

**Mobile genetic elements of *Thermus thermophilus*:
a functional insertion sequence and novel phages**

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Bacterial genetic mobile elements, including bacteriophages, plasmid and transposons, play central roles in mobilizing genes in an intra- or inter-cellular fashion. They are a major cause of genomic plasticity and are now exploited as important genetic tools for gene transfer experiments to obtain mutants. Insertion sequences or IS elements are the simplest mobile elements. They consist of a fairly short (700 - 1500 bp) DNA segment flanked by a 10 - 40 bp inverted repeat (IR) sequence. The segment encodes the protein transposase that catalyses the transposition event. In the genome of the extreme thermophile *Thermus thermophilus* several kinds of transposase-like genes have been annotated. However, many of them are partial copies instead of intact ones. Therefore, it is critical to observe transposition event experimentally for identifying a *bona fide* IS element. We found a functional IS element in a *leuC* mutant strain from *T. thermophilus* HB27 isolated after nitrosoguanidine treatment. The intact IS elements are found in the genome of HB27 and the plasmid pTT27 in the public database. Their target sequences were very different to each other, suggesting no target sequence preference.

Bacteriophages or phages are ubiquitous in our world especially in the ocean, and probably the most abundant biological entities on earth. It is thought that they drive microbial evolution at least via lateral gene transfer. Among them tailed phages constitute the largest, most widespread and most diverse group of phages. One of the families, *Myoviridae*, has a contractile tail. They show the most complex structure and the phage particle forms in a complicated and sophisticated manner. Large diversity of phages holds true with hot water environments. In general, the role of lytic phages in cellular evolution is not as clear as that of lysogenic phages, which are thought to be important vehicles for lateral gene transfer via transduction. However, lytic phages of *Thermus* species seem to significantly contribute to evolution of their host cells because DNA released from lysed cells after infection could be the good substrates for other *Thermus* cells to uptake. In addition to evolutionary interest in the thermophilic phages, the gene products related to nucleotide modification are very attractive for various molecular biology applications. More than one hundred phages with *Thermus* as host strains have been isolated, which are the largest part of the phages that infect thermophilic eubacteria. They show a large variety of morphology as seen in mesophilic phages and more than half of the isolates are tail-less. We isolated several novel myoviruses with *T. thermophilus* HB8 as an indicator strain from Mine hot spring, Shizuoka prefecture, Japan. The genome sizes were about 40 kbp. They formed clear plaques on HB8 but not HB27.