Origin of Ribonuclease P RNA (M1 RNA)

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1 Introduction

The origin of RNase P RNA is yet an unsolved problem, although one of us (K.O.) formerly pointed out some sequence similarity between RNase P RNA and virusoids (Ohnishi, 1992). Eigen hypothesized that tRNA is the first gene from theoretical standpoint. On the other hand, we have postulated poly-tRNA theory (Ohnishi; Endocytobiology V, 407: 1993; Ann. N.Y. Acad. Sci. 707: 524, 1993; Ohnishi et al.; GIW-93, 325; GIW-96, 238), in which most primitive mRNAs began to evolve from primitive tRNA(s), and at least some mRNAs (e.g., for glycyl tRNA ligase) have evolved from a poly-tRNA ribozyme closely kin to the poly-tRNA region of the B. subtilis trrnD operon transcript. Here we report a possibility that RNase P RNA might have evolved from some tRNA or oligo-tRNA region of the rrnB-type poly-tRNA.

2 Method

E. coli and *B. subtilis* RNase P RNA's were compared, by dot-matrix (Harr Plot) method (using Genentyx Software, Genentyx, Tokyo), with poly-tRNA regions of rrnB and trrnD operons, and also with rRNA regions of these operons. Most similar sequence segments found by this method were further analyzed by aligning the entire 377-base-region of RNase P RNA. The resulting alignment (n-base-long, m-base-match) was statistically evaluated by computing base-match probability by chance, Pnuc(m,n) (Origins of Life 14: 707, 1984).

3 Results and Discussions

Dot-matrix method showed three closely similar segment-pairs between E.coli RNase P RNA and B. subtilis rrnB operon poly-tRNA region; denoted here by matrix-homologies A, -B, and -C. Based on the homology-C, the entire region of the RNase P RNA was aligned against bases 5672-6032 of the rrnB poly-tRNA region, tRNA(Leu)-tRNA (Gly)-tRNA(Leu)-tRNA(Arg)-tRNA(Pro) (Fig.1). Base match level is 47.4 % (= 166/350, excluding gap positions), giving Pnuc(166,350) = 0.11 X 10E-18 in this alignment (rnpB bases 1-377). The homologies A and C satisfy this alignment, as shown in Fig. 1, in which homologies A and B correspond homology relationships among different tRNA homologs in M1 RNA. Homology search in GenBank database further revealed that Thermus thermophilus dnaJ gene (DNA region encoding aa's 98-215) is most plausibly homologous to RNase P RNA (bases 14-377) [45.3% base match, Pnuc(160,353) = 0.33E-18)].