

極域細菌のゲノム進化

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Genomic Evolutions of Polar Bacteria

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All of living organisms have been adapted to global environmental changes on the Earth. It is meaning that they have been rewriting their own genomic information again and again for their survivals, so it would be the first-step to analyze their genomes for the elucidation of adaptation strategies to their living environment. However, it is remaining unsettled of the genomic evaluation for environmental adaptations and evolutionary relationships among related species on the both polar regions and other continents. In order to address the challenge, we have isolated some of bacteria species from the biosphere of a moss pillar at Skarvsnes (69°28' S, 39°34' E) in East Antarctica and analyzed the genomes for focusing comparison with ones of related species from other continents. Consequently it was revealed that a lot of genes showed the feature of transferred ones from other species, crossing the species barriers, “horizontal gene transfer (HGT)” in technical terms of evolutionary biology. It was considered that many of important genes for material recycling and energy metabolism in the ecosystem, including the functional genes of nitrogen cycle, CO₂ fixation, photoactive-proteins and so on, had been shared or accumulated on their genomes by the highest rate of HGT. Those situations have provided increasing of biological diversity in a short span of time under the environmental condition of limited genetic resources and resulted to promote the construction of symbiotic and highly adaptive biosphere for the environmental changes. We also report about the bacterial species differentiations on local areas between Skarvsnes and Wright Valley (77°10' S, 161°50' E) on Antarctica, also on global scale among Antarctica and Arctic Spitsbergen island (79°23' N, 13°26' E) for each of genomic level. We will discuss about “the polar terrestrial biospheres as natural laboratories of biological evolutions on the Earth”.

全ての地球上の生物は環境変動に適応することで今日までの生存を可能にしてきた。それは生物が生存のために自らのゲノム情報を書き換えてきたことに他ならず、それらのゲノム解析は生物の環境への適応戦略を読み解く第一歩である。しかしながら、極域と他の大陸の生物種間での環境適応および進化に関するゲノムレベルでの評価は未解決の課題であり、そのために我々は東南極、スカルプスネス(69°28' S, 39°34' E)のコケ坊主生物圏から細菌を分離し、他の大陸の近縁種との比較ゲノム解析に取り組んできた。その結果、コケ坊主生物圏の細菌では多くの遺伝子で“種の壁”を超えて獲得されてきた痕跡（進化生物学における“遺伝子の水平伝播”）が明らかにされた。生態系における重要な物質循環やエネルギー代謝の機能性遺伝子（窒素循環、炭酸固定、光活性タンパク質など）が、これまでに無い高い割合での水平伝播により、これら細菌のゲノム上に分配あるいは集積がなされ、それにより限られた遺伝資源の環境下にあっても短期間で生物的多様性が形成され、環境変動への高い適応力や共生的な生物圏の構築を促したと考えられる。本発表では細菌の種分化、南極大陸上での局地的な種分化（スカルプスネス／ライトバレイ(77°10' S, 161°50' E)間での比較）、および南北両極における地球規模での種分化（南極大陸／北極スピッツベルゲン島(79°23' N, 13°26' E)間での比較）に関する解析結果も踏まえ、“地球上における生物進化の実験室としての極域の陸上生物圏”について議論を行う。