

Consensus Genic Sequences in Bacterial rRNA-tRNA gene clusters

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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 archaebacteria 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.

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 M
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 unmatched may be allowed as seen between M(CAT) and I(CAT) ([5], Locus names BACTGTRNE and BACRGRNB, 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 clusters may be an important key to solve phylogenetic questions. This is our current conclusion.

References

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