

古代タンパク質の復元に基づく生物進化初期の温度環境推定 Estimation of the environmental temperatures at the early evolutionary periods by resurrection of ancient proteins

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初期の生命がどのような環境下で進化したかを明らかにすることは、地球上の生命の起源と進化を理解する上で重要である。地球上の生命の初期進化に関する地質記録は極めて限られている。よって、現生生物に系譜が繋がる祖先生物が、地球上のどのような環境に生育したのかを推測することは容易ではない。

Woese et al. (1990, PNAS, 87: 4576-4579) が作製した 16S/18S rRNA に基づく系統樹は、異論はあるものの、広く「標準的」系統樹として利用されており、全生物が共通祖先を持ち、3つの生物群（古細菌 Archaea、真正細菌 Bacteria、真核生物 Eukarya）に分かれる事を示唆した。全生物の共通祖先が存在したとすると、その共通祖先がどのような生物であったかが、次の疑問となる。特に全生物の共通祖先の生育温度については、活発な議論がおこなわれて来た。「全生物の共通祖先が超好熱菌」であるという仮説が Pace (1991, Cell, 65: 531-533) によって提案されたが、その解釈に対する反論も多かった。しかしながら、これらの議論のほとんどは、分子系統解析により全生物の共通祖先の核酸の G+C 含量やアミノ酸組成を推定し、そこから生育温度を推論したものであり、実験的に検証されたものではない（例えば Galtier et al. (1999, Science, 283:220-221)）。しかし、近年、分子系統解析による祖先タンパク質のアミノ酸配列の推定と、その配列をコードする祖先型遺伝子の実験的な復元が、過去の生物の性質を理解するために行われるようになって来た（例えば Gaucher et al. (2003, Nature, 425: 285-288)）。

我々は、祖先生物の生育温度を推定するため、現存する古細菌および真正細菌由来ヌクレオシド二リン酸キナーゼ (NDK) のアミノ酸配列の多重アライメントを用いて最尤法に基づく進化系統樹を作製し、古細菌共通祖先生物と真正細菌共通祖先生物が持っていたと予想される NDK のアミノ酸配列を推定した。さらに、遺伝子工学的手法により復元した祖先型 NDK 遺伝子を大腸菌内で発現し、祖先型 NDK の精製と熱変性測定をおこなった。復元した古細菌共通祖先、真正細菌共通祖先 NDK は、どちらも変性中点温度が 100 °C を超える高い耐熱性を有していた。至適生育温度が異なる様々な微生物の NDK の変性温度が至適生育温度と強い相関を持つことから、これらの復元した NDK を持っていたと考えられる生物は超好熱菌であったと考えられる。さらに、祖先型アミノ酸配列推定の際の誤りや、祖先型配列推定の用いた系統樹の樹形が、復元した祖先型タンパク質の高い耐熱性には大きく影響しないことも明らかにした。また、古細菌共通祖先 NDK と真正細菌共通祖先 NDK の配列はよく似ており、全生物の最後の共通祖先生物 (Commonote: コモノート) の NDK も同様なアミノ酸配列を持っていたことが期待される。古細菌共通祖先 NDK と真正細菌共通祖先 NDK の配列から全生物の共通祖先 NDK の配列を作製すると、その変性温度は 90 °C 以上であり、この NDK を持った全生物の共通祖先は 75 °C 以上に生息する好熱菌であったと考えられる (Akanuma et al. 2013, PNAS, 110: 11067-11072)。以上の結果は、古細菌共通祖先生物、真正細菌共通祖先生物がともに (超) 好熱菌であり、Commonote が好熱菌であったことの実験的な証拠と言える。

キーワード: コモノート, タンパク質の祖先配列復元, ヌクレオシド 2 リン酸キナーゼ, 好熱菌

Keywords: Commonote, resurrection of proteins, nucleotide diphosphate kinase, thermophiles

地球環境の進化：堆積物記録中に残されたポルフィリンからの観点 Evolution of the Earth's environment: A view from sedimentary alkyl porphyrins

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Alkyl porphyrins are derivatives of chlorophylls that are formed in the surface of the Earth by photosynthesizers. Structural changes associated with the diagenetic processes have been intensively studied during the last half a century. Now we know that some alkyl porphyrins are derived only from specific chlorophylls that are originated from a specific type of photosynthesizers. Together with carbon and nitrogen isotopic compositions, such structural information provides a profound insight on the critical evaluation of the surface water environment in the geological past. In this presentation, I will review the diagenetic alteration of chlorophyll structures and review the current evidence.

キーワード: ポルフィリン, 堆積物, 地球表層環境

Keywords: Porphyrins, Sediment, Earth's surface environment

環境変動と後生動物進化の共進化：ゲノム重複と環境変動への急速な対応 The close correlation between environmental change and evolution of metazoans: Genome duplication and rapid adaptation

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The Neoproterozoic to Cambrian is one of the most exciting periods when Metazoa first appeared and quickly evolved. The origin and early evolution of Metazoa are very attractive firstly because the events suddenly happened after very long calmness, over 2000 m.y. since the emergence of eukaryotes, and proceeded very quickly, and secondly because appearance of new phylum was limited to this period (Cambrian explosion). Recent paleontology, biomarker study and molecular biology suggested early origin, especially of sponges and cnidarians, and cryptic evolution of the metazoans (e.g. Maloof et al., 2010; Love et al., 2010; Peterson et al., 2008; Sperling et al., 2010, Erwin et al., 2011). On the other hand, recent comprehensive study of multi-elemental and multi-isotopic chemostratigraphies of drill core samples in Three Gorges, Tianping and Beidoushan areas revealed that redox condition and bioessential element contents of seawater such as P, Ca, NO_3^- , Fe, Mn, Mo, and Sr drastically changed from the Neoproterozoic to the Early Cambrian. Sr isotope values display positive excursions at ca. 580, 570-550 and 540 Ma, indicating repeated high continental influxes at those times. P contents of carbonate minerals were very high until ca. 550 Ma, and then decreased, suggesting the seawater was enriched in phosphorus before 550 Ma and then depleted due to oxidation of seawater and deposition of phosphorite. High nitrogen isotope values of organic matter and high Ca isotope values of carbonate rocks indicate that seawater was depleted in NO_3^- and Ca contents until ca. 550 Ma, and then increased. Mo isotopes of black shale, and Fe and Mn contents and REE patterns of carbonate rocks indicate that seawater became more oxic since ca. 550 Ma. In addition, the Mo contents of black shale increased in the Late Ediacaran and Early Cambrian, indicating Mo content of seawater increased due to the oxidation of seawater. On the other hand, iron and manganese contents of carbonate rocks decreased, suggesting that iron and manganese contents of seawater decreased because of the oxidation of seawater.

Comparison of the geochemical evidence with biostratigraphy suggests that the emergence of Metazoan in the Early Ediacaran was caused under the relatively less oxic and P-rich condition, whereas their diversification occurred under oxic, NO_3^- and Ca-rich condition. Especially, the transition from phosphorus-rich to NO_3^- -rich seawater possibly increased Redfield ratio, and contributed to diversification of more actively mobile multicellular animals. In addition, the comparison of geochemical and paleontological evidence indicates that the biological evolution occurred just after the environmental changes, especially the timing of increase in nutrients, allowing a new insight of biological evolution of multicellular animals. The quick response of biological evolution to the environments suggests that the fundamental innovation for biological functions was already established long before the environmental changes. The quick adaptation implies that early metazoans or a common ancestor have genomes for the functions before they acquired the functions, indicating genome duplication plays important role on the early evolution of metazoans.

キーワード: 生命進化, 古環境解読, エディアカラ紀, 海洋栄養塩濃度変動, 後生動物進化とカンブリア爆発, ゲノム重複
Keywords: Biological evolution, paleoenvironmental change, Ediacaran, Nutrients of seawater, Evolution of Metazoa and Cambrian explosion, Genome duplication

祖先的前口動物の形態形成遺伝子セットの復元 Reconstruction of the gene sets for the developmental signaling ligands in ancestral protostome animals

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Recently, a draft genome sequence of the pearl oyster *Pinctada fucata* was reported, enabling to infer a possible evolutionary scenario of the gene sets that are important for body plan formation in protostomes including both lophotrochozoans and ecdysozoans. We report the results of phylogenetic character mapping carried out for the gene families that encode developmental signaling ligands (Fgf, Hedgehog, PDGF/VEGF, TGF- β , and Wnt families) to reconstruct possible copy numbers of signaling molecule-coding genes for hypothetical ancestral protostomes. Our reconstruction suggests that *P. fucata* retains the ancestral protostome gene complement, providing further justifications for the use of this taxon as a model organism for developmental genomics research.

キーワード: 古代ゲノム, 多細胞動物, 発生進化学, シグナル伝達遺伝子, カンブリア爆発, 冠輪動物

Keywords: paleogenomics, metazoan evolution, evo-devo, signaling ligand genes, Cambrian explosion, lophotrochozoans

マイクロシンテニーに注目した後生動物古代ゲノム情報の復元 Reconstruction of paleo genomic information of metazoan based on a microsynteny analysis

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後生動物のゲノムが幅広く解読される事により、進化速度の比較的遅い動物同士を比較すれば、ゲノム上の遺伝子の並びが比較的良好に保存されている事が分かってきた。たとえば 2007 年の Putnam らによる刺胞動物のゲノム配列と現生のヒトのゲノム配列の間に、わずかながら遺伝子配列の並びの保存性 (Macrosynteny) を見いだしている。これは 6 億年以上前にこの 2 種の生物が分岐した事を考えると驚くべき事である。さらにその後、Irimia らは、このように分岐後大きく隔たって保存されている遺伝子並びのうち、5' 側を共有して並んでいる遺伝子同士は、遺伝子発現の制御領域を共有する事により、互いの並びを変更しにくいような拘束をうけているという仮説をたて、証明しつつある。発表者はこれら最近の遺伝子の並びの保存性研究の進展に注目し、古代ゲノムの復元に応用するためのツールとする事を考えている。具体的には、発表者が現在進めているヒメギボシムシとウニやナメクジウオなどのゲノムを比較する事で、水腔動物群の共通祖先や、新口動物群の共通祖先について、それ以降に共通に維持されている発生メカニズムを示唆するデータが得られてきている。

キーワード: 後生動物, ゲノム, マイクロシンテニー, 再構築
Keywords: metazoan, genome, microsynteny, reconstruction

顕生代におけるグローバル海洋環境変遷と海底鉱床生成の因果律
A close relationship between global oceanic environmental changes and seafloor mineral
deposition during the Phanerozoic

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Metal deposition on seafloor is strongly controlled by marine redox conditions. Fe-Mn and Mn oxide deposits are formed under oxygenated oceans. In striking contrast, Cu and Zn-bearing sulfide deposits are stable under anoxic oceans. Seafloor mineral deposits in turn are good indicators to redox conditions or redox changes of modern and ancient oceans.

There are numerous strata-bound ore deposits in the Japanese accretionary complexes. These deposits are mainly divided into three types; umber (Fe-Mn), Mn-rich, and volcanogenic massive sulfide (VMS; Besshi-type). The Mn-rich deposits are further divided into two subtypes that are associated with greenstone and NOT associated. Ages of these deposits provide us important constraints for a secular change of marine redox conditions over the past ~360 Myr. Depositional ages of umber and Mn deposits were previously determined by microfossils including radiolarians and conodonts. On the other hand, ages of the Besshi-type deposits are determined by Re-Os method (Nozaki et al., 2013). Oxide ore deposits such as umbers and Mn deposits were very likely precipitated in the modern-style oxygenated deep-sea. In contrast, Mn carbonate and VMS deposits were precipitated in the stagnant, O₂-deficient deep-sea during the Triassic and Jurassic periods. Seafloor mineral deposition closely related to global oceanic environmental changes may give us a hint for exploring the causes of mass extinction, and further for elucidating the evolution of life.

Nozaki, T., Y. Kato, K. Suzuki (2013) Late Jurassic ocean anoxic event: evidence from voluminous sulphide deposition and preservation in the Panthalassa. *Scientific Reports*, 3: 1889; doi:10.1038/srep01889.

Keywords: oceanic environmental change, seafloor mineral deposit, Japanese accretionary complexes, marine redox condition, Phanerozoic

世界古地理と生命進化：その2 中生代 Global paleogeography and life evolution: 2. Mesozoic

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The Mesozoic witnessed the Pangean breakup. Since the Triassic, the southern half of Gondwana successively rifted/separated, kicking out numbers of continents northward to form Laurasia, i.e., the northern half of Pangea, ca. 200 Ma. Multiple collisions among the Russian platform, Kazakhstan, Siberia, N. China, S. China, Indochina, Tarim, and other minor continental blocks were completed mostly in the Triassic or in the Early Jurassic at the latest. Gondwana has started to be fragmented immediately after its birth at 540Ma, except the collision of Laurentia at 430 Ma. The apparent supercontinent Pangea formed when Laurasia came in shape by 200 Ma. Its disassembly began first by the opening of the central Atlantic domain induced by the eastward moving of Africa for ca. a few thousands of km. The birth of South Atlantic Ocean was delayed until ca. 120Ma, whereas the opening of Northern Atlantic already started. The separation of S. America from Africa occurred ca. 120Ma. There was a pulse period of Pacific superplume ca. 120-85Ma when the production rate of MORB was 150-300 % higher than the rest of the Mesozoic. Numbers of huge oceanic plateaus were formed in the Pacific domain, including the Caribbean plateau. The birth of Indian Ocean occurred at ca. 100-120Ma by the separation of India from Gondwana. It is composed of 4 distinct oceanic lithospheres (separated by NS-trending major transform faults) behaved uniquely. The sea-level was kept relatively high according to such Mesozoic global tectonics; warm period without global glaciation but with oceanic anoxia and remarkable production of oil, gas, and coal. The climate was generally dryer than the Cenozoic, with higher production of evaporites. The mammalian diversification was triggered by the ca. 120Ma separation of the final bridge among Africa, S. America, and Laurasia. The appearance of the fox monkey in Madagascar, and of new-world monkeies in S. America, was likely connected to Indian migration and narrow arc bridge to S. America.

キーワード: 古地理, 中生代, 超大陸, パンゲア, 大西洋, 生命進化
Keywords: paleogeography, Mesozoic, supercontinent, Pangea, Atlantic Ocean, evolution

有孔虫の石灰化に関する最近の結果 Recent results of foraminiferal calcification

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Foraminifera, marine unicellular organism, have been thought as one of the major carbonate producer in ocean. Their calcareous tests are commonly utilized as paleo-environmental indicators in various studies of earth science because their tests have been archived as numerous fossil in sediment for long time and various environmental information are brought by population, morphology and geochemical fingerprints. The calcareous test itself is interested by many foraminifer scientists. The knowledge about the cytological process on carbonate precipitation has been described for couples of decade using by many legacy technology. Cellular regulations of ions uptake into calcareous tests from seawater are of great interest for broad fields of earth science. Our recent studies showed the potential to understanding the biomineralization of foraminifera by the application of fluorescent indicators. Recently, we visualize the spatial distributions of cytological calcium and pH in living cell at same time under several pH conditions (7.5-8.1). Observed results show that foraminifera controls very detailed timing of pH variation and concentration of calcium at any stage of chamber formation dynamically even ambient pH are varied. These observations results will help to consider how the geochemical compositions arranging on the foraminiferal test, sensitivity of pH proxy of boron and others.

単細胞真核生物・浮遊性有孔虫における左右二型 Left-right reversal in unicellular eukaryotes, planktonic foraminifera

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Aquatic unicellular organisms are little motile and passively disperse in general. Holoplankton, which spend their entire life-cycle floating in the water column, are likely carried by water flow and exposed to diverse conditions of environment. Their morphology may vary over wide distribution ranges by phenotypic plasticity or allelic variation. Among these organisms, planktonic foraminifera are an excellent system to examine diversity and evolution in cellular responses to the environment because of two reasons: (1) occurrence in every ocean and (2) visible asymmetry in coiled shell. Both left- and right-coiled forms are often found within single morphospecies. Their coiling direction has traditionally been thought to change phenotypically depending on environmental factors, especially water temperature, based on coil-morph distributions but without statistical evidence. Molecular phylogenetic studies have revealed that morphospecies often contain multiple cryptic species. The arguments on the role of temperature for coil reversal most probably confused cryptic species into single taxa. In the present study, we examined the dependence of morph frequency on temperature by focusing on populations that are dimorphic for coiling direction and occur across wide ranges of temperature. *Globorotalia truncatulinoides* includes five genetically isolated species, and each of them is dimorphic for coiling direction. The statistically meaningful regression analysis was possible in three species that are distributed in global ranges. The results showed that morph frequency does not depend on water temperature in warm or cold seasons or on the annual mean temperature. Moreover, the geographic patterns of frequency variation among water masses in these species suggest that gene flow affects morph frequency. The majority exhibits the same coiling direction among populations that inhabit water masses connected by ocean circulation system. In contrast, morph frequency greatly varies between unconnected water masses regardless of climatic conditions. The present results, therefore, reject temperature-dependence of coiling direction and suggest the presence of genetic basis for coiling direction in planktonic foraminifera. Our study provides a base to explore the evolution on left-right asymmetry in unicellular eukaryotes.

キーワード: 左右非対称, 巻き方向, 隠蔽種, 単細胞真核生物

Keywords: left-right asymmetry, coiling direction, cryptic species, unicellular eukaryote

最終氷期の日本海に生息した海洋小型プランクトンは地理的に分断されていたか？ Were marine microplankton in the Japan Sea geographically isolated during the Last Glacial Maximum?

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The Japan Sea is connected by three straights (the Soya, Tsugaru, and Tsushima Straights) to the Sea of Okhotsk and Pacific Ocean with the shallow sill depth (140 m). During the last glacial maximum (LGM: 23-19 kilo years before present), the sea-level was decreased at least 120 m lower than today and the Japan Sea was almost isolated from surrounding seas. It is possible that such geographic isolation reduced and/or impeded gene flow of marine organisms between the Japan Sea and surrounding seas. Previous phylogeographic studies of coastal vertebrates (only whose larval stage is planktonic) have actually suggested that the Japan Sea was closed during the LGM. However, there is no phylogeographic study with marine microplankton, which inhabit the water column throughout their entire life cycle.

Radiolaria, the major marine planktonic protists, are passively transported in the pelagic ocean. Their geographic distribution would be easily affected by geographic changes through geological time. Moreover, their siliceous shells have been preserved in marine sediments and form a good fossil record. The sensitivity to geographic changes and well-preserved fossil record of Radiolaria could allow us to elucidate a past geographic isolation of marine microplankton. *Larcopyle buetschlii*, a morphospecies of radiolarians analyzed in the present study, is found in the surface waters in the Pacific Ocean, whereas it has a characteristic distribution vertically ranged from the surface to deep layers in the Japan Sea. In addition, its fossil specimens are continuously observed in the Japan Sea before the LGM. Therefore, *L. buetschlii* could be a good model to study a link between geographic isolation during the LGM and reproductive isolation of marine microplankton.

Heterogeneity of internal transcribed spacer regions of ribosomal DNA (ITS1 and ITS2) is observed in many eukaryotes (e.g., vertebrates, dinoflagellates, and diatoms). The ITS1 and ITS2 regions are spliced out during the maturing process of ribosome, causing a nucleotide substitution rate higher than ribosomal DNA coding regions. Nevertheless, the ITS1 and ITS2 sequences are functionally important for their splicing, because the premature transcript composed of 18S, 28S, 5.8S rRNA, ITS1, and ITS 2 is folded into a secondary structure followed by the self-splicing of ITS1 and ITS2. Based on the secondary structures of ITS1 and ITS2 sequences, compensatory base changes (CBCs: base changes occurring on both sides of a double-stranded portion) and hemi-CBCs (HCBCs: base changes occurring on one side of a double-stranded portion) are often observed among closely related species. The correlation between CBCs and HCBCs in the ITS2 sequences likely reflects sexual compatibility among individuals of a closely related species. Thus, the CBCs/HCBCs correlation is a useful marker to infer whether geographically isolated populations are reproducible.

We demonstrated that there is heterogeneity of the ITS2 sequences within an individual of *L. buetschlii* and that all individuals of *L. buetschlii* collected from the surface to deep layers in the Japan Sea do not have a significant difference in the CBCs/HCBCs of the ITS-2 sequences. Furthermore, the CBCs/HCBCs of the ITS-2 sequences do not show a significant difference between individuals of the Japan Sea and Pacific Ocean. These findings suggest that *L. buetschlii* in the Japan Sea and Pacific Ocean likely forms a reproducible single population. Thus, the geological isolation during the LGM is unlikely effective for the reproductive isolation of this radiolarian species.

Keywords: Japan Sea, *Larcopyle buetschlii*, Radiolaria, secondary deep-sea plankton

哺乳類 4 目それぞれで独自に進化的に保存された非コード領域の解析 Non-coding sequences conserved independently in four different mammalian orders

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脊椎動物において進化的に保存された非コード配列 (CNS) は、タンパク質コード遺伝子の発現調節領域と密接に関連していると考えられている。われわれは、哺乳類の 4 目 (霊長目、齧歯目、食肉目、鯨偶蹄目) について、CNS の個数とそれらのゲノム上の位置を調べた。CNS の定義にはタンパク質コード領域の保存についての 2 種類の閾値を用いた; すべてのコード領域塩基配列を用いる場合と、コドンの 1 番目と 2 番目だけを用いた場合。CNS の個数は系統によって異なっており、霊長類がもっとも多く、齧歯類がもっとも少なかった。これらの CNS は哺乳類ゲノム全体の 1.3~5.5% であり、より祖先的なもののほうがより最近に生じたものよりも保存度が高かった。CNS は、齧歯類と霊長類では、食肉目と鯨偶蹄目の場合よりもイントロンにより多く存在していた。ヒトゲノムとイヌゲノムでは、順系相同な CNS の 19% はゲノム上の異なった位置にあった。これら哺乳類の 4 目間の CNS の差は目独自の表現型を生じる原因になっている可能性がある。齧歯類で CNS の数が少ないのは、齧歯類内の多様性により遺伝子発現調節に関する進化的保存が少ないことを示唆する。霊長類の CNS は神経系に関与する遺伝子の近傍にクラスターすることが多くみられたので、霊長類の神経系の高度な複雑性に関与しているのかもしれない。この研究はすでに *Genome Biology and Evolution* (Babarinde and Saitou, 2013; vol. 5:2330-2343) に発表した。

キーワード: ゲノム, 哺乳類, 霊長目, 齧歯目, 偶蹄目, 食肉目
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古代ゲノム研究に向けたハイフネーティッド化学分析技術の開発 Development for new hyphenated analytical technologies for paleogenomics research

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Cytometry is the analytical technique, basically applied for quantitative analysis of cells and cell systems. In general, cytometry measures optical properties of cells, and most often uses fluorescence to measure specific antigen molecules, intracellular ions and DNA/RNA. Cells may be live or fixed, depending on the application, and individual cells can often be physically sorted. Other optical signals can be measured, including light scatter. The cytometry has blossomed to become the key technique to evaluate the nutritional status or to understand the elemental metabolism for animals. Several advantages can be derived by the cytometry, such as analysis speed, detection sensitivity, the ability to measure many parameters simultaneously, and the ability to sort individual cells (i.e., single cell spectroscopy). Recently, new generation cytometry utilizing the sensitive mass spectrometers (i.e., mass cytometry) was described. With the mass cytometry, further sensitive detection of ions or proteins and higher capability for the multiparameter analysis of individual adherent cells (e.g., Benfall et al., *Science*, 2011; Bodenmiller et al., *Nature Biotechnology*, 2012). With the extensive number of information collected from cells or samples through the cytometry, reliable and objective evaluation for the changes in biochemical functions could be achieved. This approach can also be applied to understand the solar system evolution based on the numerous number of age data. In recent ten years, we have demonstrated the unique study approach using the distribution pattern of sample ages based on the series of precise age data collected from large number of samples (i.e., age-cytometry) (e.g., Rino et al., *PEPI*, 2008; Iizuka et al., *Geology*, 2008; Iizuka et al., *Chem. Geol.*, 2009; Iizuka et al., *GCA*, 2010). The mass cytometry will become a powerful tool to promote the big-data science for various research fields such as metallomics, medical sciences or the geochemistry. For elemental or isotopic analysis of trace- or ultratrace-elements, plasma ion source mass spectrometry (ICP-MS) has been widely employed because of its high analytical capabilities such as high-elemental sensitivities, minimal sample preparation procedures, high-analysis throughput or user-friendly operations (Bandura et al., *Anal. Chem.*, 2009). With the laser ablation sample introduction technique, distribution of both the elemental and isotopic data for trace- or ultratrace-elements can be successfully derived directly from large-sized solid samples (>10cm). Despite the obvious success in obtaining elemental and isotopic data (age data), it should be noted that stable isotope ratio data for light elements (e.g., C and O) could not be derived by the present LA-ICPMS technique because of serious contribution mass spectrometric interferences on C and O isotopes, which provides key information concerning the physico-chemical conditions for the sample formation. To overcome this, we would like to develop a new analytical technique to measure the C isotopes, at a same time with elemental analysis using the LA-ICPMS technique. Newly developed spectroscopy technique combined to the LA-ICPMS technique can become a major analytical tool to expand the analytical capability for mass cytometry for biochemical samples and geochemical samples through precise, reliable and uniform quality data. The analytical technique develop here will promote the big-data science for various research fields including geochemistry and biochemistry.

Keywords: mass spectrometry, laser ablation, paleogenomics, hyphenated technology, analytical chemistry, geochemistry