

Search for the Origins of Prokaryotic Cell-Division Genes

Shouken Hokari

Koji Ohnishi

ohnishi@sc.niigata-u.ac.jp

Department of Biology, Faculty of Science, Niigata University
Ikarashi-2, Niigata 950-21, Japan

1 Introduction

The *E. coli* fts operon possesses ftsQ, ftsA, and ftsZ genes, which are known to be typical prokaryotic cell-division genes. The origins of these genes were analyzed from the viewpoint of molecular evolution.

2 Method

Amino acid (aa) sequence segments similar to those of these three cell-division gene products were searched for from PIR Database, by Lipman-Pearson method using Genentyx Software (Software Development Co., Tokyo). Thus found possibly homologous sequence segments were re-analyzed by dot-matrix method (Harr-Plot), and the corresponding base-sequence alignments (m-base-match in n-base-alignment) were statistically evaluated by computing base-match probability by chance, $P_{nuc}(m,n)$ (Ohnishi, Origins of Life 14: 707-715, 1984). Gene sequence data were obtained from GenBank.

3 Results and Discussions

Homology search from database resulted in finding close aa sequence similarities between ftsQ (aa's 116-171) and *Thermomyces lanuginosus* actin (aa's 98-153), between ftsA (aa's 39-103) and *D. melanogaster* insulin-receptor (Ins-R) (437-501), and between ftsZ (aa's 50-125) and *S. cerevisiae* cdc cell-division gene product (aa's 1148-1224). Based on these similarities and further matrix analyses, aa and base sequence alignments in Fig. 1 were obtained, in which similarity levels are; 16.9% aa-match (45.0 % base-match, $P_{nuc}(192, 427) = 0.29E-19$) for ftsQ (aa's 61-202)-actin (43-186) comparison, and 24.7% aa-match (35.7% base-match, $P_{nuc}(104,291) = 0.51E-4$) for ftsA (aa's 8-104)-Ins-R (410-502) comparison. Similarly, ftsZ (aa's 16-180) and cdc39 (aa's 1015-1281) were found to show a 22.9 % aa-match (22.9 % base-match), giving $P_{nuc}(208,491) = 0.35E-16$. From these results and Harr-plot graphics, genuine homology relationships were concluded for every comparisons described above.

Accordingly, ftsQ protein is considered to have originated from actin-like molecule of primitive contractile system. The ftsA protein is a homologue of Ins-R and tyrosin-kinase, both functioning as elements of tyrosin-kinase-mediated signal-transmitting system. ftsZ protein is related to the yeast cdc cell-division protein, whose exact function being unknown.