

# Origins of DNA-Binding Proteins and Their Kins: A View from Poly-tRNA Theory

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## 1 Introduction

Poly-tRNA transcripts from *B. subtilis* *trnD* and *trnB* operons have recently been proposed as relics of early peptide-synthesizing ribozyme, via which genetic codes and mRNA could have evolved (Poly-tRNA theory) (Ohnishi; *Endocytobiology* V, 407: '93; *Ann. N.Y. Acad. Sci.* 707: 524, '93; Ohnishi et al.; GIW'93, 325; GIW'96, 238). Origins of genes for DNA-binding domains and related protein genes were analyzed from Poly-tRNA viewpoint.

## 2 Method

Amino acid (aa) sequence similarity to the so-called "trnB-peptide" (See Fig.1A and GIW'93,'96) was found in DNA-binding domains from lambda-repressor (lambda-R) and homeoproteins, as well as glyceraldehyde 3-phosphate dehydrogenase (GAPDH) (Ohnishi, 1993) and adenylate kinase (AK), as shown in Fig. 1A. Based on these similarities, genes for these proteins and the *B. subtilis* *trnB* operon poly-tRNA region were compared with one another, using Lipman-Pearson's homology search (from PIR) and matrix method (Harr-Plot) (Genentyx Software, Software Development Co., Tokyo). The resulting alignments were statistically evaluated by computing m or more base-match probability by chance in n-base-alignment,  $P_{nuc}(m,n)$  (Ohnishi, *Origins of Life* 14: 707-715, 1984; GIW-93).

## 3 Results and Discussions

Aa and corresponding base sequences were aligned against hypothesized trnB-peptide (comprising 21 aa-specificities of trnB-tRNAs) and trnB-mRNA (comprising 21 codons complementary to 21 tRNA-anticodons), as shown in Fig. 1A. Gene segment coding for the helix 2-turn-helix 3 DNA-binding domain (aa's 30-57) showed a 54.0% base-match and  $P_{nuc}(46,87) = 0.24E-7$  to the tRNA-His region of the *B. subtilis* *trnB* operon. Corresponding gene-segments of AK and GAPDH showed 51% ( $P_{nuc} = 0.24E-4$ ) and 45% ( $0.59E-3$ ) base-matches. Sponge homeoprotein 1 showed 30% aa match and 47% base0-match ( $P_{nuc}=0.59E-9$ ) to GAPDH in DNA region coding for aa's 50-107 (Fig. 1B), elucidating close evolutionary relationship between these proteins. Based on matrix analysis, the entire 377-aa-encoding region of the lambda-R gene (cI) was found to be homologous to the hexa-tRNA-region, tRNA(Phe)-spacer-tRNA(His)-sp.-tRNA(Gly)-sp.-tRNA(Ile)-sp.-tRNA(Asn)-sp.-tRNA(Ser), in the *trnB*, showing 48.1% base-match and  $P_{nuc}(204,424) = 0.14E-19$ . Accordingly, the genes in Fig. 1 must have evolved from trnB-like poly-tRNA structure, as proposed by poly-tRNA theory.