

Phosphoglycerate-transporter Protein B as a Most Primitive Protein Predicted by the Poly-tRNA Theory

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1 Introduction

The poly-tRNA model can clearly explain how early tRNAs (= tRNA ribo-organisms) had associated tandemly to make *trnD*-operon-type and *rrnD*-operon-type poly-tRNA structures which could have evolved as RNA-machines for synthesizing *trnD*-type and *rrnB*-type peptides. The *trnD*-peptide is defined as a hypothetical peptide whose amino acid (aa) sequence is exactly the same order of the aa-specificities of the 16 tRNAs in the tRNA gene cluster within the *Bacillus subtilis* *trnD* operon. In hitherto published findings, Glycyl-tRNA synthetase (Gly-RS) alpha chain shows a closest similarity to the *trnD*-peptide [3].

2 Methods

Amino acid sequences similar to the *trnD* peptide, “NSEVMDFTYWHQGCLL” were searched for from Swiss Plot and PIR protein sequence databases using FASTA program [1]. *trnD*-mRNA is defined as a 48-base RNA complementary to the 64-base RNA consisting of the 16 anticodons of the 16 tRNAs in the *trnD*-poly-tRNA (Fig. 1).

3 Results and Discussions

Phosphoglycerate-transporter protein B (*pgtB*) (aa's 87-103) from *Salmonella typhimurium* (ST) was found to show the closest similarity to the *trnD*-peptide. The DNA sequence region encoding the aa's 87-103 of the *pgtB* protein was aligned with the *trnD*-mRNA, the *E. coli* GlyS gene segment encoding the aa's 139-154, *Synechococcus* sp. F0-ATP synthase a gene, and tRNA-Gly's and tRNA-Met (Fig. 1). The *trnD*-mRNA* was so defined by replacing some bases (of *trnD*-mRNA) by those bases capable of making wobble-pairing with the anticodons, that could give higher base-matches to the *pgtB* and GlyS genes (See Fig. 1). The *trnD*-mRNA* was thus found to show a 71.7% base-match to the *pgtB* gene, and 67.0% to the GlyS gene. The “eo-protein”, “NSEVXDFTYWQQGCLL”, was concluded to be an earliest protein predicted by these analyses (Fig. 1). These results strongly confirm the prediction by the poly-tRNA theory.

References

- [1] Pearson, W.R. and Lipman, D.J., Improved tools for biological sequence comparison, *Proc. Nat. Acad. Sci. USA*, 85:2444–2448, 1988.
- [2] Ohnishi, K., Tanaka, H., and Yanagawa, H., The origin of DNA-binding domains, as viewed from poly-tRNA theory, *Nucleic Acids Symp.*, Ser. 39:251–252, 1998.
- [3] Ohnishi, K. et al., Origin and evolution of early peptide-synthesizing biomachines by means of hierarchical sociogenesis of intracellular primitive tRNA-riboorganisms, *Proc. of the 4th Int. Symp. on Artificial Life and Robotics*, submitted.

(trrnD-peptide)	1 N S E V M D F T Y W H Q G C L L 16		
16 anticodons	3' UUG AGG CUU CAU UAC CUG AAG UGU AUG ACC GUG GUU CCG ACG AAU A-AC 5'		
		("*" = Watson-Crick type base-pairing)	
trrnD-mRNA	5' aac ucc gaa gua aug gac uuc aca uac ugg cac caa ggc ugc uua u-ug 3'		
	1 N S E V M D F T Y W H Q G C L L 16		
(trrnD-peptide)	1 N S E V M D F T Y W H Q G C L L 16		
16 anticodons	3' UUG AGG CUU CAU UAC CUG AAG UGU AUG ACC GUG GUU CCG ACG AAU A-AC 5'		
	* * * *	("*" = wobble pairing)	
trrnD-mRNA*	5' AAU UCC GAA GTA AUG GAU UUC ACU UAC UGG CAC CAG GGU UGC UUA U-UG 3'		
	1 N S E V M D F T Y W H Q G C L L 16		
		BASE-MATCH to ;	
		<u>trrnD-mRNA</u>	<u>trrnD-mRNA*</u>
		73.3%(33/45)	84.4%(38/45)
eo-protein (hypothetical)	1 <u>N S E V X D F T Y W Q Q G C L?</u> L 16		
	<u>AAU TCG GAA GTA XAG GAT TTT ACT TAC TGG CAG CAG GGT TGC TGX</u>		
<i>pgtB, S. typhimurium</i>	<u>AAU TCG CTG GTA CAG GAT TTT AC- --C TGG CAG CAG GGGACGC TGC T-CGAT</u>	60.9%(28/46)	71.7%(33/46)
	78 <u>N S L V Q D F T W Q Q G T L L D</u> 103		
<i>GlyS alpha, E. coli</i>	<u>GGC ATG GAA GTG ACG CAG TTC ACT TAC TTC CAG CA- GGT TGG TGG TCTG</u>	63.8%(30/47)	67.0% (31/47)
	139 <u>G M E V T Q F T Y F Q Q V G G L</u> 154		
F0-ATPase a(<i>Synechococcus</i>)	<u>GAGC TC- GAG GTC GGC CAG CAT TTT TAC TGG CAG ATC GG- --- --- ---</u>	54.1%(20/37)	54.1% (20/37)
	28 <u>E L E V G Q H F Y W Q I G</u> 40		
tRNA-Gly, <i>B.subtilis trrnD</i>	-3 <u>aat GCG GAA GTA GIT CAG T-- GG- TAG A-A CAC CA- CCT TGC CAA GGTG</u>	41 58.1%(25/43)	62.8%(27/43)
tRNA-Gly, <i>Mycopl.pneumo.</i>	-3 <u>tgc gCA GAT ATA GIT CAA T-- GC- CAG A-A CAT AA- CCT TGC CAA GGT</u>	41	
tRNA-Gly, <i>E. coli</i>	1 <u>GCG GGC ATC GTA TAA T-- GGC TAT T-A CCT CAG CCT T-C CAA GCTG</u>	42	
tRNA-Gly-3, <i>H. vulcanii</i>	1 <u>GCG CCG ATG GTC TCC AGT GG- TAG G-A CAC GAG CTT C-C CAA GCTC</u>	43	
tRNA-Met, <i>B.subtilis trrnD</i>	1 <u>CGC GGG GTG GAG CAG TTC GG- TAG C-T CGT C-G GGC T-C ATA ACCC</u>	42 48.8%(20/41)	51.2%(21/41)

Figure 1: Alignment of trrnD-mRNA with *pgtB* (*Salmonella typhimurium*) and *GlyS* (*E. coli*) genes. (Based on ref. [3]). Base- and amino acid-matches to trrnD-mRNA and trrnD-peptide are underlined. Base complementarities of Watson-Crick type and wobble type are indicated by “—” and “*”, respectively. The *trrnB*-mRNA(*) is homologous to *pgtB*, *GlyS*, and tRNA-Gly. Double-underlines denote bases capable of making wobble-pairing with trrnD-mRNA.