Planetary Science, The University of Tokyo, 2Dept. of Complexity Science & Engineering, The University of Tokyo, 3Atmosphere and Ocean Research Institute, The University of Tokyo

Earth's atmosphere and oceans are considered to have experienced stepwise and irreversible oxidation through its history (e.g. [1]), which may have paved the way to the complicated life such as eukaryotes and metazoans [2]. It is interesting to note that geological evidence suggests that a remarkable increase of oxygen concentration has occurred shortly after the Paleoproterozoic Snowball Earth event, based on widespread depositions of manganese and iron oxides immediately above the glacial diamictites found in the Paleoproterozoic sedimentary sequences from the Transvaal Supergroup, South Africa, and the Huronian Supergroup, Canada [3,4]. Carbonate precipitation occurs above the deposition of manganese and iron in both the Transvaal and Huronian Supregroups [3,5], which may represents a climate recovery from the greenhouse condition in the Snowball earth aftermath [3]. In this study we numerically investigated the linkage between a global-scale glaciation and an oxygenation of the atmosphere-ocean system, in the aim of comparing our results to the geological records.

The results of our numerical experiments with a biogeochemical cycle model indicate that the super greenhouse conditions (pCO_2˜0.7 atm and T˜320 K) in the aftermath of the Paleoproterozoic Snowball Earth event significantly enhance the chemical weathering of continents, causing ˜10 times as high as the present levels of nutrient input and the biological productivity. In the consequence of high levels of biological productivity together with a positive feedback in the atmosphere among a rise in oxygen, ozone formation, and UV shielding of methane, the atmospheric oxygen levels rapidly rise from $< 10^{-5}$ PAL to 0.01 PAL (PAL: the present atmospheric level) after the glaciation. The oxygen levels then overshoot to ˜1 PAL in ˜10^6 years after the glaciation due to the high levels of biological productivity sustained by a long-term global warming. Atmospheric oxygen then gradually decreases by oxidizing reducing materials from Earth's interior. Eventually, a steady state of atmospheric oxygen of ˜0.01 PAL is achieved in 10^8 years. Such an irreversible rise in atmospheric oxygen (i.e., from $< 10^{-5}$ PAL to ˜0.01 PAL) is explained by a transition between different steady state of atmospheric oxygen levels [6] caused by a Snowball Earth glaciation and the subsequent perturbations of biogeochemical cycles.

We found that the rapid oxygenation causes the deposition of manganese and iron in the shallow marine environments. Manganese and ferrous iron in the anoxic deep water are driven by thermohaline circulation, immediately oxidized in the shallow marine water within 10^4 years after the glaciation. Assuming deep water is initially saturated with respect to Mn-carbonates, we derive 10^{15} mol of manganese deposition, which would be sufficient to form manganese ore in the Hotazel formation, Transvaal Supergroup (˜8Gt, ˜10^{14} mol of manganese [7]). We also found that calcite precipitation is prevented in the ocean during 10^5 years after the glaciation owing to high atmospheric pCO_2. Our results imply that manganese and iron oxides deposition might precede the carbonate deposition, which is consistent with the geological records found both in the Transvaal and Huronian supergroups [3,4].

[1] Kasting (1993) Science, 259, 920-926. [2] Runnegar (1991) Palaeogeogr. Palaeoclimatol. Palaeoecol., 97, 97-111 [3] Kirschvink et al. (2000) Proc. Natl. Acad. Sci. USA, 97, 1400-1405. [4] Sekine et al. (2011) Earth Planet. Sci. Lett., 307, 201-210. [5] Bekker et al. (2006) Precambrian Research, 148, 145-180. [6] Goldblatt et al. (2006) Nature, 443, 683-686. [7] Tsicos (2003) Economic Geology, 98, 1449-1462

BAO01-11　　会場:301A　　時間:5 月 21 日 14:30-15:00

A Simple Astrobiological Scenario to go from the Great Oxygenation Event to the Origination of Eukaryotes

A Simple Astrobiological Scenario to go from the Great Oxygenation Event to the Origination of Eukaryotes

Joseph Kirschvink[1*]
Joseph Kirschvink[1*]

[1]Geological and Planetary Sciences, California Institute of Technology, Pasadena CA, USA and, [2]Earth/Life Science Institute, Tokyo Institute of Technology, Tokyo, Japan
[1]Geological and Planetary Sciences, California Institute of Technology, Pasadena CA, USA and, [2]Earth/Life Science Institute, Tokyo Institute of Technology, Tokyo, Japan

Taken in the context of Earth History, it is now clear that all previously reported Archean biomarkers indicative of oxygenic photosynthesis are most likely in error, a result of contamination during sampling. Reported geochemical whiffs of oxygen from ABDP-9 are also tightly associated with hydrothermal veins of highly crystalline clinochlore, and are thus metasomatic artifacts from hydrothermal vein deposits. Firm evidence for Archean oxygen simply does not exist.

A much simpler scenario will be presented here in which photosystem-II evolves at ˜ 3.35 Ga, causing the radiation of the Cyanobacterial clade during the Gowganda glaciation. The resulting drawdown of CO2, and destruction of CH4, triggered the Makganyene global (snowball) glaciation, freezing the ocean surfaces for ˜ 50 to 100 Myr, ending at 2.22 Ga. This is immediately followed by the deposition of the Kalahari Manganese Field, which is the oldest firm geological constraint on copious quantities of free O2 in Earth's environment. As there must be a time gap between the evolution of Photosystem-II and the origin of oxidative phosphoralization (aerobic respiration), Earth's carbon cycle must have been extremely out of balance. We interpret the Lomagundi/Jatuli Carbon Isotope excursion (about 2.2 to 2.06 Ga) as precisely this imbalance, where the oxygen produced by photosynthesis, and organic matter produced, could not be easily recycled. The fraction of organic carbon buried increased from the long-term average of about 20% up to about ˜ 75%, yielding isotopic compositions of carbonate as heavy as +15 per mil. Oxygen in the atmosphere is known to have increased to high levels ? perhaps several bars - resulting in the supergene alteration of the ˜ 2.1 Ga iron ores in the Sishen deposit of South Africa during formation of the Hekpoort Paleosol. During this Lomagundi event, the high oxygen levels would be limited by the inability of cyanobacteria to release oxygen against high back pressures, and the remineralization of organic carbon would be accomplished by oxidative weathering of sulfide minerals releasing sulfate, and by the subsequent action of sulfate reducing bacteria to break down the organic carbon.

As the radiation of the Proteobacteria post-dates the radiation of the Cyanobacteria, and the ancestor of the Eukaryotic mitochondria was once a free-living alpha-Proteobacterium, it also follows that the first organelle-bearing eukaryotes must post-date the Makganyene Snowball Earth event. Numerous eukaryotic organelles have ancestry in this bacterial endosymbiont, as do cellular components such as the hydrogenosome in basal Protists.

A puzzling organelle present in both Bacteria and Eukaryotes (including many Protists) is the magnetosome, a membrane-bound, single crystal of biological magnetite (Fe3O4) or greigite (Fe3S4). Magnetosome chains orient single cells in the geomagnetic field and allow environmental positioning. Recent work on the genetics of biomineralization in magnetotactic bacteria (MB) has shown that both the greigite and magnetite genetic pathways share a common origin, supporting an earlier suggestion that the biochemistry of magnetotaxis is monophyletic.

Small subunit RNA sequence data from hundreds of extant MB are consistent with the origin of magnetotaxis within the Bacterial domain postdating the separation of stem-group cyanobacteria, but preceding radiation of the Proteobacteria (including the mitochondrial ancestor). We propose that the free-living mitochondrion ancestor was a magnetotactic bacterium. This hypothesis presents attractive implications for adopting cytoskeletal framework throughout the eukaryotic cell, for explaining the presence of magnetosomes throughout the Eukaryotes, and for justifying the demonstrated ability of the bacterial MagA protein to induce magnetite biomineralization in mammalian cells. The radiation of the Eukaryotic Domain of Life would therefore restore balance to the carbon cycle.

キーワード: Great Oxygenation Event, Cyanobacterial Evolution, Lomagundi Event, Mitochondrial Evolution, Magnetotactic Bacteria, Sedimentary Manganese
Keywords: Great Oxygenation Event, Cyanobacterial Evolution, Lomagundi Event, Mitochondrial Evolution, Magnetotactic Bacteria, Sedimentary Manganese

Japan Geoscience Union Meeting 2013
(May 19-24 2013 at Makuhari, Chiba, Japan)

BAO01-12 会場:301A 時間:5 月 21 日 15:00-15:15

３８億年前のグラファイトのSTEMのよる観察
STEM observation of graphite from 3.8 Ga Isua Supracrustal Belt

掛川 武 [1]*
Takeshi Kakegawa[1]*

[1] 東北大大学院理
[1]Tohoku University

Graphite is known to occur in the 3.8 billion years old Isua Supracrustal Belt (ISB) of western Greenland, and 13C-depleted graphite from sedimentary rocks of the ISB have been interpreted as traces of early life. The unequivocal documentation of biogenicity for graphite is complicated by the possibility of secondary graphite precipitation from metamorphic or igneous fluids and the difficulties in distinguishing biogenic from secondary graphite.

Graphite in meta-sedimentary rocks and carbonate veins in ISB is studied by STEM and Laser-Raman spectroscopy. Previous studies proposed that graphite in meta-sedimentary rocks are biogenic in origin, and others are chemical precipitates from CO2-rich fluids. STEM observation of graphite in meta-sedimentary rocks indicated many unique textures, resemble to carbon nano-tube. On the other hand, graphite in veins show sheet-structure-dominated features. Laser-Raman analyses indicate that sedimentary graphite recorded the peak metamorphic temperature. Graphite in veins showed lower temperature than that of the peak metamorphism. Those data comprehensively provide more evidence of biogenic graphite that differ from non-biogenic graphite in ISB.

キーワード: STEM, ラマン
Keywords: STEM, Raman

BAO01-13　　会場:301A　　時間:5 月 21 日 15:15-15:45

Origin of life: Source rocks for the origin and evolution of life

Origin of life: Source rocks for the origin and evolution of life

丸山 茂徳 [1*], 戎崎 俊一 [2]
Shigenori Maruyama[1*], Toshikazu Ebisuzaki[2]

[1] 東京工業大学　地球生命研究所, [2] 理化学研究所
[1]Earth-Life Science Institute, Tokyo Institute of Technology, [2]RIKEN

One of the key factors for the origin and evolution of life is a nutrient supply which is derived from rocks. Life cannot be synthesized under nutrient-free conditions in an atmosphere as shown in the famous experiments of Miller (1953). For the beginning of life, three components are essential; (1) C (carbon)-centered sugar for fuel, (2) P (phosphorus)-centered metabolism, and (3) N (nitrogen)-centered information coded by basic pairs (DNA). Among them, P (negative ion), which is a centered nutrient coupled with K (positive ion), plays a critical role in metabolic activity. Can those nutrients be derived from any kinds of rocks on the Earth? The answer is, yes, but only three kinds of rocks as follows

(1) Granite: Granite can be formed by two-step extractions of nutrients: partial melting of mantle peridotite at a mid-oceanic ridge followed by partial melting at a subduction zone, either by slab melting or re-melting of lower mafic crust generated by partial melting of a mantle wedge. The major nutrient elements, such as P and K, are large ion lithophile elements (LILE), and hence, difficult to be bound into major mantle minerals. Plate tectonics increases the volume of calc-alkaline rocks such as TTG (tonalite-trondhjemite-granodiorite) or andesite and dacite at subduction zones through time.

Granitic rock was absent when a magma ocean was consolidated at 4.5Ga. In the Hadean, the major rock source for nutrient supply was not granite, but rather presumably the primordial continents.

(2) Primordial continents (Anorthosite with KREEP basalts): Primordial continental material is the second candidate for the source of nutrients. No remnants of those continents remain on the modern Earth (i.e., no Hadean rocks are left). Understanding of the primordial continent is developed through the geology of the Moon, and also from the concept of giant impact. The surface of Moon is covered by 50 to 70 km-thick anorthositic crust with local cover and dikes of KREEP (Potassium, Rare Earth Elements, and Phosphorus) basalt composition, and presumably underplated by KREEP-like rock types beneath the anorthositic continent. Both rock units have been interpreted as the final residue of magma ocean when the Moon was formed by the giant impact that led to the formation of the early Earth, where Mars-sized protoplanets collided with each other. If the giant impact theory is correct, the Earth must have been completely molten even up to the core. During the gradual cooling of the Moon and the Earth, the final liquid remained near the surface, forming the buoyant anorthositic crust, covered or underplated by KREEP magma similar to that observed on the Moon.

(3) Carbonatite: Carbonatite has only a single step of fractional melting of mantle peridotites under the cratons with an extremely small degree of melting. The selective removal of melt to form considerable amounts of nutrients under the sub-cratonic mantle creates carbonatite magma enriched in nutrients with highly volatile incompatible elements such as H2O and CO2 (more than 80% are volatiles). Nutrients concentrate into melt, depending on the degree of melting. Peridotite contains P=50 and K=240 (all values in ppm hereafter), but 100 times concentration of P=4495-3273 and 200-300 times of K=56118-68902 are seen in carbonatite. In general, the nutrient abundance is ideal for carbonatite, except for the U abundance. Carbonatite plays the role of milk-like materials to grow life. However, it may also function like an atomic-bomb magma to cause local mass extinctions, as well as resultant promotion of genome mutation by internal radiation through food chains.

Japan Geoscience Union Meeting 2013
(May 19-24 2013 at Makuhari, Chiba, Japan)

BAO01-14 会場:301A 時間:5月21日 16:15-16:45

火星生命探査計画：蛍光顕微鏡をもちいた火星表面での微生物探査
JAMP (Japan Astrobiology Mars Project): Search for Microbes on the Mars Surface with a Fluorescent Microscope.

山岸 明彦[1*], 吉村　義隆[2], 本多 元[3], 宮川 厚夫[1], 佐藤 毅彦[4], 石上　玄也[4], 春山 純一[4], 小林 憲正[5], 長沼 毅[6], 出村 裕英[7], 佐々木 晶[8], 宮本 英昭[9]
Akihiko Yamagishi[1*], Yoshitaka Yoshimura[2], Hajime Honda[3], Atsuo Miyakawa[1], Takehiko Satoh[4], Genya Ishigami[4], Junichi Haruyama[4], Kensei Kobayashi[5], Takeshi Naganuma[6], Hirohide Demura[7], Sho Sasaki[8], Hideaki Miyamoto[9]

[1] 東京薬科大学, [2] 玉川大学, [3] 長岡科学技術大学, [4] 宇宙科学研究所, [5] 横浜国大, [6] 広島大学, [7] 会津大学, [8] 国立天文台, [9] 東京大学
[1]Tokyo Univ. Pharm. Life Scie., [2]Tamagawa University, [3]Nagaoka University of Technology, [4]ISAS/JAXA, [5]Yokohama National Univ., [6]Hiroshima Univ., [7]Aizu Univ., [8]NAOJ, [9]The Univ. Tokyo

Introduction: Among the planets and giant satellites in our solar system, the characteristics of Mars are most similar to those of Earth. This suggests that the life similar to terrestrial life may arise and survive on Mars.

Here we propose a new life detection project on Mars within the scope of MELOS (Mars Exploration with Lander Orbiter Synergy), to search for methane-oxidizing microbes by fluorescence microscopy [1]. We propose to search for cells from a depth of about 5 - 10 cm below the surface, which is feasible with current technology. Microscopic observation has the potential to detect single cells. The subsequent anal-ysis of amino acids will provide the information need-ed to define the origin of the cell.

Survivability of Life in the Mars Environment: Physical and chemical limits for terrestrial life have been major foci in astrobiology [2], and are summa-rized in ref. [1]. Combining the environmental factors, anywhere in the Martian environment where we can find the three components, water molecules, reducing compounds and oxidative compounds could be an environment where life can be sustained for long periods of time, if other factors such as temperature, pressure, UV and other radiations permit.

Methane Oxidizing Bacteria on Earth: Recently, a microbial consortium that is capable of using manga-nese (birnessite) and iron (ferrihydrite) to oxidize me-thane has been predicted in marine methane-seep sed-iments in the Eel River Basin in California [3]. Thus, there are several mechanisms of methane oxidation carried out by Bacteria and Archaea on Earth, and pos-sibly on Mars.

Reference:

[1] Yamagishi, A, et al. (2010) Biol. Scie. Space, 24, 67-82. [2] Marion, G.M. et al. (2003) Astrobiol. 3, 785-811. [3] Beal, E. J., et al. (2009) Science, 325, 184-187.

キーワード: 火星, 微生物, 蛍光顕微鏡, 火星探査, アストロバイオロジー
Keywords: Mars, microbes, fluorescence microscope, Mars exploration, Astrobiology

Japan Geoscience Union Meeting 2013
(May 19-24 2013 at Makuhari, Chiba, Japan)

BAO01-15 会場:301A 時間:5 月 21 日 16:45-17:00

Amazonis and Elysium basins and Their Link, Marte Vallis (AME), Tharsis/Elysium Corridor, Mars

Amazonis and Elysium basins and Their Link, Marte Vallis (AME), Tharsis/Elysium Corridor, Mars

Dohm James[1]*, 丸山 茂徳 [1], 宮本 英昭 [2]
James Dohm[1]*, Shigenori Maruyama[1], Hideaki Miyamoto[2]

[1] 東京工業大学　地球生命研究所, [2] 東京大学総合研究博物館
[1]Earth-Life Science Institute, Tokyo Institute of Technology, [2]The University Museum, The University of Tokyo

The geologic provinces of Mars, as identified through a synthesis of geologic, paleohydro-logic, topographic, geophysical, spectral, and elemental information [1], are windows into its evolution, with the youthful province, the Tharsis/Elysium corridor [2-4], recording hydrologic, tectonic, and volcanic activity, including fissure-fed eruptions and shield-volcano field development, within at least tens of millions of years.

Geologically recent activity in the Tharsis/Elysium corridor region is particularly high-lighted in the Amazonis and Elysium basins and their link, Marte Vallis (hereafter referred to as AME). A youthful shield-volcano field with at least seven gentle sloping shield volcanoes and fissure-fed vent structures have been identified, mapped, and characterized in the western part of the Elysium. In addition, the lava flows on and near the margins of the shield volcanoes display crenulated lava flow margins, possibly marking lava-water-ice interactions. Both the shield volcanoes and pristine lavas located within AME, which are marked by a paucity of relatively small (~few-km-diameter) superposed impact craters and modified by faults and fractures and valleys, point to geological and hydrological activity on Mars in recent geologic time, making AME a significant target for future reconnaissance, including testing the hypotheses of whether Mars is geologically, hydrologically, and biologically active.

Specifically, the following questions might be addressed through international reconnaissance missions to AME, which would include instrument suites with optimal geologic, geochemical, geophysical (including seismic), environmental, and biological capabilities, including whether Mars: (1) is geologically and hydrologically active, (2) contains salty groundwater and magma at relatively shallow depths, (3) has sustained elevated heat flow, (4) records seismic activity, and (5) comprises fossilized and/or extant life.

References

[1] Dohm, J.M. et al., (2013?in press), Nova Science Publishers, Inc.
[2] Dohm, J.M., et al., 2008, Planetary and Space Science 56, 985?1013, doi:10.1016/j.pss.2008.01.001
[3] Dohm, J.M., (2004) Planetary and Space Science 52, 189?198, doi:10.1016/j.pss.2003.08.013.
[4] Miyamoto, H., (2004) Journ. of Geophy. Res. 109, E06008, doi:10.1029/2003JE002234.

Japan Geoscience Union Meeting 2013
(May 19-24 2013 at Makuhari, Chiba, Japan)

BAO01-16 会場:301A 時間:5月21日 17:00-17:15

たんぽぽ計画の準備状況と微生物宇宙生存可能性の検討
Current status of preparation of TANPOPO mission and investigation of survivability of microbes in space

横堀 伸一[1*], 河口 優子[1], 橋本 博文[7], 林 宣宏[6], 東出 真澄[7], 今井 栄一[8], 河合 秀幸[9], 小林 憲正[10], 三田 肇[11], 中川 和道[2], 鳴海 一成[3], 奥平 恭子[12], 清水 康之[1], 田端 誠[9], 薮田 ひかる[14], 太刀川 純孝[4], 富田ー横谷 香織[13], 山下 雅道[4], Yang Yinjie[1], 矢野 創[4], 吉田 聡[5], 山岸 明彦[1]
Shin-ichi Yokobori[1*], Yuko Kawaguchi[1], Hirofumi Hashimoto[7], HAYASHI, Nobuhiro[6], HIGASHIDE, Masumi[7], Eiichi Imai[8], KAWAI, Hideyuki[9], Kensei Kobayashi[10], Hajime Mita[11], NAKAGAWA, Kazumichi[2], Issay Narumi[3], Kyoko Okudaira[12], SHIMIZU, Yasuyuki[1], TABATA, Makoto[9], Hikaru Yabuta[14], TACHIKAWA, Sumitaka[4], Kaori Tomita-Yokotani[13], YAMASHITA, Masamichi[4], Yinjie Yang[1], Hajime Yano[4], YOSHIDA, Satoshi[5], Akihiko Yamagishi[1]

[1] 東京薬大・生命科学, [2] 神戸大・院人間発達環境学, [3] 原子力機構・量子ビーム, [4]JAXA/ISAS, [5] 放医研・福島復興支援, [6] 東京工大・院生命理工, [7]JAXA・未踏技術研究セ, [8] 長岡科技大・生物, [9] 千葉大・院理, [10] 横浜国大・院工, [11] 福岡工大・工, [12] 会津大, [13] 筑波大・院生命環境, [14] 大阪大・院理
[1]Sch. Life Sci., Tokyo Univ. Pharm. Life Sci., [2]Grad. Sch. Human Develop. Environ., Kobe Univ., [3]Quantum Beam, JAEA, [4]JAXA/ISAS, [5]NIRS, [6]Grad. Sch. Biosci. Biotech., Tokyo Inst. Tech., [7]JAXA, [8]Nagaoka Univ. Tech., [9]Grad. Sch. Sci., Chiba Univ., [10]Grad. Sch. Eng. Yokohama Natl. Univ., [11]Facl. Eng., Fukuoka Inst. Tech., [12]Univ. Aizu, [13]Grad. Sch. Life Environ. Sci., Univ. Tsukuba, [14]Grad. Sch. Sci., Osaka Univ.

Microbes have been collected from high altitude using balloons, aircraft and meteorological rockets since 1936, even it is not clear how those microbes could be ejected up to such high altitude. Spore forming fungi, spore-forming Bacilli, and Deinococci (e.g. *Deinococcus aerius* and *Deinococcus aetherius*) have been isolated in these experiments. If microbes could be found even at the higher altitude of low earth orbit (400 km), the fact would endorse the possibility of interplanetary migration of terrestrial life.

For the origin of life on Earth emerged within a short period after the end of heavy bombardment, Panspermia hypothesis was proposed. Recent the reports on the possible fossils of microbes in the Martian meteorite promote the debate on the possible existence of extraterrestrial life, and interplanetary migration of life as well.

On the other hand, it is the question where precursors of materials such as protein and nucleic acids came from in the era of ”chemical evolution” on the Earth? Recent studies suggest that the some of such organic compounds were created in space. Then, they reached the surface of Earth via meteorites, cosmic dusts, and so on. Avoiding contamination of terrestrial materials from the extraterrestrial materials is quite important issues for the analysis of extraterrestrial materials. Capturing such extraterrestrial materials before falling down on the surface of Earth might be one of possible solutions.

We have proposed a mission, named TANPOPO, to examine possible interplanetary migration of microbes, and organic compounds at the Exposure Faculty of Japan Experimental Module (JEM) of the International Space Station (ISS). The Tanpopo mission consists of six subthemes ? capture of microbes in space, exposure of microbes in space, capture of organic compounds in space, exposure of organic compounds in space, measurement of space debris at the ISS orbit, and evaluation of ultra low-density aerogel special for the TANPOPO mission.

Ultra low-density aerogel will capture micrometeoroid and space debris. Particles captured by aerogel will be analyzed from biological, chemical, and meteorological aspects.

In addition to particle-capture on ISS, we also proposed direct exposure experiments of microbial cell aggregates that might protect the microbes themselves from UV and cosmic rays. Deinococci (*Deinococcus radiodurans*, *D. aerius*, and *D. aetherius*), terrestrial cyanobacteria, and fungi are under consideration for space exposure. Amino acids and complex organic compounds that can be formed in space are also planed for space exposure.

In this paper, we overview the TANPOPO mission and discuss the current status of experiments related to the microbe existence/survival set for this mission.

キーワード: パンスペルミア, 宇宙曝露, 生命の起原
Keywords: Panspermia, Space exposure, Origin of life

Japan Geoscience Union Meeting 2013
(May 19-24 2013 at Makuhari, Chiba, Japan)

BAO01-17 会場:301A 時間:5月21日 17:15-17:30

サブミリメーターサイズの*Deinococcus*属の凝集細胞は宇宙空間でUVを遮蔽することが可能である

The sub-millimeter-sized aggregated deinococcal cells could be shield from solar UV

河口 優子[1*], Yinjie Yang[1], 川尻成俊[1], 白石啓祐[1], 高須昌子[1], 鳴海一成[2], 佐藤勝也[2], 橋本 博文[3], 中川和道[4], 谷川能章[4], 桃木洋平[4], 田邊真依子[4], 杉野朋弘[1], 高橋勇太[1], 清水康之[1], 吉田聡[5], 小林 憲正[6], 横堀 伸一[1], 山岸 明彦[1]
Yuko Kawaguchi[1*], Yinjie Yang[1], Narutoshi Kawashiri[1], Keisuke Shiraishi[1], Masako Takasu[1], Issay Narumi[2], Katsuya Satoh[2], Hirofumi Hashimoto[3], Kazumichi Nakagawa[4], Yoshiaki Tanigawa[4], Yoh-hei Momoki[4], Maiko Tanabe[4], Tomohiro Sugino[1], Yuta Takahashi[1], Yasuyuki Shimizu[1], Satoshi Yoshida[5], Kensei Kobayashi[6], Shin-ichi Yokobori[1], Akihiko Yamagishi[1]

[1] 東京薬科大学生命科学, [2] 日本原子力機構量子ビーム, [3]JAXA/ISAS, [4] 神戸大学大学院人間発達科学, [5] 放射線医科学研究所福島復興支援, [6] 横浜国立大学大学院工学府, [7] 東京都医学総合研究所
[1]Department of Applied Molecular Biology, School of Life Sciences, Tokyo University of Pharmacy and L, [2]Ion Beam Mutagenesis Research Group, Quantum Beam Science Directorate, [3]Institute of Space and Astronautical Science, JAXA, [4]Graduate School of Human Development and Environment, Kobe University, [5]National Institute of Radiological Sciences, [6]Graduate School of Engineering, Yokohama National University, [7]Protein Metabolism Project, Tokyo Metropolitan Institute of Medical Science

To investigate the interplanetary transfer of life, numerous exposure experiments have been carried out on various microbes in space since 1960s. The results suggested that microbe spores might survive for a long period if the spores are shielded from intense solar radiation [1]. In the Tanpopo mission, we have proposed to carry out the experiments on capture and space exposure of microbes at International Space Station (ISS) [2]. Microbial candidates for the exposure experiments in space include *Deinococcus radiodurans*, *D. aerius* and *D. aetherius*. We have examined the survivability of *Deinococcus* spp. under the environmental conditions on ISS in orbit (i.e., long exposure to heavy-ion beams, temperature cycles, vacuum and UV irradiation). Among the space environmental factors, solar UV is most lethal to microbes, and damage is caused by the absorption of UV by DNA [3].

In this report, we examined the effect of solar UV radiation (172 nm, 254 nm and 280?315 nm respectively) on the deinococcal cell aggregates with different thicknesses to determine whether the size of the cell aggregate influences the cell survivability. Though the cells in thin layers of aggregates were killed by UV radiation, large number of cells survived the radiation when the cell layer was thick. The similar trend of survivability was observed for other UV range. Supposing that the aggregates are sphere, the diameter of the aggregate that is sufficient to shield the cells in the inner layer from solar UV radiation is 200 micrometer for *D. radiodurans*, 850 micrometer for *D. aerius*, and 700 micrometer for *D. aetherius*. We propose the microbial cell aggregate as an ark for the interplanetary transfer of microbes, and name it the 'masspanspermia' hypothesis.

[References]
[1] Horneck et al., (1994) Adv. Space Res. 14, 41?45 [2] Yamagishi et al., (2008) Int. Symp. Space Tech. Sci. (ISTS) Web Paper Archives 2008-k-05 [3] Horneck (1993) Orig. Life Evol. Biosph. 23, 37?52

キーワード: パンスペルミア仮説, 宇宙実験, Deinococcus, 微生物凝集体, マサパンスペルミア仮説
Keywords: Panspermia hypothesis, Space exposure experiments, Deinococcus, Cell aggregation, Massapanspermia hypothesis

BAO01-18 会場:301A 時間:5 月 21 日 17:30-17:45

復元した祖先型タンパク質を用いた単純型アミノ酸組成の検討
Restricting the amino acid usage of a resurrected ancestral protein

赤沼 哲史 [1*], 島田真実 [1], 中島慶樹 [1], 横堀伸一 [1], 山岸明彦 [1]
Satoshi Akanuma[1*], Masami Shimada[1], Yoshiki Nakajima[1], Shin-ichi Yokobori[1], Akihiko Yamagishi[1]

[1] 東京薬科大学 生命科学部 応用生命科学科
[1]Department of Applied Bioscience, Tokyo University of Pharmacy and Life Sciences

It is common among life on Earth that proteins are composed of 20 or nearly 20 kinds of amino acids. However, it is uncertain that, from the standpoint of astrobiology, proteins are always composed of the 20 kinds of amino acids. Even for the evolution of proteins on Earth, it has been argued that primordial proteins that existed before the last universal common ancestor involved less than 20 kinds of amino acids (Crick, 1968). Given simpler protein synthesis system, the primitive proteins, which might have comprised a reduced set of amino acids, must have had a sufficiently adequate structure for functional interactions and catalysis. To address this issue experimentally, we used the protein simplification engineering (Akanuma et al., 2002) to examine whether a protein composed of less than 20 types of amino acids can retain its stable structure and biological function. To this end, we first resurrected several ancestral proteins and then restricted the amino acid usage of a resurrected protein to a reduced amino acid set.

As the model protein, we chose a house keeping enzyme, nucleoside diphosphate kinase (NDK). Because extant genes are evolutionary descendants of ancient genes, ancestral sequences of a particular protein can be inferred by comparing extant homologous protein sequences. Along this line, we first inferred several ancestral amino acid sequences of NDK by phylogenetic analysis of the extant homologous sequences. The inferred sequences were then genetically reconstructed. One of the reconstructed protein, Arc1, is very thermally stable (unfolding temperature = 113oC) and shows catalytic efficiency similar to those of the modern NDKs.

It is currently impossible to infer amino acid sequences that existed before the last universal common ancestor. Therefore, using Arc1 as the starting molecule, we reconstructed a reduced amino acid set variant, Arc1-s2, in which Met, Gln, Lys, Tyr and Asn were replaced by other amino acids. Because cysteine is absent from Arc1, Arc1-s2 consists of only 14 amino acid letters. Arc1-s2 retains thermal stability similar to that of Arc1; whereas, no detectable level of catalytic activity was observed for Arc1-s2. Therefore, the fourteen amino acid types are sufficient to encode a thermally stable protein but more amino acid types would be required for its function. To reevaluate the individual contributions of the 20 amino acid types to the stability and activity of Arc1, we reconstructed 19 Arc1 variants in which one of the 19 amino acid types was all replaced by other amino acids. The result will be also present in the meeting.

(1) Crick, JMB 38, 367 (1968); (2) Akanuma et al., PNAS 99, 13549 (2002)

BAO01-P01 会場:コンベンションホール 時間:5月21日 18:15-19:30

系外惑星のバイオマーカーのための光合成光吸収についての理論的研究
Theoretical investigation on the absorption spectrum of photosystem for the biomarker of extrasolar planets

田口 真彦[1], 小松勇[1], 佐藤皓允[1], 庄司 光男[1]*, 栢沼愛[2], 神谷克政[1], 白石賢二[1], 矢花一浩[1], 梅村雅之[1]
Masahiko Taguchi[1], Yu Komatsu[1], Akimasa Sato[1], Mitsuo Shoji[1]*, Megumi Kayanuma[2], Katsumasa Kamiya[1], Kenji Shiraishi[1], Kazuhiro Yabana[1], Masayuki Umemura[1]

[1] 筑波大学数理物質科学研究科, [2] 筑波大学システム情報研究科
[1]Graduate School of Pure and Applied Science, University of Tsukuba, [2]Department of Computer Science, University of Tsukuba

Over 800 extrasolar planets have been discovered, and more than 20,000 candidates have been detected. Planets in habitable zone have been observed, and the discovery of Earth-like planets is expected. Great attentions have been paid to the detection of life in extrasolar planets. For the detection, various indices have been proposed as biomarkers. One of the indicators is red edge[1], which is a characteristic steep gradient observed in the near-infrared region of around 750 nm in plant's reflection spectra [2]. In fact, red edge can be observed in the reflection spectrum of the Earth via the Moon (earthshine [3]). Since red edge is affected by many factors, its pricise predictions is not simple. However, a leaf chlorophyll absorption is thought to be the major factor of red edge [2].

On Earth, photosynthetic organisms have evolved through the collection of sunlight. On the other hand for the extrasolar planets, whose surrounding space environment has different spectrum from their primary star, photosystems should be different in many parts, such as pigment types and arrangements even though the environment is similar to the Earth.

Before predictions of biomakers of extrasolar planets, we examine the basic characters of chlorophylls in photosystems. It is also important for the study of the diverse photosystems on Earth. Chlorophylls are concentrated in a chloroplast, and form pigments-protein complexes in the photochemical systems.

The purpose of this research is to characterize the absorption spectrum of chlorophylls in a photosystem. First of all, we calculated the absorption spectrum of the pigment in methanol using DFT based polarization continuum model (PCM) method, and confirmed the validity of our calculation method. Then, quantum mechanics/molecular mechanics (QM/MM) calculations were performed for the absorption spectrums of the photosystem. Each chlorophyll was included in the QM region. We found that the absorption wavelengths are shifted about +10 nm by the effects of the protein environment. Similar influence was observed by the effect of amino acid coordination to the central Mg ion in the chlorophyll. These calculated results indicate a fine modulation character of the adsorption wavelength for the photosystem. This character is important for photosystems in extrasolar planets as well as in extreme conditions on Earth.

[1] N. Y. Kiang et al., Astrobiology, 7 (1), 252, 2007
[2] S. Seager et al., Astrobiology, 5 (3), 372, 2005
[3] L. Arnold et al., Astronomy&Astrophysics, 392, 231, 2002

キーワード: バイオマーカー, 系外惑星, 光合成, 量子古典混合計算, 光吸収
Keywords: biomarker, extrasolar planet, photosystem, QM/MM, absorption spectrum

Japan Geoscience Union Meeting 2013
(May 19-24 2013 at Makuhari, Chiba, Japan)

BAO01-P02　　会場:コンベンションホール　　時間:5月21日 18:15-19:30

宇宙線による星間物質からのアミノ酸前駆体生成の実験的検証
Experimental studies on abiotic formation of amino acid precursors from interstellar media by cosmic rays

江藤 碧[1]*, 岡部 拓人[1], 金子 竹男[1], 大林 由美子[1], 福田 一志[2], 小栗 慶之[2], 吉田 聡[3], 小林 憲正[1]
Midori Eto[1]*, Takuto Okabe[1], Takeo Kaneko[1], Yumiko Obayashi[1], Hitoshi Fukuda[2], Yoshiyuki Oguri[2], Satoshi Yoshida[3], Ken-sei Kobayashi[1]

[1] 横浜国立大学, [2] 東京工業大学, [3] 放射線医学総合研究所
[1]Yokohama National University, [2]Tokyo Institute of Technology, [3]National Institute of Radiological Sciences

地球生命の誕生に用いられたアミノ酸などの有機物の起源として，隕石等による地球外有機物の供給が注目されている。隕石や彗星の有機物は太陽系生成前の分子雲環境下で，星間分子に宇宙線などにより生成した可能性が考えられている。本研究では，模擬星間物質（一酸化炭素・メタノール・アンモニア・水など）に東工大タンデム加速器からの陽子線，もしくは放医研 HIMAC からの重粒子線を照射し，生成物を加水分解の後，アミノ酸の定量を行った。出発物質の組成，照射条件などの違いによるアミノ酸生成量の違いを調べ，アミノ酸生成機構などを考察した。

キーワード: 宇宙線, 星間物質, アミノ酸前駆体, 陽子線照射, 生命の起源, 重粒子線
Keywords: cosmic rays, interstellar media, amino acid precursors, proton irradiation, origins of life, heavy ions

BAO01-P03 会場:コンベンションホール 時間:5月21日 18:15-19:30

たんぽぽ計画エアロゲル試料の初期分析とその後の分析フロー
Preliminary examination plan and subsequent analytical procedure of captured samples by aerogel in the Tanpopo mission

奥平 恭子[1]*, 山岸 明彦[2], 矢野 創[3], 薮田 ひかる[4], 田端　誠[3], 横堀 伸一[2], 今井 栄一[5], 小林 憲正[6], 三田 肇[7], 河合　秀幸[8], 東出　真澄[3], 佐々木　聰[9], たんぽぽWG[3]
Kyoko Okudaira[1]*, Akihiko Yamagishi[2], Hajime Yano[3], Hikaru Yabuta[4], Makoto Tabata[3], Shin-ichi Yokobori[2], Eiichi Imai[5], Kensei Kobayashi[6], Hajime Mita[7], Hideyuki Kawai[8], Masumi Higashide[3], Satoshi Sasaki[9], Tanpopo WG[3]

[1] 会津大学, [2] 東京薬科大学, [3] 宇宙航空研究開発機構, [4] 大阪大学, [5] 長岡技術科学大学, [6] 横浜国立大学, [7] 福岡工業大学, [8] 千葉大学, [9] 東京工科大学
[1]The University of Aizu, [2]Tokyo University of Pharmacy and Life Science, [3]JAXA, [4]Osaka University, [5]Nagaoka University of Technology, [6]Yokohama National University, [7]Fukuoka Institute of Technology, [8]Chiba University, [9]Tokyo University of Technology

The Tanpopo mission is a Japanese astrobiological experiment which will be conducted on the Japanese Experiment Module (JEM) of the International Space Station (ISS) [1]. The Tanpopo mission consists of several subthemes: 1) capture of microbes in space, 2) exposure of microbes in space, 3) exposure of organic compounds in space, 4) capture of organic compounds (in micrometeoroids) in space, 5) evaluation of ultra low-density aerogel developed for the Tanpopo mission, and 6) capture of space debris at the ISS orbit (approximately 400 km altitude).

Here, we overview Preliminary Examination Team (PET) analysis and subsequent analytical procedure of aerogel samples for the mission, i.e. analyses for the subthemes 1, 3, 5, and 6 described above. Silica aerogel with 0.01 g cm^{-3} density supported by higher density aerogel [2] will be used to capture micrometeoroid and space debris at LEO. Captured particles and their penetration tracks will be offered for various analyses after retrieval to Earth. These samples will be analyzed for mineralogical, organic and microbiological characteristics.

In this paper, current status of Tanpopo-Aerogel-PET preparation will be introduced. In Preliminary Examination (PE), Curation team covers the receipt of retrieved samples (Sample Aerogel Panels), sample catalog preparation for data archiving and sample storage. Whole documentation team deals with penetration track mapping, penetration track measurement (e.g. incoming angle, track depth and track volume) and evaluation of aerogel as a capture medium. Processing team prepares keystones and quickstones (small pieces of aerogel) containing particles and their penetration tracks for allocation to researchers. After preliminary characterization, the samples (tracks and/or particles in keystones/quickstomes) will be properly processed in accordance with a request by each sub team for the subsequent detailed analyses.

Aerogel panels attached to zenith (space)-facing side will be allocated mainly to Organic and Inorganic Sub-Teams, and ones attached to ram-facing side (facing east) to both Debris and Microbe (terrestrial origin) Sub-Teams, while ones facing north to all Sub-Teams. We plan to preserve basically one of each aerogel panel for storage in the scope of future analyses and possible provision to researchers.

References

[1] Yamagishi A. et al., Trans. JSASS Space Tech. Jpn, 7, (2009) Tk_49-Tk_55.
[2] Tabata M. et al., Biol. Sci. Space, 25 (2011), 7-12.

Keywords: Tanpopo mission, International Space Station, Silica aerogel, Micrometeoroid, Space debris, Curation

BAO01-P04 会場:コンベンションホール 時間:5 月 21 日 18:15-19:30

エアロゲルで捕集した微小粒子中のアミノ酸分析法の検討
Analysis of amino acids in small particles captured with aerogel

古川 天[1*], 河口 優子[2], 奥平 恭子[3], 三田 肇[4], 田端 誠[5], 今井 栄一[6], 長谷川 直[5], 河合 秀幸[7], 矢野 創[5], 橋本 博文[5], 横堀 伸一[2], 山岸 明彦[2], 大林 由美子[1], 金子 竹男[1], 小林 憲正[1]
Taka Kogawa[1*], Yuko Kawaguchi[2], Kyoko Okudaira[3], Hajime Mita[4], Makoto Tabata[5], Eiichi Imai[6], Sunao Hasegawa[5], Hideyuki Kawai[7], Hajime Yano[5], Hirofumi Hashimoto[5], Shin-ichi Yokobori[2], Akihiko Yamagishi[2], Yumiko Obayashi[1], Takeo Kaneko[1], Kensei Kobayashi[1]

[1] 横浜国立大学, [2] 東京薬科大学, [3] 会津大学, [4] 福岡工業大学, [5] 宇宙科学研究所, [6] 長岡技術科学大学, [7] 千葉大学
[1]Yokohama National University, [2]Tokyo University of Pharmacy and Life Science, [3]Aizu University, [4]Fukuoka Institute of Technology, [5]JAXA/ISAS, [6]Nagaoka University of Technology, [7]Chiba University

たんぽぽ計画においては，国際宇宙ステーション曝露部上にエアロゲルを設置し，これで高速に飛来する惑星間塵などの微小粒子を捕集する予定である。これを地球に回収した後，アミノ酸分析等により微小粒子のキャラクタリゼーションを行うが，その予備実験として，二段式軽ガス銃を用いて射出した模擬宇宙塵をエアロゲルで捕集し，その分析を行った。エアロゲル中のアミノ酸ブランクの測定などを行い，実験計画の評価を行った。

キーワード: たんぽぽ計画, 惑星間塵, 微小粒子, 微生物, エアロゲル, アミノ酸
Keywords: the Tanpopo Mission, interplanetary dust particles, small particles, microorganisms, aerogel, amino acids

Japan Geoscience Union Meeting 2013
(May 19-24 2013 at Makuhari, Chiba, Japan)

BAO01-P05 会場:コンベンションホール 時間:5 月 21 日 18:15-19:30

衝撃波を用いたカルボン酸およびアンモニアからのアミノ酸合成
Synthesis of an amino acid from carboxylic acid and ammonia with shock wave

鈴木 千月香 1*, 古川 善博 1, 小林 敬道 2, 関根 利守 3, 掛川 武 1
Chizuka Suzuki1*, Yoshihiro Furukawa1, Takamichi Kobayashi2, Toshimori Sekine3, Takeshi Kakegawa1

1 東北大学理学研究科, 2 物質・材料研究機構 超高圧グループ, 3 広島大学理学研究科
1Graduate School of Science, Tohoku University, 2National Institute for Materials Science, 3Graduate School of Science, Hiroshima University

Proteins are composed of twenty kinds of amino acids and are essential biomolecules for life on the Earth. Therefore, origins of amino acids on the early Earth have been an important concern. Many previous studies indicate that the late heavy bombardment (LHB) of extraterrestrial objects had occurred during 3.8-4.0 billion years ago. These impacts might have delivered and produced prebiotic organic compounds including amino acids, amines, and carboxylic acids as well as ammonia (Cronin and Pizzarello et al., 1988; Furukawa et al. 2009). However, the number of biomolecule by these processes was limited number of amino acids among protein-constituent amino acids. The organic compounds supplied by the impacts of extraterrestrial objects to the oceans must have experienced further impacts, because the LHB is a successive impact event. In this study, we demonstrated shock-recovery experiments on a solution of formic acid and ammonia to investigate whether amino acids form from low molecular weight organic compounds by oceanic impacts on the early Earth.

Shock-recovery experiments were performed with a single-stage propellant gun using an improved sample container. Starting material is a mixture of 13C-formic acid and ammonia. After the impact experiments, soluble organic compounds were extracted into water and then amines and amino acids were analyzed with liquid chromatography-mass spectrometer (LC/MS). Glycine, methylamine and ethylamine whose carbons are composed of 13C were identified in all of the samples. The amounts of glycine were almost constant regardless of the impact velocity (0.7-0.8 km/s). The amounts of produced amines increased depending on the impact velocity. The present results suggest that shock wave converts a low molecular weight organic compound to larger molecular weight organic compounds. The successive impacts might have contributed to chemical evolution providing variety in biomolecules on the prebiotic Earth.

BAO01-P06 会場:コンベンションホール 時間:5 月 21 日 18:15-19:30

D-型と L-型のアミノ酸の同位体化学：生物起源と非生物起源のシグナル識別法
Enantiomer-specific isotope analysis (ESIA): D- and L-amino acids by biotic and abiotic processes

高野 淑識 [1]*
Yoshinori Takano[1]*

[1] 海洋研究開発機構
[1]JAMSTEC

Introduction

The one-handedness of terrestrial L-amino acids in proteins and in D-sugars of DNA and RNA are primary formation, structure and function of biopolymers for life on the Earth. Recently D-alanine has been recognized as a physiologically essential enantiomer for microbial growth and metabolic maintenance. The cell wall of domain Bacteria, especially for Gram-positive Bacteria, consists of a thick and uniform peptidoglycan layer that includes D-amino acids. Laboratory studies of the degradation of peptidoglycan showed it to decompose more slowly than proteins, indicating semi-labile compounds in nature. We have developed an analytical method to determine the ESIA of individual amino acid enantiomers and revealed nitrogen isotopic hetero- and homogeneity for D-alanine and L-alanine in terms of microbial processes in domain Bacteria and chemical processes in organic symmetric synthesis.

Experimental

The nitrogen isotopic composition of the individual amino acids was determined using a gas chromatograph/combustion/isotope ratio mass spectrometer (GC/C/IRMS) with a ThermoFinnigan Delta Plus XP combined with an Agilent Technologies 6890N GC and an Ultra-2 capillary column. Novel derivatization of amino acid diastereomers by optically active (R)-(-)-2-butanol or (S)-(+)-2-butanol with pivaloyl chloride produces N-pivaloyl-(R,S)-2-butyl esters (NP/2Bu) of the amino acid diastereomers. The elution order of these compounds on the chromatogram can be switched by a designated esterification reaction. We used purified peptidoglycans from domain Bacteria (phylum Firmicutes and Actinobacteria; Enterococcus faecalis, Staphylococcus aureus, Staphylococcus staphylolyticus, Lactobacillus acidophilus, Bacillus subtilis, Micrococcus luteus and Streptomyces sp.), (pseudo)-peptidoglycan from domain Archaea (Methanobacterium sp.), cell walls from domain Eukarya (Saccharomyces cerevisiae). Racemic D- and L-alanine were synthesized by a nucleophilic substitution 1 (SN1) reaction via an intermediate carbocation formed between α-bromopropionic acid (as amino acid racemic precursors) and aqueous ammonia.

Results and Discussion

The nitrogen isotopic difference of peptidoglycan defined as Δ15ND-L in bacteria, representative gram-positive phylum Firmicutes and Actinobacteria, tended to be 15N-depleted in D-alanine, suggesting that heterogeneous components are mainly controlled by enzymatic pathways prior to formation of the bacterial cell wall. Alanine racemase (Enzyme Commission, EC; 5.1.1.1) that interconvert L-alanine to D-alanine, one of isomerases for chiral amino acids, previously indentified in a biosynthetic pathway, participates in crucial enzymatic reaction to form D-alanine before D-alanine-D-alanine ligase (EC; 6.3.2.4) pathway in peptidoglycan metabolism. In contrast, the Δ15ND-L of racemic alanine in the chemical pathway during the nucleophilic substitution reaction between 2-bromopropionic acid and ammonia showed infinitely homogeneous components for each enantiomers. We present recent preliminary results in terms of abiotic geochemical samples for ESIA.

References

Takano, Y., Chikaraishi, Y. and Ohkouchi, N. (2010) Enantiomer-specific isotope analysis (ESIA) of D- and L-alanine: nitrogen isotopic hetero- and homogeneity by microbial process and chemical process. Earth, Life, and Isotopes . Kyoto University Press., pp. 387-402.

Chikaraishi Y., Takano Y., Ogawa O. N., and Ohkouchi, N. (2010) Instrumental optimization for compound-specific nitrogen isotope analysis of amino acids by gas chromatography/combustion/isotope ratio mass spectrometry. Earth, Life, and Isotopes. Kyoto University Press., pp. 365-386.

Takano, Y., Chikaraishi, Y., Ogawa, O. N., Kitazato, H., and Ohkouchi, N. (2009) Compound-specific nitrogen isotope analysis of D-alanine, L-alanine, and valine: application of diastereomer separation to delta 15 N and microbial peptidoglycan studies. Analytical Chemistry, 81, 394-399.

Japan Geoscience Union Meeting 2013
(May 19-24 2013 at Makuhari, Chiba, Japan)

BAO01-P07 会場:コンベンションホール 時間:5 月 21 日 18:15-19:30

高温高圧下でのメチオニン重合に対するグリシン及びその分解物の影響: 海洋堆積物内における化学進化の可能性
Effects of glycine and its decomposition products on polymerization of methionine under high temperature and pressure

黄 叡 [1*], 古川 善博 [1], 掛川 武 [1]
Rui Huang[1*], Yoshihiro Furukawa[1], Takeshi Kakegawa[1]

[1] 東北大学大学院理学研究科
[1]Graduate school of Science, Tohoku University

It is widely believed that abiotic polymerization of amino acids is an important process for the formation of the first life. Several geological settings have been proposed as the place for the polymerization: sub-marine hydrothermal vents (Imai et al., 1999), tidal flats (Lahav et al., 1978), and marine sediments (Nakazawa et al., 1993). A unique point of the marine sediment is its pressurized conditions. Previous studies have suggested the importance of pressurized conditions for the production of longer peptides (Ohara et al., 2007; Otake et al., 2011; Furukawa et al., 2012). These previous studies also indicate that the reactivity of each amino acid is widely different, leading to skepticism about the formation of peptides composed of plural amino acids. In this study, we investigated oligomerization of methionine and glycine under the conditions of high temperature and high pressure (at 175^{o}C, 150 MPa, and 0-96 hours).

Methionine and glycine were used for representatives of each low and high reactive amino acid, respectively. Starting materials were solid methionine or solid methionine mixed with solid glycine, water, aqueous ammonia, or ammonium hydrogen carbonate. The additives other than glycine (water, aqueous ammonia, and ammonium hydrogen carbonate) are simulated decomposition products of glycine. Ammonium hydrogen carbonate decompose at about 60^{o}C and yields ammonia, carbon dioxide, and water. For each starting material, 0.43 mmol of methionine were used. The amounts of each additive were 0.43 mmol. Each starting material was sealed into a gold tube of 25 mm length and 5.5mm diameter. Then, high temperature and pressure conditions were applied using a test-tube-type autoclave system. After these experiments, amino acids and their oligomers were extracted into aqueous solution from the experimental products and analyzed with a high performance liquid chromatograph connected to a mass spectrometer (LC/MS).

In all experiments, methionine decomposed with elapsed time. Peptides longer than di-methionine were not formed in experiments without the additives. On the other hand, methionine was oligomerized to di-methionine, tri-methionine and methionine diketopiperazine in the experiments with additives. Methionyl-glycine and glycyl-methionine were also produced in experiments containing such additives. The rates of methionine decomposition and methionine-peptide formation were increased in experiments with additives. These rates were especially increased in samples containing aqueous ammonia, and ammonium hydrogen carbonate, suggesting that ammonia promote both the production rates of peptides and the decomposition reactions of methionine. The difference in reaction rates might have been caused by the difference in pH as suggested in a previous study (Sakata et al., 2010). When these results are applied to diagenesis in Hadean marine sediments, these results suggest that amino acids of lower reactivity may have been activated by amino acids of higher reactivity and might have produced peptides composed of plural amino acids.

BAO01-P08 会場:コンベンションホール 時間:5月21日 18:15-19:30

モンモリロナイト-グリシン-水混合物を用いた開放系における加圧加熱実験
Open system incubation experiments of glycine-montmorillonite-water mixture at high temperature and high pressure

小口 健太郎[1*], 古川 善博[1], 掛川 武[1]
Kentaro Oguchi[1*], FURUKAWA, Yoshihiro[1], KAKEGAWA, Takeshi[1]

[1] 東北大学大学院理学研究科
[1]Graduate School of Science, Tohoku University

There are several theories as to the place where primordial protein formed. Most of studies assume that polymerization of amino acids occurred in oceanic environments. However, there is a difficulty in the oligomerization of amino acids in oceans where huge amount of water exit, because the oligomerization of amino acid is a dehydration reaction. To address this contradiction, a model that hypnotizes the oligomerization proceeded in oceanic sediments was proposed. The effects of pressure in this model have been investigated previously. Clay minerals play an important role for the accumulation of amino acids in this model. However, the effect of clay minerals remains unclear. Therefore, this study investigated the effects of a typical clay mineral on the oligomerization of amino acids in a simulated diagenetic condition.

Glycine (Gly) adsorbed on montmorillonite was compressed and heated at 90^{o}C and 9 MPa with a piston cylinder for 7 days using silica powder as a pressure medium. Samples were collected and divided into three sections (S1, S2, and C1). The S1 was the outermost part of the sample, which was composed of mainly silica. S2 was the part between S1 and C1. Most of the S2 sample was silica. C1, the part of the center of the sample, was composed of mainly montmorillonite. Gly and peptides in these three samples were extracted with ammonia water. The extracted solution were filtered and concentrated to analyze the amount of Gly and peptides with LC/MS. Results show that Gly, diketopiperazine of Gly (Gly_{DKP}), and Gly dimer (Gly_2) were detected from three samples. The amount of Gly_2 and Gly_{DKP} were higher in C1 than in S1 and S2. Therefore, montmorillonite was considered to be effective to form peptides.

Japan Geoscience Union Meeting 2013
(May 19-24 2013 at Makuhari, Chiba, Japan)

BAO01-P09 会場:コンベンションホール 時間:5月21日 18:15-19:30

隕石海洋衝突によるアラニンの化学進化と酸素分圧の影響
Effect of oxygen fugacity in chemical processes of alanine during oceanic impacts of meteorites

梅田 悠平[1*], 関根 利守[1], 古川 善博[2], 掛川 武[2], 小林 敬道[3]
Yuhei Umeda[1*], Toshimori Sekine[1], Yoshihiro Furukawa[2], Takeshi Kakegawa[2], KOBAYASHI, Takamichi[3]

[1] 広島大学理学研究科, [2] 東北大学理学研究科, [3] 物質・材料研究機構
[1]Graduate School of Science, Hiroshima University, [2]Graduate School of Science, Tohoku University, [3]National Institute for Materials Science

The biomolecules on the Earth are thought either to have come from the extraterrestrial parts carried with flying meteorites or to have been formed on the Earth from the inorganic materials through given energy. From the standpoint to address the importance of impact energy, it is required to simulate experimentally the chemical reactions during impacts, because violent impacts may have occurred 3.8-4.0 Gyr ago to create biomolecules initially. It has been demonstrated that shock reactions between ocean and meteoritic constitutions can induce locally reduction environment to form bioorganic molecules such as amino acid (Nakazawa et al., 2005; Furukawa et al., 2009). We need to know possible processes how further chemical evolutions proceed by repeated impacts and how more complicated biomolecules are formed.

In this study, we carried out shock recovery experiments to investigate the chemical reactions of alanine in aqueous solutions and the effect of oxygen fugacity. Experiments were carried out with a propellant gun. We used alanine labeled by ^{13}C to distinguish products from contaminants. Sample of aqueous solution immersed in olivine or hematite powders, sealed in a stainless steel container, was used as a target. The sample space has air gap behind the sample. The powder, solution, and air correspond to meteorite, ocean, and atmosphere on early Earth, respectively. Two powders of olivine and hematite can keep the oxygen fugacity low and high during experiments, respectively. After shots, the steel containers, after cleaned, were immersed into liquid nitrogen for sample solution to be frozen and then we drilled on the impact surface to extract water-soluble components from the sample using pure water in a beaker. After that, water-soluble components were analyzed by LC/MS for four amino acids (glycine, alanine, valine, and phenylalanine) and four amines (methylamine, ethylamine, propylamine, and butylamine).

The results indicate the formation of decomposition products (glycine, methylamine, ethylamine, and propylamine) of alanine and butylamine as a new biomolecule. However, the results did not detect any formation of valine and phenylalanine those could be expected to form by reactions. Glycine and some amines were detected in samples under low oxygen fugacity, while these molecules were hardly detected in samples under high oxygen fugacity. Therefore, oxidative conditions are not preferable to the formation of biomolecules. On the other hand, the present experimental results suggest that the survival rate of alanine depends on pressure and temperature but that it is not dependent on oxygen fugacity. In applying the present results to actual meteorite impacts, the physical condition during impact is a key factor in chemical reactions, although it also must be taken into account the heterogeneous distribution of impact energy in an impact that may cause a significant effect on the chemical reactions.

Japan Geoscience Union Meeting 2013
(May 19-24 2013 at Makuhari, Chiba, Japan)

BAO01-P10 会場:コンベンションホール 時間:5月21日 18:15-19:30

熱水条件下におけるAla-DKP生成時におけるジアステレオマーの過剰とカンラン石の役割
Diastereoisomeric excess of Ala-DKP during condensation of racemic-Ala on olivine under hydrothermal condition

淵田 茂司[1]*, 奈良岡浩[2], 益田晴恵[1]
Shigeshi Fuchida[1]*, Hiroshi Naraoka[2], Harue Masuda[1]

[1] 大阪市立大学 理学研究科, [2] 九州大学 地球惑星科学科
[1]Faculty of Science, Osaka City University, [2]Department of Earth and Planetary Science, Kyusyu University

<Introduction>

When peptides are abiotically formed from amino acid monomers under thermal condition, cyclic dipeptides, diketopiperazine (DKP), are intensely dominant. DKP was defined as an obstacle for peptide elongation (Basiuk et al., 1990), while, Nagayama et al. (1990) supposed that the DKP was an effective intermediate phase to provide internal free energy necessary to form additional peptide bond. If DKP play as an intermediate phase, DKP formation must be important as the first step of chemical evolution of peptides continuing to life. Minerals promote the DKP formation under laboratory thermally condition (e.g., Bujdak and Rode, 1996; Meng et al., 2004); e.g., DKP formation would be promoted on olivine surface, where amino acid monomers are dehydrated and the olivine is hydrated (serpentinization). Diastereoisomeric DKPs (*cis/trans*) are formed, when chiral amino acids are dimerized. In this study, the diastereoisomeric excess (*de*) of DKP formed from the simplest chiral amino acid, alanine (Ala), was observed on the surface of olivine (during aqueous reaction with olivine) at 120 degree C for 8 days.

<Experiment>

DL-Ala powder was reacted with/without powdered olivine and a small amount of ultrapure water in sealed glass ampoules under Ar atmosphere. The ampoules were heated in a drying oven at 120 degree C for 1-8 days. After cooling at room temperature, the reacted product was suspended in 5 mL ultrapure water and the dissolved diastereoisomers of DKP were quantified using a high performance liquid chromatograph with UV detection.

<Result and Discussion>

When the DL-Ala was heated without olivine, 3.0 % DL-Ala transformed into DKPs. On the other hand, 12.2 % of Ala changed to DKPs when the olivine coexisted. Olivine would be a good catalyst for DKPs formation. The DKPs were not detected even if the olivine coexisted after heating for 8 days, when a small amount of water was not added. A small amount of water would play a role to break the strong bonds of Ala crystals and promote the DKP formation reaction.

When *de* ({[*cis* DKP] - [*trans* DKP]}/ {[*cis* DKP] + [*trans* DKP]} is defined, positive *de* means *cis* DKP excess. The *de* of DKP formed from the reaction without olivine heating for 8 days was +7.3 %. On the contrast, it was +16.3 % when reacted with olivine. It was reported that *trans* DKP is preferentially formed relative to *cis* DKP during recemic amino acid condensation, then the *de* gradually decreased with increasing reaction time (Naraoka and Harada, 1986). In this study, the *de* of DKP considerably increased when reacted with olivine. Olivine would be not only an efficient catalyst to promote the DKPs formation but also a determining factor on the selectivity of diastereoisomeric DKPs. Thus, serpentinization of ultramafic rock would have connection to DKP formation with regulation of peptide stereoisomers in the primitive ocean on planets.

Keywords: diketopiperadine, diastereoisomeric excess, olivine, alanine

BAO01-P11 会場:コンベンションホール 時間:5月21日 18:15-19:30

五炭糖の分解速度に対するケイ酸の影響
Effects of silicate on the decomposition rates of pentoses

新田 祥子[1]*, 古川 善博[1], 掛川 武[1]
Sakiko Nitta[1]*, Yoshihiro Furukawa[1], Takeshi Kakegawa[1]

[1] 東北大学大学院理学研究科地学専攻
[1]Graduate School of Science, Tohoku University

RNA is considered as a very important molecule for the origin of life because RNA carries genetic information and several RNA catalyze biological reactions. Ribose is an essential constituent of RNA. Ribose as well as the other pentoses can be produced abiotically through formose reaction. However, ribose is the most unstable pentose among of the pentoses produced by the formose reaction. Therefor, stabilization of ribose has been very important issue. For the solution of this problem, a previous study proposed that pentoses including ribose are stabilized forming complexes with silicate. Because of technical difficulties, it has not been clear which pentoses are stabilized by silicate. This study adopted a new application of liquid chromatography-mass spectrometry for the pentose analysis. The method made it possible to determine the concentration of each uncomplexed pentose. Incubation experiments of aldopentoses, ribose, lyxose, xylose, and arabinose, with three concentration of silicate have conducted in this study. In silicate-free solution, ribose had the highest rate of decrease. The rate of decrease for all aldopentoses became smaller with the concentration of silicate. In particular, the rate of decrease for ribose was significantly decreased. This result shows that silicate stabilize aldopentoses, especially ribose. Silicate is common in all over the world as silicate minerals and might have been common on the early Earth. Therefore, the selective stabilization of ribose by silicate might have provided a mechanism for the selection of ribose as the sugar in RNA on the early Earth.

キーワード: RNA, ケイ酸塩, リボース, 五炭糖, 液体クロマトグラフ/質量分析計
Keywords: RNA, silicate, ribose, pentose, liquid chromatography-mass spectrometry

Japan Geoscience Union Meeting 2013
(May 19-24 2013 at Makuhari, Chiba, Japan)

BAO01-P12 会場:コンベンションホール 時間:5月21日 18:15-19:30

初期の地球において原始的なリポソームを生成したメカニズム
The mechanism that had formed the primitive liposome in the early Earth

唐澤 信司 [1]*
Shinji Karasawa[1]*

[1] 宮城高専　名誉教授
[1]Miyagi National College of Technology: Professor emeritus

[はじめに]

初期のリポソームの形成過程を探求する次ぎの実験に用いた物質は初期の地球には存在していた。炭酸水に鉄の微粉末を加えると気泡ができた。その気泡は、アミノ酸を加えると寿命が長くなり、その数が増えた。そこで、気泡の膜の表面にアミノ酸の側鎖が吸着して、吸着したアミノ酸の熱運動は抑制され、そのペプチド結合の分解が抑制されるとして最初のタンパク質が膜に組み込まれて生成されたと考えた。水中の気泡は浮上し、水面で破裂する。このことが繰り返されると水面が気泡と同じ膜で覆われる。そして、水底と水面の中間に層をなして停留する小胞が生成されることが観測された。この小胞は、水面で破裂する際に、その内部に膜および水を吸い込んで発生したと考えられる。本報告でこのような実験結果と原始のリポソームを発生するメカニズムを報告する。

[炭酸水に鉄粉を混ぜて発生する気泡に及ぼすアミノ酸の効果を調べる実験]

鉄粉を炭酸水に混ぜて発生する気泡はアミノ酸を添加することにより、その寿命が長くなり、その存在の数が増加した。この実験で使われた物質は、炭酸水75 cc、鉄粉5g、アミノ酸（グルタミン:143mg、バリン; 36mg、ロイシン:71mg、イソロイシン:36mg、）である。数日間にわたって生成された水面に浮かぶ物質は、攪拌すると水に溶解する。その攪拌の後で、雰囲気を大気圧のCO_2で満たしていると再び鉄粉等の底質から気泡が生成される。生成された泡が水中を浮上し、水面で破裂して気泡を作る物質は水底に沈降する。そのような上昇と下降が繰り返されることが続いて、しばらくすると水の中間部分に停留する小胞が現れ、その小胞は寿命が長く、時間経過に沿ってその数を増した。

[理論による理解]

炭酸水に鉄の微粉末を混入することにより気泡が生成される理由は次の通りである。炭素原子の電気陰性度が水素原子のそれよりも大きいので、鉄原子は、二酸化炭素の酸素原子と反応する。酸素から放出された炭素原子が電気陰性度の関係で鉄原子と反応し、生成された炭化鉄が水と反応する。その結果、遊離炭素原子と自由水素原子が発生して気泡を形成する。水に溶けない気体が水中で発生すると水中の有機分子が気泡の膜を組織する。気泡は浮上するが、水面に到達した気泡は破裂する。やがて、気泡の膜を構成する有機分子が水面を覆うようになる。

他方、アミノ酸は水に溶けて、油には溶けない。しかし、炭酸水に鉄粉を混ぜて発生する気泡の膜には有機分子が存在し、アミノ酸分子の側鎖には気泡や水面の膜の有機分子に吸着するものがある。膜に付着したアミノ酸の分子の熱運動は抑制され、アミノ酸分子相互間のペプチド結合の分解も抑制される。その会合状態は環境に敏感ではある。一種の原始的なタンパク質ともいえる会合物質が有機分子の膜に吸着して合成される。

会合分子を持つ膜を持つ気泡が水面で破裂すると、破裂する際に気泡を形成するメカニズムが作用して、水面の膜と水を内部に吸い込み、原始的なリポソームができる。この特殊な小胞は水面と水底の間に停留する。このアミノ酸分子が膜に組織されて寿命が長くなると、その小胞の個数が増加する。水面に浮かぶ膜の断片を単位として組織される複雑な小胞や複数のリポソームを飲み込んだ小胞もできる。このようなメカニズムで原始的なリポソームと初期のタンパク質が生成されるという仮説を実験結果に添えて報告する。

キーワード: 気泡, 膜, アミノ酸, ペプチド結合, タンパク質, リポソーム
Keywords: bubble, membrane, amino acid, peptide bond, protein, liposome

Japan Geoscience Union Meeting 2013
(May 19-24 2013 at Makuhari, Chiba, Japan)

BAO01-P13 会場:コンベンションホール 時間:5月21日 18:15-19:30

気球による成層圏微生物捕集実験
Stratospheric Microorganisms Collection Using a Balloon

大野 宗祐[1*], 石橋 高[1], 山岸 明彦[2], 河口 優子[2], 仁田原 翔太[2], 瀬川 高弘[3], 所源亮[4], 山内　一也[4], 石川　裕子[5], 三宅 範宗[1], 小林 正規[1], 松井孝典[1]
Sohsuke Ohno[1*], Ko Ishibashi[1], Akihiko Yamagishi[2], Yuko Kawaguchi[2], Shota Nitahara[2], Takahiro Segawa[3], Gensuke Tokoro[4], Kazuya Yamanouchi[4], Yuko Ishikawa[5], Norimune Miyake[1], Masanori Kobayashi[1], Takafumi Matsui[1]

[1] 千葉工業大学惑星探査研究センター, [2] 東京薬科大学, [3] 極地研究所, [4] アリジェン製薬, [5] 日本バイオロジカルズ
[1]Planetary Exploration Research Center, Chiba Institute of Technology, [2]Tokyo University of Pharmacy and Life Sciences, [3]National Institute of Polar Research, [4]aRigen Pharmaceuticals, Inc., [5]Nippon Biologicals, Inc.

本講演では、我々が計画している、大気球を使い成層圏中の微生物を採集する実験について紹介する。

キーワード: アストロバイオロジー, パンスペルミア, 成層圏, 気球, 極限環境微生物
Keywords: Astrobiology, Panspermia, Stratosphere, Balloon, Extremophile

Japan Geoscience Union Meeting 2013
(May 19-24 2013 at Makuhari, Chiba, Japan)

BAO01-P14 会場:コンベンションホール 時間:5月21日 18:15-19:30

ホスファターゼ活性を用いた極限環境生物活動評価
Evaluation of biological activity in extreme environments by phosphatase activity

栗塚 泰平[1*], 古川 天[1], 大林 由美子[1], 金子 竹男[1], 三田 肇[2], 吉村 義隆[3], 高野 淑識[4], 小川 麻里[5], 小林 憲正[1]
Taihei Kurizuka[1*], Taka Kogawa[1], Yumiko Obayashi[1], Takeo Kaneko[1], Hajime Mita[2], Yoshitaka Yoshimura[3], Yoshinori Takano[4], Mari Ogawa[5], Kensei Kobayashi[1]

[1] 横浜国立大学, [2] 福岡工業大学, [3] 玉川大学, [4] 海洋研究開発機構, [5] 安田女子大学
[1]Yokohama National University, [2]Fukuoka Institute of Technology, [3]Tamagawa University, [4]JAMSTEC, [5]Yasuda Women's University

地球極限環境における生物活動評価にホスファターゼ活性を用いることを検討した。試料としては，南極土壌や海底熱水噴出孔チムニー等を用いた。ホスファターゼ活性は４?メチルウンベリフェリルリン酸を基質とする蛍光法を用いた。同じ試料のアミノ酸濃度も定量した。ホスファターゼ活性値やアミノ酸濃度は，生物活動とよい相関を示した。試料から抽出したホスファターゼの熱安定性や活性の温度依存性を調べると，その環境での主要生物種の生息温度に依存する傾向がみられた。

キーワード: ホスファターゼ活性, 生物活動, 極限環境, アミノ酸, 南極, 海底熱水系
Keywords: phosphatase activity, biological activity, extreme environments, amino acids, Antarctica, submarine hydrothermal systems

Japan Geoscience Union Meeting 2013
(May 19-24 2013 at Makuhari, Chiba, Japan)

BAO01-P15 会場:コンベンションホール 時間:5月21日 18:15-19:30

好塩性アーキアに特徴的なC_{20}-C_{25}ジエーテルの分析?幾つかの好塩性アーキアの生育環境による脂質成分変化

Analysis of C_{20}-C_{25} isoprenoidal diether of halophilic archaea-lipid content changes in the incubation

田上 諒[1], 山内 敬明[2]*
TANOUE, Ryo[1], Noriaki YAMAUCHI[2]*

[1] 九州大学大学院理学研究科地球惑星科学専攻, [2] 九州大学大学院理学研究院地球惑星科学部門
[1]Dept. Earth and Planetari Sci., Grad. School Sci., Kyushu Univ., [2]Dept. Earth and Planetari Sci., Fac. Sci., Kyushu Univ.

アーキア（古細菌）は，海底の熱水噴出口（高温，低pH），底泥（無酸素），塩田（高い塩濃度）といった他の生物の生育が困難な環境に多く存在する微生物で，16SrRNAによる分子系統樹や，高温，低pHでの生育が原始地球環境と類似すると想定されることなどから，生命の起源を探る為のツールとして，極めて重要な微生物である。好塩性アーキアは，通常生物のグリセリンと脂肪酸がエステル結合したものでなくグリセリンとイソプレノイドと呼ばれるC_5単位が重合したC_{20}の枝分かれ炭化水素がエーテル結合したC_{20}-C_{20}ジエーテル（アーキオール）(**1**)が脂質の主成分である。さらに，他の古細菌にはほとんど見られない特徴的なC_{20}-C_{25}ジエーテル(**2**)が存在する。好塩性アーキアは岩塩や高塩濃度環境での存在が示されているので，C_{20}-C_{25}ジエーテル脂質は高塩濃度環境としてのバイオマーカーとしての利用の可能性が考えられる。一方，沿岸域生物圏でのバイオマス推定は例がなく，従ってこういったごく“ 普通 ”の環境での好塩性アーキアがどの程度この生物圏に影響をおよぼしているのかは不明である。好塩性古細菌の環境耐性を考え，本微生物のごく普通の沿岸域でバイオマス推定を，脂質構造の特徴に注目し，有機物の微量迅速分析という典型的な有機地球化学的手法で明らかにしたいと考えている。

さて，好熱好酸性古細菌においては，テトラエーテル脂質に五員環化合物が存在し，温度に対しては五員環の数と五員環化合物の割合が多くなるように変化することが特徴的で，これが高温耐性の一つとされる。また南極で発見された好冷性アーキアは，脂質主成分は1であるが低温で二重結合を**1**の中間に持つような脂質の割合が増大することが示されている。すでに予備的実験で我々は*N. pallidum* JCM 8980では**1**と2の存在比が培養条件により変化することを示唆する結果を得ているが一方アーキアの環境変化に対応する膜成分変化は極性基変化の影響が大きいとする説も有る。そこで，好塩性古細菌の環境変化に対応するコア脂質部分の変化について2種の性質がやや異なる種について，生育条件変化による脂質成分の変化を検討した。

微生物*Natronomonas pharaonis* JCM 8858は，好アルカリ性古細菌で至適条件がpH 8.5という特徴があり，その他（温度37 °，NaCl濃度は20%程度）はJCM 8980とよく似た至適条件を持つ。この好塩性古細菌培地300 ml（カザミノ酸4.5 g, クエン酸ナトリウム0.9 g, グルタミン酸0.75 g, $MgSO_4$・7H2O 0.75g，KCl 0.6 g，NaCl 20%）に，N. pharaonisを1 ml加え12日間培養し（この条件が定常期（またはその直前）というのを増殖曲線観察で確認），遠心分離にて集菌，Bligh-Dyer法にて脂質抽出の後溶媒を除いて，3 % HCl-MeOH，引き続き7 M NaOHを加えて加水分解した。得られた脂質コアはシリカゲルカラムクロマトグラフィーにてhexane, hexane-ethyl acetate (10:1), hexane-ethyl acetate (2:1)で精製， hexane-ethyl acetate (10:1)溶出分（約1˜1.5 mg）をESI-MSにて分析した。温度としては27度から42度，温度37度でかつpHを変化させるという条件で培養を行い，脂質を分析した。まず，低温（27 °）で増殖は著しく遅く，ほぼ3倍の日数を要した。その他でこのような著しい増殖度の変化は見られなかった。文献で報告されている**1**と(**2**の存在比は本実験によるESI-MS分析においてもほぼ確保されていた。さらに条件を変化させた場合，高温で(**2**の割合が増加する傾向にあった。一方pHは至適条件でほぼ最大でその他は減少する傾向にあった。一般に好塩性古細菌の耐塩性は主にタンパク質の性質と，細胞質内の高カリウム濃度で確保されていると言われているが，温度環境の変化に対応する変化は*N. pallidum*と同様であり，好塩性古細菌に一般的な温度変化への適応の一端ではないかと考えられる。現在さらに好アルカリ性の古細菌*Natronobacterium gregoryi*の培養と脂質変化の研究を行っているのでこれについても報告予定である

キーワード: アーキア, バイオマーカー, ジエーテル脂質, 高塩濃度環境
Keywords: halophilic, archaea, biomarker, hypersaline environment

BAO01-P16 会場:コンベンションホール 時間:5月21日 18:15-19:30

南アフリカバーバートン地域ムーディーズ層(32億年前)砕屑性堆積岩の鉱物学的研究

Mineralogical study of clastic sedimentary rocks in the 3.2 Ga Moodies Group, South Africa

川井 祥二[1]*, 掛川 武[1]
Shohji Kawai[1]*, Takeshi Kakegawa[1]

[1] 東北大学大学院理学研究科地学専攻
[1]Graduate School of Science, Tohoku University

It is important to investigate the timing of emergency of oxygenic phototrophs (i.e., cyanobacteria) on the early Earth. To approach this problem, Sakamoto (2012) studied chemical sedimentary rocks (Banded Iron Formation:BIF) deposited in shallow ocean environments in Moodies Group in the Barberton Greenstone Belt, South Africa (ca.3.2Ga). Sakamoto (2012) concluded that chromite in Moodies BIFs is a chemical precipitates from oxygenated 3.2 Ga ocean water. However, absence of knowledge of a clastic chromite creates ambiguity if Sakamoto's chromite was a real chemical precipitate. Therefore the objectives of this study is set: (1) to constrain paragenesis and find minerals formed under oxic environments in shallow water clastic sediments, (2) to determine the chemical compositions and occurrence of clastic chromite, and (3) to discuss microbial ecosystem through stable carbon isotopic compositions.

We collected of the Moodies Group from the under-ground mining site (Sheba mine). Chromite in the examined samples is rounded or angular and surrounded by fuchsite and Cr-bearing biotite, contrasting chemical precipitated euhedral chromite surrounded by magnetite. Mg# of clastic chromite is 0.012 to 0.043, which differs from Mg# of chemical precipitated chromite (Mg# = 0.000). Such contrast suggests that both detrital and chemical precipitated chromites are present in Moodies sedimentary rocks. Additionally, stable carbon isotopic compositions are within a range of organic matter produced by cyanobacteria. Overall results of this study indicated that presence of 3.2 Ga oxygenic shallow oceans in where cyanobacteria were active.