環境ストレスへの耐性史アーカイブとしてのインテグロン遺伝子の可能性

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Applicability of integron genes as potential archives for bio-history of resistances to environmental stresses

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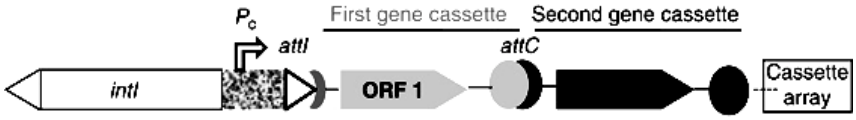
インテグロンは多薬剤耐性菌で発見された「動く遺伝子」である。新しい薬剤が開発されても、やがて病原菌はそれへの耐性遺伝子を獲得し、その遺伝子はインテグロンという「動く遺伝子」に乗せられて他の病原菌へ伝播する。近年の研究により、環境微生物にもインテグロン遺伝子が広く分布していることがわかってきた。これらの環境インテグロンが乗せている耐性遺伝子は、ひとつやふたつではなく、1000 個以上にもなることがある。それらは、その時その時の環境ストレスへの応答遺伝子であり、その順序は環境ストレスの変遷史を反映している。この発表では極域における環境ストレス変遷史の再構築にインテグロン遺伝子を用いることを提案する。

Integrons are mobile DNA elements first described in multidrug-resistant pathogenic bacteria. Now, integrons are known to occur widely in non-pathogencic microorganisms in natural environments. Microbes in nature use integrons as “reservoir” of “imported” stress response genes to cope with various environmental stresses. Such imported genes are present in the reservoir regions (gene cassettes, as stated below) for certain duration, and the numbers of imported genes reach 1000 or more. That is, the “storage” regions may act as bio-records of environmental stresses that occurred against their natural habitats.



The defining features of integrons are an integrase gene, *intI*, which encodes a site-specific recombinase, IntI, and an integron-associated recognition site designated *attI*. This recombination system is designed to capture individual genes when such genes are part of a mobilizable genetic element known as gene cassette. Insertion of a cassette into an integron occurs via an IntI-mediated site-specific recombination reaction between *attI* and the cassette-associated recombination site, *attC*.

Integrons are phylogenetically diverse elements and are dispersed among a wide range of both pathogenic and environmental bacteria. At least three integron classes contribute to the spread of antibiotic resistance. Outside the antibiotic-resistance domain, the biological significance of environmental integrons was demonstrated in their flexibility to acquire and express adaptive genes for several environmental stresses. This unique integron feature creates a system that provides for an enormous pool of adaptive genes to be mobilized, rearranged and disseminated among environmental bacteria. Indeed, the reservoir of integrons has as yet no known upper limit but must, at the very least, number in the thousands..

Environmental integron genes have been studied based on random PCR against bulk environmental DNA, particularly from extreme environments such as deep-sea hydrothermal vents. Similar ventures are applicable to the environmental samples from snow, icebergs, ice cores, permafrost, *etc* of Polar regions. History of environmental stresses causing biological responses are thus recorded in integron genes, and re-constructed by metagenomic analyses of bulk environmental DNA, particularly from well-preserved cryosphere habitats.

References

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