2-01

栄養の代謝に注目したケモスタット数理モデル

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ケモスタット数理モデルとは、連続培養器内における微生物の個体数の時間変化を微分方程式によって記述したものである。

今回、細胞外酵素による微生物の栄養有機物の代謝過程を模式化し、微生物の代謝に対する数理・理論的枠組みを発展させたので、その結果を紹介する。

理論的枠組みを、実際に農薬を共生的に分解する微生物集団のダイナミクスの理解へと応用し、微生物集団内の栄養共生関係がいかにして成立するか、その機構を数理モデルによって明らかにする。

2-02

The genome sequences of a cyanophage Ma-LMM01 infecting toxic *Microcystis aeruginosa*.

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Here, we report the complete genome sequence of a T4-like cyanophage Ma-LMM01 infecting the toxic strain of cyanobacterium *Microcystis aeruginosa*. The phage genome, a linear double-stranded DNA with 1,620,109 bp was circularly permuted. 184 potential open reading frames (ORFs) and two tRNA genes were identified. Of these ORFs, only 24% (44 ORFs) exhibited significant sequence matches (BLAST, E-value<10-5) in viral (22 ORFs) and/or cellular genomes (41 ORFs). Except for sheath structure protein, homologs in phage virion were not found. Thus Ma-LMM01 possessed a limited number of ORFs with homologs in the current sequence databases, indicating that this phage is distinctive from other phages reported. The genome lacked homologs for the photosynthetic genes that are ubiquitous among marine cyanophages. Alternatively, it encoded *nblA* involved in degradation of the major light-harvesting complexes, phycobiliproteins. Ma-LMM01 has a site-specific recombinase gene and two putative antirepressors, suggesting that Ma-LMM01 has a potential lysogeny. Ma-LMM01 possessed also several genes including three transposase genes highly similar to the homologs found in cyanobacteria, suggesting that relatively recent gene transfers have occurred between Ma-LMM01 and its host. Integration of these leads a fascinating hypothesis that reducing absorption of excess light energy is advantageous for propagation of Ma-LMM01 rather than maintenance of host photosynthetic activity. Thus, Ma-LMM01-Microcytis system seems to provide a new window to understand the phage adaptation for infection to photosynthetic hosts.
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