PI-128:

Transcriptome analysis of *Microcystis aeruginosa* during Ma-LMM01 infection

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【Introduction】The cyanobacterium *Microcystis aeruginosa* is a toxic, bloom-forming bacterium in eutrophic freshwaters throughout the world. A member of myoviridae, Ma-LMM01 can infect only a strain of *M. aeruginosa*. No detectable homologues involved in highjack of host metabolism were found in the phage genome. Here, we examined the dynamics of gene expression in the host cells infected by Ma-LMM01 to find a clue of the mechanism.
【Methods】After *M. aeruginosa* NIES-298 cells were inoculated with Ma-LMM01, culture was collected every 2h from 0 to 6 h. Total RNA was extracted from the collected samples. After removing rRNA, cDNA was synthesized from them. Host genome was extracted from *M. aeruginosa* NIES-298 cells. cDNA and host genome were sequenced using MiSeq and Nextera XT library preparation.
【Results and Discussion】Sequence reads of the *M. aeruginosa* NIES-298 genome were assembled to 589 contigs comprising 4.89×10^6 bp. 4666 CDSs were predicted on the genome. Of these, 4431 genes (95%) did not show significant change in expression when the rate of variability between two controls was discarded. Twenty two genes were up-regulated by more than 16 fold and 33 genes were down-regulated by more than 11 fold. In addition, 175 genes completely shut off and 5 genes expressed by viral infection. This result indicates that infection of Ma-LMM01 generally does not cause obvious shut off of host gene transcription. Virus infection with drastic change in host physiology during infection is disadvantageous for the phage due to induction of the host defense system. *Microcystis* possesses highest number of defense system against foreign genetic elements among all sequenced procaryotes. In particular, cell death caused by toxin-antitoxin systems can be robustly influenced by host transcription activity, suggesting that Ma-LMM01 may maintain host transcription so as not to induce host defense systems.

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