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“Multiple genome comparison within a species reveals a unit of evolution spanning two ORFs in tandem paralog clusters”

A genome sequence is just a snapshot, but a large number of such snapshots, when compared, will reveal dynamics of genome evolution. Comparison of closely related genome sequences would provide insights as to how genome sequences evolve. Recent innovation in DNA sequencing is making this approach practical and productive. Prokaryotes provide particularly suitable targets because a large number of closely related genome sequences are being produced. I here introduced an example.

We tend to assume that an open reading frame (ORF) represents a unit of gene evolution as well as a unit of gene expression and function. On the contrary, I here report a case in which a unit of [3'-region of an ORF – intergenic region – 5'- region of its downstream ORF] has been conserved and has served as a unit of gene evolution. This is for tandem paralogous *lpl* genes of bacterium *Staphylococcus aureus*, for which more than 20 entire genomes have been decoded. A highly conserved nucleotide sequence within every *lpl* gene is likely to provide a site for recombination. Multiple crossing-over events there appear to have caused rearrangements, shuffling the 5'- and 3'- variable regions within one ORF but maintaining the unit spanning two adjacent ORFs. A similar pattern of paralog evolution was observed at another locus.
T. Tsuru & I. Kobayashi, *Molecular Biology and Evolution* 25: 2457-2473 (2008)

Short CV

2006-: Ph. D Course in Department of Biophysics and Biochemistry, Graduate School of Science, University of Tokyo, Japan.

2007-: Research fellow of the Japan Society for the Promotion of Science (JSPS).