Table 1. Promising consensus fragments of the rRNA-tRNA gene clusters.
(+ :found; - : not found as yet)

| Sequence | Holder A N P M | Sequence | Holder A N P M | Sequence | Holder A N P N |
|---|---|---|---|---|---|
| T P | + - - - A | L P | - + - - N | G R V | - - + - P |
| 5 D | + - - - A | R H | - + - - N | G C V | - - + - P |
| D K | + - - - A | V V V K | - + - - N | 23 5 V T K | - - + + PM |
| A 16 23 M | + - - - A | V V V | - + + - | (Q) K L (16) | - - + + PM |
| 7 S 16 A 23 | + - - - A | V K | - + - - N | (G L) R P A | - - + + PM |
| 16 A 23 | + - + - | M M | - + - - N | A M I S | - - + + PM |
| 5 C | + - - - A | T Y G T | - + - - N | K D F | - - + + PM |
| S L | + - - - A | Y G T | - + - - N | H G I N S E | - - + + PM |
| W W | + - - + | P H P | - + - - N | 23 5 N | - - + + PM |
| 16 I A 23 5 | - + - - N | A A | - + - - N | N S E V M D | - - + + PM |
| 16 I A 23 | - + + + | L L | - + + - | Y M D F | - - + + PM |
| 16 E 23 | - + - - N | fM F | - - + - P | N E V T | - - - + M |

Choice of the promising fragments is subjectively performed. Only one allowed union of categories is PM. It should be noted that, in principle, exact match is necessary not only between amino acids but also between anticodons as seen in a certain case of L(TAA) [2]:

*B.subtilis* --V(TAC)-T(TGT)-K(TTT)-L(CAG)-G(GCC)-L(TAA)-------
*A.ladilawii* --V(TAC)-T(TGT)-K(TTT)---------------L(TAA)-------

Exceptionally, evolutionally interpretable unmatch may be allowed as seen between M(CAT) and I(CAT) ( [5], Locus names BACTGTRNE and BACRGRRNB, respectively), and between L(CAG) and L(TAG) [2]. To estimate the ability of the set summarized in Table 1, three test sequences were processed;(1) From *Anacytics aueus* : 16 I A (23); (A) 23 5 [5]. There is no effective clue. (2) From *B.subtilis* : N S Q E K L L [6]. A fragment, K L, may suggest PM. (3) From *Staphylococcus aureus*: 23 5 V T K L G L G L R P A M I S D S fM D F T Y W H Q C G G G L [7]. This is enough information to suggest, again, PM.

The result of the first test would reveal the limit of the present set of consensus fragments because the bacteria is cyanobacteria, which is out of the four categories. The last two suggest that the concept of the consensus fragments of the rRNA-tRNA gene cluters may be an important key to solve phylogenetic questions. This is our current conclusion.

# References


[1] P.J.Keeling et al., *Current Opinion in Genetics and Development*, 4, 816-822, 1994.

[2] R.Tanaka et al., *Nucl.Acid.Res.*, 19, 6787, 1985.

[3] M.Akira et al., *ibid*,18, 5037, 1990.

[4] KUDO, Yoshihiro and KANAYA, Shigehiko, *Bull.Yamagata Univ.(Eng.)*, 23,113, 1995.

[5] DNA Data Base of Japan. DDBJ Distribution No.16.(Jan. 1994)

[6] D. B. Garrity et al., *J. Bacteriol.*., 175, 6512 (1993).

[7] Christopher J. Green et al., *ibid*, 5091.

# Consensus Genic Sequences in Bacterial rRNA-tRNA gene clusters

KUDO Yoshihiro
ykudo@eie.yz.yamagata-u.ac.jp

KANAYA Shigehiko
kanaya@eie.yz.yamagata-u.ac.jp

Dep. of Electric and Inf. Eng., Fac. of Eng., Yamagata Univ.
Yonezawa, Yamagata-ken 992,Japan

## 1 Introduction

Organization of rRNA-tRNA gene clusters has combined with a better understanding of bacterial molecular biology. It is known that archaebacteria has several consensus genic sequences in their rRNA-tRNA gene clusters[1]: 16 23...5 in some species of the crenarchaeota, and `16 A 23 5` in many species of the euryarchaeota, where 16, 23, and 5 stand for 16S, 23S and 5S rRNA genes, respectively, and "A" represents tRNA(Ala) gene. Moreover, a set of *Batillis subtilis* clusters is often compared with those of *Mycoplasmas* [2][3]. That is, attention has been mainly paid to search closely kindred bacteria for consensus sequences in their clusters. To the contrary, we have attempted to find (bacterial) holders holding the same fragments of the clusters. A preliminary experiment showed that `A M I(or M) S`, which had been found in *B.subtilis* and some *Mycoplasmas* species[2][3], was detected in neither arcaebacteria nor Gram-negative bacteria as yet[4]. The present article reports ability of candidates of consensus fragments of the rRNA-tRNA gene clusters.

## 2 Methodology

The procedure is as follows: (1) Bacteria is classified into four categories: Archaebacteria (code A), Gram-negative (N) and Gram-positive (P) bacteria and Mycoplasmas (M). (2) Sequences of the rRNA-tRNA gene clusters are collected. (3) They are arranged in the KWIC indexing manner, and promising ones of sets of the same fragments are chosen with the category names of their holder bacteria.

## 3 Results and Discussion

(1) Bacteria is classified into the four categories. (2) Necessary sequences of rRNA-tRNA gene clusters were picked up from the DDBJ[5]. The numbers of species concerned are 14 (A), 14 (N), 24(P), and 21(M). (3) The results were summarized in Table 1.

工藤喜弘, 金谷重彦 : 山形大学工学部・電子情報工学科・生体システム講座, 992 米沢市城南 4-3-16