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Effective procedure to develop alternative annotations of bacterial tRNA genes by means of deductive inference on the basis of characteristic tandems of tRNA genes

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Abstract

In a series of analysis of genomic DNA sequences, we have established an induction-deduction method to dig up hidden tRNA and rRNA genes from bacterial genome DNA sequences by means of a concept of a characteristic tRNA-gene tandem we have developed, and are accumulating information on positions of putative tRNA and rRNA genes to be proposed as alternative annotations to the DDBJ/GenBank/EMBL Database. We have searched the DNA sequences near the existing tRNA genes as golcondas for tRNA genes, and found more than fifty genes, e.g. tRNA-Ser and tRNA-Met in [AB013377], and 5S rRNAs in [AE014192], [AE017000], and others. A part of miserable states of the Database was partly introduced, and it is discussd how such status will be dissolved. In addition, we proposed some ideas to maintain and improve the DDBJ/GenBank/EMBL database.

1. Introduction(*)

It is known that Archaebacteria has several consensus gene clusters, e.g. , “ΣAΛΦ” (note: our notation for [16S rRNA][tRNA-Ala][23S rRNA][5S rRNA]; See Appendix 1) in many species of *eutyarchaeota* and “ΣΛ----Φ” in some species of *crenarchaeota*1). Phylogenetical relationship among *Bacillus subtilis*2) and some Mycoplasmas species (*Acholeoplasma laidlawii*,3) *Mycoplasma mycoides*4), *Mycoplasma capricolum*5) and *Spiroplasma melliferum*6)) was discussed using several consensus clusters such as AtgcMcatIcatStga. We made an optimistic hypothesis that the cluster AMIS is characteristic of Gram-positive bacteria (including Mycoplasmas), and would be found neither in Gram-negative bacteria nor Archaebacteria, and then made it clear that, in many cases, the AMIS consisted of Atgc of a cluster RacgPtggAtgc and another cluster McatIcatStga7). Since, at that time, we began to consider importance of the order of genes in a cluster, we temporalily used a term genic sequence of tRNA genes to avoid confusion with a DNA nucletide sequence, and now we adopt a term tandem (See Appendix 1 on Notations.) We have edited an ongoing tandem index. Entries that were registered in our eariest time are exemplified as follows.: (M: Mycoplasmas, P: Gram-positive bacteria, N: Gram-negative bacteria, and A: Archae bacteria)

M :Y(UAC)Q(CAA), and K(AAA)L(UUA),
M & P : M(AUG)M/I(AUG)S(UCA), E(GAA)D(GAC), and K(AAA)L(CUA),
P : H(CAC)Q(CAA), and K(AAA)L(CUG),
N :RH, LP, PHP, NL, G(GGA)T(ACC), M(AUG)M(AUG), and ΣE(GAA)Λ,

A :T(ACA)P(CCA), D(DAC)K(AAA), and Φ C(UGC),
M, P, N, & A(i.e. ubiquitous) : I(AUC)A(GCA)

Studying tandems annotated in the DDBJ/GenBank/EMBL Database, near the tandem D(ATC)F(GGC) of [U15182] of a Gram-positive bacterium *Mycobacterium lepae* , we accidentallly found a new putative tandem EttcDgtc, and then detected deductively Fgaa (See [U15182] in Table 4). In order to know whether this induction-deduction method is useful, we tried to detect tRNA and/or rRNA genes. The present paper enumerates a collection of putative tRNA and sometimes also rRNA genes that we detected. They may be used as alternatives of the Annotations in the Database. Moreover, we insist necessity of any cooperation system for maintenance and improvement of quality of sets of original data and annotations in this complicated discipline.

2. Method

We use more than one procedure. A main one is a set of inductive and deductive inferences where we select arbitrarily a tRNA gene (as a part of a tandem) or a tandem as a clue to detect any hidden gene(s). The clue is treated as an imperfect tandem, and compared with other tandems to be perfect ones in the alignment manner and the like. Considering that a logical difference between them suggests a missing link, we search the DNA sequence containing subsequence of the clue for DNA subsequences of any hidden genes to be obtained as the logical difference between the (imperfect) clue and one of the (perfect) templates.

3. Result

We collected about 3200 tRNA-gene tandems from the DDBJ/GenBank/EMBL, Release 58. Table 1 displays a small part of them. Then we picked up about eight hundred names of relevant bacteria (data not shown). Table 2 shows our own classification system and a genus index consisting of names and class codes of the genera. Table 3 exemplifies all of the tandems beginning with “H” for His. Table 4 lists the putative tRNA and rRNA genes we found which are underlined. Because the Annotations are always updated and improved, a part of our sauce data cited from the Database may be changed.

4. Consideration

We could show more examples, but stopped because we think these cases are enough to prove the power and usefulness of our induction-deduction method.

4.1 Detection of putative genes

4.1.1 tRNA genes (Direct)

A few of the results are explained as follows.

We discovered accidently a putative tandem EttcDgtc in [U15182] of the Gram-positive bacterium (*Mycobacterium laprae* B6-2-1-1-3-2-1) when we attempted to construct cloverleaf structures of the annotated tandem D(ATC)F(GGC). Then we made [ED] a clue, and searched our tandem index for any template tandems, which are VED ([X15246] *Lactobacillus* B6-1-2-1) and KEDF ([X00889] *Bacillus* B6-1-1-1-1). We found Fgtt downstream of the clue.

A clue [RG] [AB031213] (*Bacillus halodurans*). A template is RPG of [AP001508] (the same) and we found Ptgg at the corresponding position, the middle of the clue.

A clue [G] (a single gene) [AB031215] (*Bacillus halodurans*). The clue is compared with GRG [AP001516] (*Bacillus halodurans*), and R was found downstream of the first G.

A clue [AYHQGR] [AB013377] (*Bacillus halodurns*). The clue was aligned with ASMYHQQGRG of [AP001516] (*Bacillus halodurans*), and we found a tandem SM between A and Y, and Q just on the second H, respectively. The subsequence downstream of R is too short for the second G to be found.

A clue [Q(CAA)V YQK] [AY224382] (*Bacillus cereus* B6-1-1-1-1). The clue was aligned with

Table 1 A list of the tandems (Part)

@ A name of a bacterium(Genus and species,(strain)
Classification in the database
a tandem:tRNA genes(, rRNAs and CDS) and space length (bp) between them
[Accesion Number] Complete/Fragment

@ Acholeplasma laidlawii
Bacteria; Firmicutes; Mollicutes; Acholeplasmatales; Acholeplasmataceae; Acholeplasma
16S 139 Igat 22 Atgc 70 23S [D13259] Frag.
S??? 2 Ettc [X61065] Frag.
Hgtg 23 Qttg 28 Ltag [X61067] Frag.
23S 63 5S 28 Vtac 8 Ttgt 6 Kttt 14 Ltaa 22 Atgc 45 Mcat 4 Mcat 22 Stga 40 Mcat 24 Dgtc 7 Fgaa [X61068] Frag.

@ Agrobacterium tumefaciens str. C58
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium
16S 321 Igat 55 Atgc 471 ~Atu0056 2978 5S 235 Mcat 152 recQ [AE008980] Frag.
~Vtac 445 Dgtc 38 Dgtc [AE009088] Frag.
~Atu1993 306 Ygta 22 Gtcc 266 Atu1990 [AE009151*] Frag.
~purC 585 16S 321 Igat 55 Atgc 15 ~Atu2544 [AE009201*] Frag.
Igat 55 Atgc 471 ~Atu3940 2978 5S 235 Mcat 46 Atu3945 [AE009325] Frag.
~Atu4179 103 16S 308 Igat 55 Atgc 403 ~Atu4183 2932 5S 236 Mcat -25 ~Atu4188 [AE009348] Frag.

@ Bacillus amyloliquefaciens
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
16S 98 Igat 18 Atgc 83 23S [AF478079] Frag.

@ Bacillus anthracis str. Ames
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group
purA 139 Kttt 13 Ettc 20 Dgtc 41 Fgaa 403 yycF 548601 BA5126 131 16S 178 23S 101 5S 4 Vtac 4 Ttgt 9 Hgtg 22 Ltag 29 Ggcc 16 Ltaa 3 Racg 10 Ptgg 15 Atgc 20 Mcat 4 Mcat 17 Stga 27 Mcat 1 Dgtc 12 Fgaa 14 Ttgt 10 Kttt 13 Gtcc 10 Igat 7 Ngtt 7 Sgct 6 Ettc 657 ldh-2 360546 BA4712 -15 Gtcc 1 Rtct 407 BA4711 3538237 ~BA0720 138 ~Ettc 1 ~Ngtt 8 ~Igat 10 ~Wcca 6 ~Ttgt 9 ~Fgaa 8 ~Dgtc 4 ~Mcat 20 ~Stga 54 ~Stga 20 ~Atgc 16 ~Ptgg 10 ~Racg 3 ~Ltaa 16 ~Ggcc 29 ~Ltag 14 ~Kttt 4 ~Qttg 11 ~Vtac 5 ~5S 101 ~23S 178 ~16S 722 BA0719 198628 BA0540 207 ~Lcaa 10 ~Cgca 14 ~Ggcc 5 ~Qt

tg 63 ~Hgtg 19 ~Wcca 7 ~Ygta 10 ~Ttgt 18 ~Fgaa 9 ~Dgtc 3
~Mcat 24 ~Vtac 5 ~Ettc 17 ~Sgga 2 ~Ngtt 8 ~5S 100 ~23
S 171 ~16S -5 ~BA0539 236341 ~purE 698 ~5S 50 ~23S 178 ~16S 504
BA0287 2748 bacA-1 450 ~5S 50 ~23S 178 ~16S -5 ~BA0281 7355 B
A0273 137 ~5S 49 ~23S 178 ~16S 322 ~BA0272 13177 ~BA0258 174 ~Dgtc 3
~Mcat 12 ~5S 49 ~23S 178 ~16S 103 ~Gtcc 1 ~Ptgg 4 ~Ra
cg 95 ~Lgag 17 ~Kttt 5 ~Qttg 88 ~Dgtc 46 ~Vtac 4 ~Ettc 8
~Sgct 3 ~Ngtt 114 ~BA0257 90939 ~rocF 1470 ~Atgc 10 ~Ggcc 5 ~Kt
tt 5 ~Qttg 65 ~Ygta 17 ~Vtac 5 ~Ettc 24 ~Tggt 4 ~Ngtt 9
~5S 86 ~23S 178 ~16S -5 ~BA0152 57544 ~ctsR 206 ~5S 49 ~23
S 178 ~16S 400 ~lysS 13236 ~spoIIE 352 ~Ettc 13 ~Mcat 160 ~BA0060 292
99 ~BA0025 190 ~5S 48 ~23S 94 ~Atgc 8 ~Igat 150 ~16S 245 ~bo
fA 11682 ~guaB 1149 ~5S 48 ~23S 94 ~Atgc 8 ~Igat 150 ~16S 268
~gyrA [AE016879*] Comp.
gyrA 268 16S 150 Igat 8 Atgc 94 23S 48 5S 1149 guaB 116
82 bofA 245 16S 150 Igat 8 Atgc 94 23S 48 5S 190 B
A0025 29299 BA0060 160 Mcat 13 Ettc 352 spoIIE 13236 lysS 400 16S 178
23S 49 5S 206 ctsR 57544 BA0152 -5 16S 178 23S 86 5S
9 Ngtt 4 Tggt 24 Ettc 5 Vtac 17 Ygta 65 Qttg 5
Kttt 5 Ggcc 10 Atgc 1470 rocF 90939 BA0257 114 Ngtt 3 Sg
ct 8 Ettc 4 Vtac 46 Dgtc 88 Qttg 5 Kttt 17 Lgag 95
Racg 4 Ptgg 1 Gtcc 103 16S 178 23S 49 5S 12 M
cat 3 Dgtc 174 BA0258 13177 BA0272 322 16S 178 23S 49 5S 137
~BA0273 7355 BA0281 -5 16S 178 23S 50 5S 450 ~bacA-1 2748 ~ B
A0287 504 16S 178 23S 50 5S 698 purE 236341 BA0539 -5 16S 171
23S 100 5S 8 Ngtt 2 Sgga 17 Ettc 5 Vtac 24 M
cat 3 Dgtc 9 Fgaa 18 Ttgt 10 Ygta 7 Wcca 19 Hgtg 63
Qttg 5 Ggcc 14 Cgca 10 Lcaa 207 ~BA0540 198628 ~BA0719 722 16
S 178 23S 101 5S 5 Vtac 11 Qttg 4 Kttt 14 Ltag 29
Ggcc 16 Ltaa 3 Racg 10 Ptgg 16 Atgc 20 Stga 54 St
ga 20 Mcat 4 Dgtc 8 Fgaa 9 Ttgt 6 Wcca 10 Igat 8
Ngtt 1 Ettc 138 BA0720 3538237 ~BA4711 407 ~Rtct 1 ~Gtcc -15 ~ B
A4712 360546 ~ldh-2 657 ~Ettc 6 ~Sgct 7 ~Ngtt 7 ~Igat 10 ~Gtcc 13
~Kttt 10 ~Ttgt 14 ~Fgaa 12 ~Dgtc 1 ~Mcat 27 ~Stga 17 ~ M
cat 4 ~Mcat 20 ~Atgc 15 ~Ptgg 10 ~Racg 3 ~Ltaa 16 ~Ggcc 29
~Ltag 22 ~Hgtg 9 ~Ttgt 4 ~Vtac 4 ~5S 101 ~23S 178 ~16
S 131 ~BA5126 548601 ~yycF 403 ~Fgaa 41 ~Dgtc 20 ~Ettc 13 ~Kttt 139
~purA [AE016879] Comp.
gyrA 268 16S 150 Igat 8 Atgc 94 23S 48 5S 1149 guaB 116
82 bofA 245 16S 150 Igat 8 Atgc 94 23S 48 5S 190 ?C
DS 29299 ?CDS 160 Mcat 13 Ettc 352 spoIIE 13236 lysS 400 16S 178
23S 49 5S 206 ctsR 57544 ?CDS -5 16S 178 23S 86 5S

9 Ngtt 4 Tggt 24 Ettc 5 Vtac 17 Ygta 65 Qttg 5 Kttt 5 Ggcc 10 Atgc 1470 rocF 90939 ?CDS 114 Ngtt 3 Sgct 8 Ettc 4 Vtac 46 Dgtc 88 Qttg 5 Kttt 17 Lgag 95 Racg 4 Ptgg 1 Gtcc 103 16S 178 23S 49 5S 12 Mcat 3 Dgtc 174 ?CDS 13177 ?CDS 322 16S 178 23S 49 5S 137 ~?CDS 7355 ?CDS -5 16S 178 23S 50 5S 450 ~bacA-1 [AE017024] Comp.

16S 178 23S 50 5S 698 purE 236341 ?CDS -5 16S 171 23S 100 5S 8 Ngtt 2 Sgga 17 Ettc 5 Vtac 24 Mcat 3 Dgtc 9 Fgaa 18 Ttgt 10 Ygta 7 Wcca 19 Hgtg 63 Qttg 5 Ggcc 14 Cgca 10 Lcaa 207 ~?CDS [AE017025] Comp.

~?CDS 722 16S 178 23S 101 5S 5 Vtac 11 Qttg 4 Kttt 14 Ltag 29 Ggcc 16 Ltaa 3 Racg 10 Ptgg 16 Atgc 20 Stga 54 Stga 20 Mcat 4 Dgtc 8 Fgaa 9 Ttgt 6 Wcca 10 Igat 8 Ngtt 1 Ettc 138 ?CDS [AE017026] Comp.

?CDS -15 Gtcc 1 Rtct 407 ?CDS [AE017038*] Comp.

?CDS 131 16S 178 23S 101 5S 4 Vtac 4 Ttgt 9 Hgtg 22 Ltag 29 Ggcc 16 Ltaa 3 Racg 10 Ptgg 15 Atgc 20 Mcat 4 Mcat 17 Stga 27 Mcat 1 Dgtc 12 Fgaa 14 Ttgt 10 Kttt 13 Gtcc 10 Igat 7 Ngtt 7 Sgct 6 Ettc 657 ldh-2 [AE017039*] Comp.

purA 139 Kttt 13 Ettc 20 Dgtc 41 Fgaa 403 yycF [AE017041*] Comp.

@ Chlamydia muridarum

Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia

TC0495 199 Vtac 7 Dgtc 23 TC0494 16343 kdtA 26 Mcat 16 Mcat 26 ~pfkA-2 29450 TC0453 190 Atgc 4 Igat 27 TC0452 69432 ~TC0419 164 ~Ygta 7 ~Ttgt 50 ~TC0418 315690 ~tkt 250 ~5S 114 ~23S 242 ~16S 507 TC0126 16741 TC0114 -502 ~23S 241 ~16S 78007 frr 101 Ettc 17 Kttt 79 TC0047 [AE002160*] Comp.

~TC0047 79 ~Kttt 17 ~Ettc 101 ~frr 78007 16S 241 23S -502 ~TC0114 16741 ~TC0126 507 16S 242 23S 114 5S 250 tkt 315690 TC0418 50 Ttgt 7 Ygta 164 TC0419 69432 ~TC0452 27 ~Igat 4 ~Atgc 190 ~TC0453 29450 pfkA-2 26 ~Mcat 16 ~Mcat 26 ~kdtA 16343 ~TC0494 23 ~Dgtc 7 ~Vtac 199 ~TC0495 [AE002160] Comp.

frr 101 Ettc 17 Kttt 79 ?CDS [AE002272*] Comp.

?CDS 50 Ttgt 7 Ygta 164 ?CDS [AE002308] Comp.

?CDS 190 Atgc 4 Igat 27 ?CDS [AE002314*] Comp.

kdtA 26 Mcat 16 Mcat 26 ~pfkA-2 [AE002316*] Comp.

?CDS 199 Vtac 7 Dgtc 23 ?CDS [AE002318*] Comp.

rrf 101 Ettc 17 Kttt [U60196] Frag.

Table 2 The genera classification system and a genus index

(a) Our classification system

Class code and name

A Archaea
A1 Euryarchaeota
A1-1 Archaeoglobi
A1-1-1Archaeoglobales
A1-1-1Archaeoglobaceae

A1-2 Halobacteria
A1-2-1Halobacteriales
A1-2-1-1Halobacteriaceae

A1-3 Methanobacteria
A1-3-1Methanobacteriales
A1-3-1-1Methanobacteriaceae
A1-3-1-2Methanothermaceae

A1-4 Methanococci
A1-4-1Methanococcales
A1-4-1-1 Methanocaldococcaceae
A1-4-1-2Methanococcaceae

A1-5 Methanomicrobia
A1-5-1Methanosarcinales
A1-5-1-1-Methanosarcinaceae

A1-6 Methanopyri
A1-6-1Methanopyrales
A1-6-1-1Methanopyraceae

A1-7 Thermococci
A1-7-1Thermococcales
A1-7-1-1Thermococcaceae

A1-8 Thermoplasma
A1-8-1Thermoplasmatales
A1-8-1-1Thermoplasmataceae

A2 Crenarchaeota
A2-1 Thermoprotei
A2-1-1Sulfolobales
A2-1-1-1Sulfolobaceae

A2-1-2Thermoproteales
A2-1-2-1Thermofiliaceae

A2-1-2-2Thermoproteaceae

B Bacteria
B1 Nitrospirae
B1-1Nitrospirales
B1-1-1Nitrospiraceae

B2 Aquificae
B2-1Aquificales
B2-1-1 Aquificaceae

B3 Thermotoga
B3-1Thermotogales
B3-1-1Thermotogaceae

B4 Deinococcus-Thermus
B4-1 Deinococci
B4-1-1Deinococcales
B4-1-1-1Deinococcaceae
B4-1-2Thermales
B4-1-2-1 Thermaceae

B5 Cyanobacteria
B5-1 Chroococcales
B5-1-1 Chroococcales
B5-1-2Chroococcales
B5-1-3 Chroococcales
B5-2 Nostocales
B5-2-1 Microchaetaceae
B5-2-2Nostocaceae
B5-2-3 Rivulariaceae
B5-2-4 Scytonemataceae
B5-3 Oscillatoriales
B5-4 Prochlorophytes
B5-5 Stigonematales

B6 Firmicutes
B6-1 Low GC G-P
B6-1-1 Bacillales
B6-1-1-1 Bacillaceae
B6-1-1-2 Paenibacillaceae
B6-1-1-3Listeriaceae
B6-1-1-4Staphylococcus
B6-1-2 Lactobacillales
B6-1-2-1 vCarnobacteriaceae
B6-1-2-2Enterococcaceae
B6-1-2-3 Lactobacillaceae
B6-1-2-4 Streptococcaceae
B6-1-2-5 Weissella
B6-1-3 Mollicutes
B6-1-3-1 Acholeplasmatales
B6-1-3-1-1 Acholeplasmataceae
B3-1-3-2 Anaeroplasmatales
B6-1-3-2-1Anaeroplasmataceae

B6-1-3-3Entomoplasmatales
B6-1-3-3-1 Spiroplasmataceae
B6-1-3-4 Mycoplasmataceae
B6-1-3-4-1Mycoplasmataceae
B6-1-4 Clostridia
B6-1-4-1 Clostridiales
B6-1-4-1-1 Acidaminococcaceae
B6-1-4-1-2 Clostridiaceae
B6-1-4-1-3 Ethanologenbacterium
B6-1-4-1-4 Peptostreptococcaceae
B6-1-4-2 Thermoanaerobacteriales
B6-1-4-2-1 Thermoanaerobacteriaceae
B6-2 High GC G-P
B6-2-1 Actinobacteria
B6-2-1-1Actinobacteridae
B6-2-1-1-1 Actinomycetales
B6-2-1-1-1-1Propionibacterineae
B6-2-1-1-1-1-1Nocardioidaceae
B6-2-1-1-2Streptomycineae
B6-2-1-1-2-1 Streptomycetaceae
B6-2-1-1-3 Corynebacterineae
B6-2-1-1-3-1Corynebacteriaceae
B6-2-1-1-3-2 Mycobacteriaceae
B6-2-1-1-4 Micrococcineae
B6-2-1-1-4-1 Cellulomonadaceae
B6-2-2¥1-1-4-2 Micrococcaceae
B6-2-1-1-2 Bifidobacteriales
B6-2-1-1-2-1 Bifidobacteriaceae

B7 Fusobacteria
B7-1 Fusobacterales
B7-1-1Fusobacteriaceae

B8 Bacteroidetes
B8-1 Bacteroides (class)
B8-1-1 Bacteroidales
B8-1-1-1Bacteroidaceae
B8-1-1-2Porphyromonadaceae
B8-1-1-3 Prevotellaceae
B8-2 Sphingobacteria
B8-2-1 Sphingobacteriales
B8-2-1-1 Crenotrichaceae
B8-2-1-2 Saprospiraceae

B9 Chlorobi
B9-1 Chlorobia
B9-1-1 Chlorobiales
B9-1-1-1Chlorobiaceae

B10 Spirochaetes
B10-1 Spirochaetales
B10-1-1 Leptospiraceae
B10-1-2 Spirochaetaceae

B11 Chlamydiae & Planctomycetes
B11-1 Planctomycetes
B11-1-1 Planctomycetacia
B11-1-1-1 Planctomycetales
B11-2 Chlamydiae
B11-2-1 Chlamydiales
B11-2-1-1Chlamydiaceae
B11-2-2 Parachlamydiaceae

B12 Proteobacteria
B12-1 Alphaproteobacteria
B12-1-1 Rhodospirillales
B12-1-1-1 Acetobacteraceae
B12-1-1-2 Rhodospirillaceae
B12-1-2 Rhodobacterales
B12-1-2-1 Rhodobacteraceae
B12-1-3 Rhizobiales
B12-1-3-1 Rhizobiaceae
B12-1-3-2Bradyrhizobiaceae
B12-1-3-3 Brucellaceae
B12-1-3-4 Methylobacteriaceae
B12-1-3-5 Phyllobacteriaceae
B12-1-3-6 Bartonellaceae
B12-1-4 Sphingomonadales
B12-1-4-1 Sphingomonadaceae
B12-1- 5Caulobacterales
B12-1-5-1 Caulobacteraceae
B12-1-6 Rickettsiales
B12-1-6-1 Rickettsiaceae

B12-2 Betaproteobacteria
B12-2-1 Neisseriales
B12-2-1-1Neisseriaceae
B12-2-2 Burkholderiales
B12-2-2-1Alcaligenaceae
B12-2-2-2Burkholderiaceae
B12-2-2-3Thiomonas
B12-2-2-4
B12-2-3 Nitrosomonadales
B12-2-3-1Nitrosomonadaceae

B12-3 Gammaproteobacteria
B12-3-1 Acidithiobacillales
B12-3-1-1 Acidithiobacillaceae
B12-3-2 Aeromonadales
B12-3-2-1 Aeromonadaceae
B12-3-3 Alteromonadales
B12-3-3-1 Alteromonadaceae
B12-3-4 Enterobacteriales
B12-3-4-1 Enterobacteriaceae
B12-3-5 Oceanospirillales
B12-3-5-1 Alcanivoraxaceae
B12-3-5-2 Halomonadaceae
B12-3-6 Pasteurellales
B12-3-6-1 Pasteurellaceae
B12-3-7 Pseudomonadales
B12-3-7-1 Moraxellaceae
B12-3-8 Pseudomonadales
B12-3-8-1Pseudomonadaceae
B12-3-9 Thiotrichales
B12-3-9-1 Piscirickettsiaceae
B12-3-10 Vibrionales
B12-3-10-1 Vibrionaceae
B12-3-11 Xanthomonadales
B12-3-11-1Xanthomonadaceae
B12-3-12 Cardiobacteriales
B12-3-12-1 Cardiobacteriaceae
B12-3- 13 Legionellales
B12-3-13-1 Coxiellaceae
B12-3-13-2 Pasteurellaceae

B12-4 Deltaproteobacteria
B12-4-1 Desulfovibrionales
B12-4-2 Desulfuromonadales
B12-4-3 Myxococcales
B12-4-3-1 Sorangineae
B12-4-3-1-1 Polyangiaceae

B12-5Epsilonproteobacteria
B12-5-1 Campylobacterales
B12-5-1-1Campylobacteraceae
B12-5-1-2 Helicobacteraceae

(b) a genera index

Acetobacter	B12-1-1-1-1
Acholeplasma	B6-1-3-1-1-1
Acidithiobacillus	B12-3-1-1-1
Acinetobacter	B12-3-7-1-1
Actinobacillus	B12-3-13-2-1
Aeromonas	B12-3-2-1-1
Afipia	B12-1-3-2-1
Agrobacterium	B12-1-3-1-1
Alcanivorax	B12-3-5-1-1
Aquifex	B2-1-1-1
Anabena	B5-2-2-1
Anaeroplasma	B6-1-3-2-1-1
Archaeoglobus	A1-1-1-1
Antarctbacter	B12-1-2-1-1
Arsenophonus	B12-3-4-1-1
Arthrospira	B5-3-1
Azospirilum	B12-1-1-2-1
Bacillus	B6-1-1-1-1
Bacteroides	B8-1-1-1-1
Bartonella	B12-1-3-6-1
Bifidobacterium	B6-2-1-1-2-1-1
Blastobacter	B12-1-3-2-2
Blochmannia(Candidatus)	B12-3-4-1-11
Bordetella	B12-2-2-1-1
Borrelia	B10-1-2-1
Bradyrhizobium	B12-1-3-2-3
Brevibacillus	B6-1-1-2-1
Brocadia (Candidatus)	B11-1-1-1-2
Brucella	B12-1-3-3-2
Buchnera	B12-3-4-1-2
Burkholderia	B12-2-2-2-1
Calothrix	B5-2-3-1
Campylobacter	B12-5-1-1-1
Caulobacter	B12-1-5-1-1
Carnobacterium	B6-1-2-1-1
Chlamydia	B11-2-1-1-1
Chlamydophila	B11-2-1-1-2
Chlorobium	B9-1-1-1-1
Chlorogloeopsis	B5-5-1
Chromobacterium	B12-2-1-1-1
Clostridium	B6-1-4-1- 2-1
Coleodesmium	B5-2-1-1
Coxiella	B12-3-13-1-1
Corynebacterium	B6-2-1-1-3-1-1
Cyanobium	B5-1-1-1
Deinococcus	B4-1-1-1-1
Desulfovibrio	B12-4-1-1
Dichelobacter	B12-3-12-1-1
Enterococcus	B6-1-2-2-1
Erwinia	B12-3-4-1-3
Escherichia	B12-3-4-1-4
Ethanologenbacterium	B6-1-4-1- 3-1
Finegoldia	B6-1-4-1-4-1
Fischerella	B5-5-2
Fusobacterium	B7-1-1-1
Geitlerinema	B5-3-2
Geobacter	B12-4-2 -1
Gloeotrichia	B5-2-3-2
Gluconacetobacter	B12-1-1-1-2
Gluconobacter	B12-1-1-1-3
Haemophilus	B12-3-6-1-1
Haloarcula	A1-2-1-1-1
Halobacterium	A1-2-1-1-2
Halococcus	A1-2-1-1-3
Helicobacter	B12-5-1-2-1
Kuenenia (Candidatus)	B11-1-1-1-3
Lactobacillus	B6-1-2-3-1
Lactococcus	B6-1-2-4-1
Leptospira	B10-1-1-1
Leptospirillum	B1-1-1-1
Liberibacter (candidatus)	B12-1-3-1-4
Limnothrix	B5-3-5
Listeria	B6-1-1-3-1
Listonella	B12-3-10-1-1
Marinibacillus	B6-1-1-1-2
Mesorhyzobium	B12-1-3-5-1
Methanobacterium	A1-3-1-1-2
Methanocaldococcus	A1-4-1-1-1
Methanococcus	A1-4-1-2-1
Methanopyrus	A1-6-1-1-1
Methanosarcina	A1-5-1-1-1
Methanothermobacter	A1-3-1-1-1
Methanothermus	A1-3-1-2-1
Methylobacterium	B12-1-3-4 -1
Microchaetaceae	B5-2-1-3
Micrococcus	B6-2-1-1-4-2-1
Microcoleus	B5-3-3
Microvirgula	B12-2-1-1-2
Mycobacterium	B6-2-1-1-3-2-1
Mycoplasma	B6-1-3-4-1-1
Neisseria	B12-2-1-1-3
Nitrosomonas	B12-2-3-1-1
Nocardioides	B6-2-1-1-1-1-1-1
Nostoc	B5-2-2-2
Novosphingobium	B12-1-4-1-1
Oceanobacillus	B6-1-1-1-3
Ochrobactrum	B12-1-3-3-1
Oscillatoria	B5-3-4
Paenibacillus	B6-1-1-1-2-2
Parachlamydia	B11-2-2-1
Paracoccus	B12-1-2-1-2
Pectobacterium	B12-3-4-1-5
Pelagibacter(candidatus)	B12-1-6-1-3
Photobacterium	B12-3-10-1-2
Photorhabdus	B12-3-4-1-6
Phytoplasma	B6-1-3-1-1-2
Pirellula	B11-1-1-1-1
Piscirickettsia	B12-3-9-1-1
Polyanguim	B12-4-3-1-1-1
Porphyromonas	B8-1-1-2-1
Prevotella	B8-1-1-3-1
Prochlorococcus	B5-4-1
Pseudaminobacter	B12-1-3-5-2
Pseudomonas	B12-3-8-1-1
Pyrobaculum	A2-1-2-2-1
Pyrococcus	A1-7-1-1-1
Ralstonia	B12-2-2-2-2
Renibacterium	B6-2-1-1-4-2-2
Rhizobium	B12-1-3-1-2
Rhodobacter	B12-1-2-1-3
Rhodopseudomonas	B12-1-3-2-4
Rhodothermus	B8-2-1-1-1
Rickettsia	B12-1-6-1-1
Roseobacter	B12-1-2-1-4
Roseovarius	B12-1-2-1-5
Ruegeria	B12-1-2-1-6
Salinibacter	B8-2-1-1-2
Salinivibrio	B12-3-10-1-3
Salmonella	B12-3-4-1-7
Saprospira	B8-2-1-2-1
Scytonema	B5-2-4-1
Selenomonas	B6-1-4-1-1-1
Shewanella	B12-3-3-1-1
Shigella	B12-3-4-1-8
Sinorhyzobium	B12-1-3-1-3
Sodalis	B12-3-4-1-9
Sphingomonas	B12-1-4-1-2
Spiroplasma	B6-1-3-3-1-1
Staphylococcus	B6-1-1-4-1
Streptococcus	B6-1-2-4-2
Streptomyces	B6-2-1-1-2-1-1
Sulfolobus	A2-1-1-1-1
Synechococcus	B5-1-2-1
Synechocystis	B5-1-3-1
Thermoanaerobacter	B6-1-4-2-1-1
Thermococcus	A1-7-1-1-2
Thermofilum	A2-1-2-1-1
Thermoplasma	A1-8-1-1-1
Thermotoga	B3-1-1-1
Thermus	B4-1-2-1-1
Thiomonas	B12-2-2-3-1
Tolypothrix	B5-2-1-2
Treponema	B10-1-2-2
Trichodesmium	B5-3-6
Tropheryma	B6-2-1-1-4-1-1
Ureaplasma	B6-1-3-4-1-2
Vibrio	B12-3-10-1-4
Wautersia	B12-2-2-2-3
Weissella	B6-1-2-5-1
Wolbachia	B12-1-6-1-2
Xanthomonas	B12-3-11-1-1
Xylella	B12-3-11-1-2
Xylophilus	B12-2-2-4-1
Yersinia	B12-3-4-1-10
Zymobacter	B12-3-5-2-1
Zymomonas	B12-1-4-1-3

Table 3.(1) A list of tRNA gene tandems (The H section for His)

					Heading												Class code	bacterial name	Acc. No
---	----	---	----	---	@Hatg	15	Hatg	23	~gseA	---	----	---	----	---	----	---	B11-2-1-1-2	Chlamydophila pneumoniae CWL029	[AE001602*]
34	tauB	68469	CPj01!	94	@Hatg	15	Hatg	23	~gseA	---	----	---	----	---	----	---	B11-2-1-1-2	Chlamydophila pneumoniae J138	[AP002545*]
34	tauB	68558	CPn01!	94	@Hatg	15	Hatg	23	~gseA	---	----	---	----	---	----	---	B11-2-1-1-2	Chlamydophila pneumoniae	[AE001363*]
21	Ettc	39	Ltag	14	@Hgtg	299	16S	65	Atgc	207	23S	---	----	---	----	---	A1-4-1-1-1	Methanocaldococcus jannaschii	[U67517]
106	Ptgg	31	Rtct	27	@Hgtg	51	Ettc	233	pheT	---	----	---	----	---	----	---	B9-1-1-1-1	Chlorobium tepidum TLS	[AE012843]
106	Ptgg	31	Rtct	27	@Hgtg	51	Ettc	233	pheT	####	~CT07‹	141	~Lcaa	26	~Ltag	->	B9-1-1-1-1	Chlorobium tepidum TLS	[AE006470]
---	----	---	~BB060!	9	@Hgtg	264	Ggcc	40	BB061	---	----	---	----	---	----	---	B10-1-2-1	Borrelia burgdorferi B31	[AE001162]
4	Dgtc	4	Fgaa	26	@Hgtg	22	Gtcc	26	Igat	6	Ngtt	36	Sgct	5	Ettc	->	B6-1-1-3-1	Listeria innocua	[AL592022*]
4	Dgtc	4	Fgaa	26	@Hgtg	22	Gtcc	26	Igat	6	Ngtt	36	Sgct	5	Ettc	->	B6-1-1-3-1	Listeria innocua	[AL596170*]
4	Dgtc	4	Fgaa	28	@Hgtg	23	Gtcc	25	Igat	6	Ngtt	34	Sgct	5	Ettc	->	B6-1-1-3-1	Listeria monocytogenes	[AL591980*]
4	Dgtc	4	Fgaa	28	@Hgtg	23	Gtcc	25	Igat	6	Ngtt	34	Sgct	5	Ettc	->	B6-1-1-3-1	Listeria monocytogenes EGD-e	[NC_003210*]
4	Dgtc	4	Fgaa	28	@Hgtg	24	Gtcc	25	Igat	6	Ngtt	34	Sgct	5	Ettc	->	B6-1-1-3-1	Listeria monocytogenes str. 4b F2365	[AE017327*]
11	Dgtc	12	Fgaa	16	@Hgtg	10	Gtcc	15	Igat	10	Ngtt	3	Sgct	25	Ettc	---	B6-1-1-1-1	Bacillus subtilis	[K00637]
11	Dgtc	12	Fgaa	16	@Hgtg	10	Gtcc	15	Igat	10	Ngtt	3	Sgct	25	Ettc	->	B6-1-1-1-1	Bacillus subtilis	[AL009126*]
11	Dgtc	12	Fgaa	16	@Hgtg	10	Gtcc	15	Igat	10	Ngtt	3	Sgct	25	Ettc	->	B6-1-1-1-1	Bacillus subtilis	[AF008220]
11	Dgtc	12	Fgaa	17	@Hgtg	10	Gtcc	15	Igat	10	Ngtt	3	Sgct	25	Ettc	->	B6-1-1-1-1	Bacillus subtilis subsp. subtilis str. 168	[Z99119*]
13	Dgtc	12	Fgaa	17	@Hgtg	10	Gtcc	15	Igat	10	Ngtt	3	Sgct	25	Ettc	---	B6-1-1-1-1	Bacillus subtilis	[K01390]
14	Dgtc	10	Fgaa	13	@Hgtg	17	Gtcc	9	Ngtt	1	Ettc	53	Sgga	209	~?CDS	---	B6-1-1-4-1	Staphylococcus epidermidis ATCC 12228	[AE016749*]
21	Dgtc	16	Fgaa	13	@Hgtg	15	Gtcc	14	Ngtt	1	Ettc	54	Sgga	1244	~MW17'	---	B6-1-1-4-1	Staphylococcus aureus subsp. aureus MW2	[AP004828*]
14	Dgtc	10	Fgaa	13	@Hgtg	17	Gtcc	9	Ngtt	1	Ettc	53	Sgga	209	~SE15(	->	B6-1-1-4-1	Staphylococcus epidermidis ATCC 12228	[AE015929*]
21	Dgtc	16	Fgaa	13	@Hgtg	15	Gtcc	17	Ngtt	1	Ettc	54	Sgga	213	seo	---	B6-1-1-4-1	Staphylococcus aureus subsp. aureus N315	[AP003135*]
21	Dgtc	16	Fgaa	13	@Hgtg	15	Gtcc	17	Ngtt	1	Ettc	54	Sgga	213	seo	->	B6-1-1-4-1	Staphylococcus aureus subsp. aureus N315	[BA000018*]
21	Dgtc	19	Fgaa	13	@Hgtg	18	Gtcc	20	Ngtt	4	Ettc	54	Sgga	213	seo	---	B6-1-1-4-1	Staphylococcus aureus subsp. aureus Mu50	[AP003363*]
21	Dgtc	19	Fgaa	13	@Hgtg	18	Gtcc	20	Ngtt	4	Ettc	54	Sgga	213	seo	->	B6-1-1-4-1	Staphylococcus aureus subsp. aureus Mu50	[BA000017*]
18	Rtct	27	Hgtg	45	@Hgtg	26	Hgtg	31	~?CDS	---	----	---	----	---	----	---	B12-2-1-1-1	Chromobacterium violaceum ATCC 12472	[AE016916*]
18	Rtct	27	Hgtg	45	@Hgtg	26	Hgtg	31	~CV192	####	~CV16:	360	~Sgga	53	~Sgga	->	B12-2-1-1-1	Chromobacterium violaceum ATCC 12472	[AE016825*]
225	Ptgg	18	Rtct	27	@Hgtg	45	Hgtg	26	Hgtg	31	~?CDS	---	----	---	----	---	B12-2-1-1-1	Chromobacterium violaceum ATCC 12472	[AE016916*]
225	Ptgg	18	Rtct	27	@Hgtg	45	Hgtg	26	Hgtg	31	~CV19:	####	~CV16:	360	~Sgga	->	B12-2-1-1-1	Chromobacterium violaceum ATCC 12472	[AE016825*]
176	Ptgg	63	Rtct	39	@Hgtg	110	Kctt	494	?CDS	---	----	---	----	---	----	---	B12-3-11-1-2	Xylella fastidiosa Temecula1	[AE012561]
162	Ptgg	43	Rtct	31	@Hgtg	83	Kctt	77	Ltag	202	tig	4962	hupB	11	Vtac	->	B12-3-11-1-1	Xanthomonas campestris pv. campestris str. ATCC 33913	[AE012195]
162	Ptgg	43	Rtct	31	@Hgtg	83	Kctt	77	Ltag	202	tig	4962	hupB	11	Vtac	->	B12-3-11-1-1	Xanthomonas campestris pv. campestris str. ATCC 33913	[AE008922]
176	Ptgg	63	Rtct	39	@Hgtg	110	Kctt	494	PD210	---	----	---	----	---	----	---	B12-3-11-1-2	Xylella fastidiosa Temecula1	[AE009442]
176	Ptgg	61	Rtct	39	@Hgtg	110	Kctt	311	~XF276	---	----	---	----	---	----	---	B12-3-11-1-2	Xylella fastidiosa 9a5c	[AE004082]
176	Ptgg	61	Rtct	39	@Hgtg	110	Kctt	311	~XF276	---	----	---	----	---	----	---	B12-3-11-1-2	Xylella fastidiosa	[AE003849]
107	Ptgg	7	Gtcc	10	@Hgtg	3	Kttt	12	Ltag	40	Qttg	175	FN19!	---	----	---	B7-1-1-1	Fusobacterium nucleatum subsp. nucleatum ATCC 25586	[AE010498*]
107	Ptgg	7	Gtcc	10	@Hgtg	3	Kttt	12	Ltag	40	Qttg	175	FN19!	7054	FN19‹	->	B7-1-1-1	Fusobacterium nucleatum subsp. nucleatum ATCC 25586	[AE009951*]
53792	ansP3	148	Rccg	83	@Hgtg	16	Lcag	-38	~?CDS	####	~?CDS	51	~5S	-1	~23S	->	B12-3-4-1-10	Yersinia pestis biovar Mediaevails str. 91001	[AE017042]
53792	ansP3	148	Rccg	83	@Hgtg	16	Lcag	-38	~?CDS	####	~?CDS	51	~5S	-1	~23S	->	B12-3-4-1-10	Yersinia pestis biovar Mediaevails str. 91001	[AE017139]
---	----	---	Rccg	49	@Hgtg	20	Lcag	71	Ptgg	---	----	---	----	---	----	---	B12-3-2-1-1	Aeromonas hydrophila	[X12977]
---	----	---	Rccg	57	@Hgtg	20	Lcag	42	Ptgg	---	----	---	----	---	----	---	B12-3-4-1-4	Escherichia coli	[K01994]
---	?CDS	102	Rccg	53	@Hgtg	20	Lcag	42	Ptgg	---	----	---	----	---	----	---	B12-3-4-1-7	Salmonella typhimurium	[M95047]

---	yifK	102	Rccg	57	@Hgtg	20	Lcag	42	Ptgg	---	----	---	----	---	----	---	B12-3-4-1-4	Escherichia coli K12	[AE000455]
45462	yifK	283	Rccg	76	@Hgtg	15	Lcag	42	Ptgg	987	ISPl	####	orn	199	Ggcc	->	B12-3-4-1-6	Photorhabdus luminescens subsp. laumondii TTO1	[BX470251*]
45462	yifK	283	Rccg	76	@Hgtg	15	Lcag	42	Ptgg	987	ISPl	####	orn	199	Ggcc	->	B12-3-4-1-6	Photorhabdus luminescens subsp. laumondii TTO1	[BX571874*]
---	ECs47	102	Rccg	58	@Hgtg	20	Lcag	43	Ptgg	22	Lcag	42	Ptgg	146	ECs4	->	B12-3-4-1-4	Escherichia coli O157:H7	[AP002567]
32881	ECs47	102	Rccg	58	@Hgtg	20	Lcag	43	Ptgg	22	Lcag	42	Ptgg	146	ECs4	->	B12-3-4-1-4	Escherichia coli O157:H7	[BA000007]
70027	STY36	102	Rccg	54	@Hgtg	20	Lcag	42	Ptgg	581	~STY3	####	STY3	380	16S	->	B12-3-4-1-7	Salmonella enterica subsp. enterica serovar Typhi	[AL513382*]
55124	YPO38	148	Rccg	83	@Hgtg	16	Lcag	75	Ptgg	866	YPO3	---	----	---	----	---	B12-3-4-1-10	Yersinia pestis CO92	[AJ414159*]
---	yifK	102	Rccg	57	@Hgtg	20	Lcag	42	Ptgg	146	aslB	---	----	---	----	---	B12-3-4-1-4	Escherichia coli O157:H7 EDL933	[AE005611]
---	yifK	233	Rccg	58	@Hgtg	20	Lcag	42	Ptgg	116	aslB	---	----	---	----	---	B12-3-4-1-8	Shigella flexneri 2a str. 301	[AE015394]
32046	yifK	102	Rccg	57	@Hgtg	20	Lcag	42	Ptgg	146	aslB	---	----	---	----	---	B12-3-4-1-4	Escherichia coli CFT073	[AE016769]
---	yifK	102	Rccg	58	@Hgtg	20	Lcag	42	Ptgg	146	aslB	####	hemG	377	16S	->	B12-3-4-1-8	Shigella flexneri 2a str. 2457T	[AE016990*]
32000	yifK	233	Rccg	58	@Hgtg	20	Lcag	42	Ptgg	116	aslB	####	hemG	377	16S	->	B12-3-4-1-8	Shigella flexneri 2a str. 301	[AE005674]
32000	yifK	102	Rccg	58	@Hgtg	20	Lcag	42	Ptgg	146	aslB	####	hemG	377	16S	->	B12-3-4-1-8	Shigella flexneri 2a str. 2457T	[AE014073*]
32046	yifK	102	Rccg	57	@Hgtg	20	Lcag	42	Ptgg	146	aslB	####	hemG	377	16S	->	B12-3-4-1-4	Escherichia coli CFT073	[AE014075]
33128	yifK	102	Rccg	57	@Hgtg	20	Lcag	42	Ptgg	146	aslB	####	hemG	380	16S	->	B12-3-4-1-4	Escherichia coli O157:H7	[AE005174]
33151	yifK	102	Rccg	57	@Hgtg	20	Lcag	42	Ptgg	146	aslB	####	hemG	377	16S	->	B12-3-4-1-4	Escherichia coli	[U00096]
7202	rho	296	Rccg	71	@Hgtg	30	Lcag	12	Ptgg	101	~hemD	####	~purH	428	16S	->	B12-3-4-1-11	Candidatus Blochmannia floridanus	[BX248583*]
7202	rho	296	Rccg	71	@Hgtg	30	Lcag	12	Ptgg	101	~hemD	####	~purH	428	16S	->	B12-3-4-1-11	Candidatus Blochmannia floridanus	[BX248586*]
---	yifK	102	Rccg	57	@Hgtg	23	Lcag	45	Ptgg	584	~hemY	---	----	---	----	---	B12-3-4-1-7	Salmonella typhimurium LT2	[AE008883]
70027	yifK	102	Rccg	54	@Hgtg	20	Lcag	42	Ptgg	581	~hemY	---	----	---	----	---	B12-3-4-1-7	Salmonella enterica subsp. enterica serovar Typhi	[AL627279*]
70029	yifK	102	Rccg	54	@Hgtg	20	Lcag	42	Ptgg	581	~hemY	####	hemG	387	16S	->	B12-3-4-1-7	Salmonella enterica subsp. enterica serovar Typhi Ty2	[AE016845*]
70029	yifK	102	Rccg	54	@Hgtg	20	Lcag	42	Ptgg	581	~hemY	####	hemG	387	16S	->	B12-3-4-1-7	Salmonella enterica subsp. enterica serovar Typhi Ty2	[AE014613*]
33026	yifK	102	Rccg	57	@Hgtg	23	Lcag	45	Ptgg	584	~hemY	####	hemG	377	16S	->	B12-3-4-1-7	Salmonella typhimurium LT2	[AE006468]
55124	YPO38	148	Rccg	83	@Hgtg	16	Lcag	75	Ptgg	866	tnp	####	hemG	501	16S	->	B12-3-4-1-10	Yersinia pestis	[AL590842*]
---	y0375	148	Rccg	86	@Hgtg	19	Lcag	-35	~y0376	---	----	---	----	---	----	---	B12-3-4-1-10	Yersinia pestis KIM	[AE013638]
55125	y0375	148	Rccg	86	@Hgtg	19	Lcag	-35	~y0376	####	hemG	475	16S	59	Igat	->	B12-3-4-1-10	Yersinia pestis KIM	[AE009952]
96981	~folD-	293	Rtct	51	@Hgtg	56	Ltag	571	?CDS	---	----	---	----	---	----	---	B12-3-8-1-1	Pseudomonas syringae pv. tomato str. DC3000	[AE016869*]
39	?CDS	1E+05	?CDS	28	@Hgtg	50	Ltag	37	?CDS	####	~?CDS	52	~Rtct	35	~Gtcc	->	B4-1-2-1-1	Thermus thermophilus HB27	[AE017221]
39	?CDS	1E+05	?CDS	28	@Hgtg	50	Ltag	37	?CDS	####	~?CDS	52	~Rtct	35	~Gtcc	->	B4-1-2-1-1	Thermus thermophilus HB27	[AE017301]
---	----	---	~DR092	176	@Hgtg	52	Ltag	141	DR092	---	----	---	----	---	----	---	B4-1-1-1-1	Deinococcus radiodurans R1	[AE001945*]
-398	DR126	3E+05	~DR092	176	@Hgtg	52	Ltag	141	DR092	####	~DR06	197	Ptgg	20	Gtcc	->	B4-1-1-1-1	Deinococcus radiodurans	[AE000513*]
361	Vtac	4	Ttgt	9	@Hgtg	22	Ltag	29	Ggcc	16	Ltaa	3	Racg	10	Ptgg	->	B6-1-1-1-1	Bacillus cereus ATCC 14579	[AE017013*]
361	Vtac	4	Ttgt	9	@Hgtg	22	Ltag	29	Ggcc	16	Ltaa	3	Racg	10	Ptgg	->	B6-1-1-1-1	Bacillus cereus ATCC 14579	[AE016877*]
4	Vtac	4	Ttgt	9	@Hgtg	22	Ltag	29	Ggcc	16	Ltaa	3	Racg	10	Ptgg	->	B6-1-1-1-1	Bacillus cereus	[AY224388]
4	Vtac	4	Ttgt	9	@Hgtg	22	Ltag	29	Ggcc	16	Ltaa	3	Racg	10	Ptgg	->	B6-1-1-1-1	Bacillus anthracis str. Ames	[AE016879*]
4	Vtac	4	Ttgt	9	@Hgtg	22	Ltag	29	Ggcc	16	Ltaa	3	Racg	10	Ptgg	->	B6-1-1-1-1	Bacillus anthracis str. Ames	[AE017039*]
4	Vtac	4	Ttgt	9	@Hgtg	22	Ltag	29	Ggcc	16	Ltaa	3	Racg	10	Ptgg	->	B6-1-1-1-1	Bacillus anthracis str. Ames 0581	[AE017334*]
---	~folD	278	Rtct	51	@Hgtg	54	Ltag	66	Hgtg	697	~?CDS	---	----	---	----	---	B12-3-8-1-1	Pseudomonas aeruginosa PAO1	[AE004605]
1E+06	~folD	278	Rtct	51	@Hgtg	54	Ltag	66	Hgtg	697	~PA17	####	PA28	-124	~Ggcc	->	B12-3-8-1-1	Pseudomonas aeruginosa	[AE004091]
96981	~folD-	293	Rtct	51	@Hgtg	56	Ltag	571	PSPTO	####	~PSPT	1722	16S	103	Igat	->	B12-3-8-1-1	Pseudomonas syringae pv. tomato str. DC3000	[AE016853*]
47	Ptgg	5	Rtct	25	@Hgtg	62	Ltag	115	tig	1885	loN-	139	Dgtc	11	Vtac	->	B12-4-2-1	Geobacter sulfurreducens PCA	[AE017180*]
47	Ptgg	5	Rtct	25	@Hgtg	62	Ltag	115	tig	1885	loN-	139	Dgtc	11	Vtac	->	B12-4-2-1	Geobacter sulfurreducens PCA	[AE017213*]
719	Ngtt	1	Mcat	13	@Hgtg	26	Mcat	13	Stga	152	Fgaa	169	OB19	---	----	---	B6-1-1-1-3	Oceanobacillus iheyensis HTE831	[AP004599*]

719	Ngtt	1	Mcat	13	@Hgtg	26	Mcat	13	Stga	152	Fgaa	169	OB19	####	~OB09	->	B6-1-1-1-3	Oceanobacillus iheyensis	[BA000028*]
---	----	---	Ptgg	8	@Hgtg	53	Ptgg	---	----	---	----	---	----	---	----	---	B11-2-1-1-2	Photobacterium phosphoreum	[X12975]
34	Hgtg	76	Ptgg	49	@Hgtg	64	Ptgg	---	----	---	----	---	----	---	----	---	B12-3-10-1-4	Vibrio harveyi	[M29762]
53	Ptgg	174	Ptgg	8	@Hgtg	149	Ptgg	---	----	---	----	---	----	---	----	---	B11-2-1-1-2	Photobacterium phosphoreum	[X12976]
---	Mcat	2418	Rccg	29	@Hgtg	24	Ptgg	180	16S	131	Ettc	274	23S	247	5S	->	B12-3-6-1-1	Haemophilus influenzae Rd KW20	[U32697*]
1283	Mcat	2418	Rccg	29	@Hgtg	24	Ptgg	180	16S	131	Ettc	274	23S	247	5S	->	B12-3-6-1-1	Haemophilus influenzae Rd	[L42023*]
57958	wecG	157	Rccg	30	@Hgtg	29	Ptgg	202	16S	80	Ettc	198	23S	242	5S	->	B12-3-6-1-1	Haemophilus ducreyi 35000HP	[AE017156*]
57958	wecG	157	Rccg	30	@Hgtg	29	Ptgg	202	16S	80	Ettc	198	23S	242	5S	->	B12-3-6-1-1	Haemophilus ducreyi 35000HP	[AE017143*]
41	Hgtg	29	Ptgg	77	@Hgtg	27	Ptgg	1282	?CDS	####	?CDS	167	Ettc	4	Kttt	->	B12-3-10-1-4	Vibrio vulnificus CMCP6	[AE016800]
34	Hgtg	66	Ptgg	9	@Hgtg	51	Ptgg	723	AGAD	---	----	---	----	---	----	---	B11-2-1-1-2	Photobacterium profundum	[CR378663]
---	----	---	Rccg	34	@Hgtg	76	Ptgg	49	Hgtg	64	Ptgg	---	----	---	----	---	B12-3-10-1-4	Vibrio harveyi	[M29762]
14144	~?CDS	254	Rccg	41	@Hgtg	29	Ptgg	77	Hgtg	27	Ptgg	1282	?CDS	####	?CDS	->	B12-3-10-1-4	Vibrio vulnificus CMCP6	[AE016800]
14517	~NMB16	294	Rccg	34	@Hgtg	66	Ptgg	9	Hgtg	51	Ptgg	723	AGAD	---	----	---	B11-2-1-1-2	Photobacterium profundum	[CR378663]
---	~VC016	289	Rccg	35	@Hgtg	61	Ptgg	70	Hgtg	61	Ptgg	435	~VC01	---	----	---	B12-3-10-1-4	Vibrio cholerae O1 biovar eltor str. N16961	[AE004107]
9186	~VC016	289	Rccg	35	@Hgtg	61	Ptgg	70	Hgtg	61	Ptgg	435	~VC01	####	VC03	->	B12-3-10-1-4	Vibrio cholerae	[AE003852]
9312	~VP004	337	Rccg	32	@Hgtg	72	Ptgg	49	Hgtg	24	Ptgg	66	~VP00	---	----	---	B12-3-10-1-4	Vibrio parahaemolyticus	[AP005073]
9312	~VP004	337	Rccg	32	@Hgtg	72	Ptgg	49	Hgtg	24	Ptgg	66	~VP00	####	VP05	->	B12-3-10-1-4	Vibrio parahaemolyticus RIMD 2210633	[BA000031]
9269	~VV004	254	Rccg	38	@Hgtg	26	Ptgg	74	Hgtg	24	Ptgg	942	~VV00	####	~VV01	->	B12-3-10-1-4	Vibrio vulnificus YJ016	[AP005330]
9269	~VV004	254	Rccg	38	@Hgtg	26	Ptgg	74	Hgtg	24	Ptgg	942	~VV00	####	~VV01	->	B12-3-10-1-4	Vibrio vulnificus YJ016	[BA000037]
14144	~VV110	254	Rccg	41	@Hgtg	29	Ptgg	77	Hgtg	27	Ptgg	1282	VV11	####	VV11	->	B12-3-10-1-4	Vibrio vulnificus CMCP6	[AE016795]
---	~?CDS	206	Rccg	52	@Hgtg	15	Ptgg	53	Ptgg	184	~?CDS	---	----	---	----	---	B12-3-3-1-1	Shewanella oneidensis MR-1	[AE015865*]
176	Ptgg	176	Ptgg	8	@Hgtg	53	Ptgg	174	Ptgg	8	Hgtg	149	Ptgg	---	----	---	B11-2-1-1-2	Photobacterium phosphoreum	[X12976]
2E+05	~SO432	206	Rccg	52	@Hgtg	15	Ptgg	53	Ptgg	184	~SO43	####	secA	716	16S	->	B12-3-3-1-1	Shewanella oneidensis MR-1	[AE014299*]
35	Hgtg	61	Ptgg	70	@Hgtg	61	Ptgg	435	~VC016	---	----	---	----	---	----	---	B12-3-10-1-4	Vibrio cholerae O1 biovar eltor str. N16961	[AE004107]
35	Hgtg	61	Ptgg	70	@Hgtg	61	Ptgg	435	~VC016	####	VC03	-25	16S	63	Igat	->	B12-3-10-1-4	Vibrio cholerae	[AE003852]
32	Hgtg	72	Ptgg	49	@Hgtg	24	Ptgg	66	~VP004	---	----	---	----	---	----	---	B12-3-10-1-4	Vibrio parahaemolyticus	[AP005073]
32	Hgtg	72	Ptgg	49	@Hgtg	24	Ptgg	66	~VP004	####	VP05	85	16S	177	Aggc	->	B12-3-10-1-4	Vibrio parahaemolyticus RIMD 2210633	[BA000031]
38	Hgtg	26	Ptgg	74	@Hgtg	24	Ptgg	942	~VV004	####	~VV01	537	16S	68	Ettc	->	B12-3-10-1-4	Vibrio vulnificus YJ016	[AP005330]
38	Hgtg	26	Ptgg	74	@Hgtg	24	Ptgg	942	~VV004	####	~VV01	537	16S	68	Ettc	->	B12-3-10-1-4	Vibrio vulnificus YJ016	[BA000037]
41	Hgtg	29	Ptgg	77	@Hgtg	27	Ptgg	1282	VV110	####	VV11	167	Ettc	4	Kttt	->	B12-3-10-1-4	Vibrio vulnificus CMCP6	[AE016795]
---	rho	100	Rccg	39	@Hgtg	33	Ptgg	1773	~cyaY	---	----	---	----	---	----	---	B12-1-3-3-2	Buchnera aphidicola str. Sg (Schizaphis graminum)	[AE014131*]
---	rho	282	Rccg	40	@Hgtg	35	Ptgg	91	~cyaY	####	aroE	204	Ettc	159	23S	->	B12-1-3-3-2	Buchnera aphidicola str. Bp (Baizongia pistaciae)	[AE014017*]
---	rho	100	Rccg	39	@Hgtg	33	Ptgg	1773	~cyaY	####	dut	734	~Mcat	133	Ngtt	->	B12-1-3-3-2	Buchnera aphidicola str. Sg (Schizaphis graminum)	[AE013218*]
---	rho	282	Rccg	40	@Hgtg	35	Ptgg	91	~cyaY	####	~pyrE	118	~Mcat	193	Ngtt	->	B12-1-3-3-2	Buchnera aphidicola (Baizongia pistaciae)	[AE016826*]
---	rho	188	Rccg	29	@Hgtg	36	Ptgg	757	~hemC	####	aroE	152	Ettc	161	23S	->	B12-1-3-3-2	Buchnera aphidicola str. APS (Acyrthosiphon pisum)	[AP001119*]
---	rho	188	Rccg	29	@Hgtg	36	Ptgg	757	~hemC	####	~pyrE	95	~Mcat	134	Ngtt	->	B12-1-3-3-2	Buchnera sp. APS	[AP000398*]
4	Ygta	8	Wcca	2	@Hgtg	11	Qttg	5	Cgca	9	Gtcc	14	Gtcc	11	Gtcc	->	B6-1-1-4-1	Staphylococcus epidermidis ATCC 12228	[AE015929*]
4	Ygta	8	Wcca	2	@Hgtg	11	Qttg	5	Cgca	9	Gtcc	14	Gtcc	11	Gtcc	->	B6-1-1-4-1	Staphylococcus epidermidis ATCC 12228	[AE016749*]
5	Ygta	15	Wcca	2	@Hgtg	11	Qttg	5	Cgca	7	Gtcc	103	Gtcc	38	Lcaa	->	B6-1-1-4-1	Staphylococcus aureus subsp. aureus N315	[AP003135*]
5	Ygta	15	Wcca	2	@Hgtg	11	Qttg	5	Cgca	7	Gtcc	103	Gtcc	38	Lcaa	->	B6-1-1-4-1	Staphylococcus aureus subsp. aureus MW2	[AP004828*]
5	Ygta	15	Wcca	2	@Hgtg	11	Qttg	5	Cgca	7	Gtcc	103	Gtcc	38	Lcaa	->	B6-1-1-4-1	Staphylococcus aureus subsp. aureus N315	[BA000018*]
8	Ygta	15	Wcca	5	@Hgtg	11	Qttg	5	Cgca	10	Gtcc	106	Gtcc	41	Lcaa	->	B6-1-1-4-1	Staphylococcus aureus subsp. aureus Mu50	[AP003363*]
8	Ygta	15	Wcca	5	@Hgtg	11	Qttg	5	Cgca	10	Gtcc	106	Gtcc	41	Lcaa	->	B6-1-1-4-1	Staphylococcus aureus subsp. aureus Mu50	[BA000017*]

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  5 Ygta     4  Wcca    36 @Hgtg    14  Qttg    25  Cgca    13  Lcaa   576 ~?CDS ---    ---- --- B6-1-2-2-1   Enterococcus faecalis V583                            [AE016950]
  4 Ygta     7  Wcca    14 @Hgtg     4  Qttg    20  Cgca    31  Lcaa   115  ?CDS 2136  ?CDS ->  B6-1-2-3-1   Lactobacillus johnsonii NCC 533                       [AE017198*]
  4 Ygta     7  Wcca    14 @Hgtg     4  Qttg    20  Cgca    31  Lcaa   115  ?CDS 2136  ?CDS ->  B6-1-2-3-1   Lactobacillus johnsonii NCC 533                       [AE017205*]
  5 Ygta     4  Wcca    36 @Hgtg    14  Qttg    25  Cgca    13  Lcaa   576 ~EF10 ####  EF13 ->  B6-1-2-2-1   Enterococcus faecalis V583                            [AE016830]
  5 Ygta     7  Wcca    59 @Hgtg     9  Qttg    27  Cgca    37  Lcaa    89  labJ ---    ---- --- B6-1-2-3-1   Lactobacillus sakei                                   [AF401668]
  5 Ygta     8  Wcca     5 @Hgtg     7  Qttg    22  Cgca    55  Lcaa   150 ~lp_1 ####  lp_1 ->  B6-1-2-3-1   Lactobacillus plantarum WCFS1                         [AL935263]
  5 Ygta     8  Wcca     5 @Hgtg     7  Qttg    22  Cgca    55  Lcaa   150 ~lp_1 ####  uvrA ->  B6-1-2-3-1   Lactobacillus plantarum WCFS1                         [AL935255]
 10 Ygta     7  Wcca    19 @Hgtg    63  Qttg     5  Ggcc    14  Cgca    10  Lcaa ---    ---- --- B6-1-1-1-1   Bacillus cereus                                       [AY224386]
 20 Ygta     7  Wcca    15 @Hgtg    29  Qttg     5  Ggcc    19  Cgca    45  Lcaa  348  ?CDS --- B6-1-1-3-1   Listeria monocytogenes str. 4b F2365                  [AE017330*]
 10 Ygta     7  Wcca    19 @Hgtg    63  Qttg     5  Ggcc    14  Cgca    10  Lcaa  206 ~?CDS --- B6-1-1-1-1   Bacillus cereus ATCC 14579                            [AE016999]
 10 Ygta     7  Wcca    19 @Hgtg    63  Qttg     5  Ggcc    14  Cgca    10  Lcaa  207 ~?CDS --- B6-1-1-1-1   Bacillus anthracis str. Ames                          [AE017025]
 10 Ygta     7  Wcca    19 @Hgtg    63  Qttg     5  Ggcc    14  Cgca    10  Lcaa  207 ~?CDS ->  B6-1-1-1-1   Bacillus anthracis str. Ames 0581                     [AE017334]
 10 Ygta     7  Wcca    19 @Hgtg    63  Qttg     5  Ggcc    14  Cgca    10  Lcaa  487  ?CDS ->  B6-1-1-1-1   Bacillus cereus ATCC 10987                            [AE017266]
 10 Ygta     7  Wcca    19 @Hgtg    63  Qttg     5  Ggcc    14  Cgca    10  Lcaa  207 ~BA05 ->  B6-1-1-1-1   Bacillus anthracis str. Ames                          [AE016879]
 10 Ygta     7  Wcca    19 @Hgtg    63  Qttg     5  Ggcc    14  Cgca    10  Lcaa  206 ~BC05 ->  B6-1-1-1-1   Bacillus cereus ATCC 14579                            [AE016877]
 15 Ygta    15  Wcca     5 @Hgtg    24  Qttg     2  Ggcc     8  Cgca     4  Lcaa  186  OB09 --- B6-1-1-1-3   Oceanobacillus iheyensis HTE831                       [AP004596]
 15 Ygta    15  Wcca     5 @Hgtg    24  Qttg     2  Ggcc     8  Cgca     4  Lcaa  186  OB09 ->  B6-1-1-1-3   Oceanobacillus iheyensis                              [BA000028]
 22 Ygta     7  Wcca    14 @Hgtg    31  Qttg     5  Ggcc    19  Cgca    45  Lcaa  187  lin2 --- B6-1-1-3-1   Listeria innocua                                      [AL596172*]
 22 Ygta     7  Wcca    14 @Hgtg    31  Qttg     5  Ggcc    19  Cgca    45  Lcaa  187  lin2 ->  B6-1-1-3-1   Listeria innocua                                      [AL592022*]
 20 Ygta     7  Wcca    15 @Hgtg    29  Qttg     5  Ggcc    19  Cgca    45  Lcaa  351  lmo2 --- B6-1-1-3-1   Listeria monocytogenes                                [AL591983*]
 20 Ygta     7  Wcca    15 @Hgtg    29  Qttg     5  Ggcc    19  Cgca    45  Lcaa  351  lmo2 ->  B6-1-1-3-1   Listeria monocytogenes EGD-e                          [NC_003210*]
 19 Ygta     5  Wcca    24 @Hgtg     9  Qttg    46  Ggcc     5  Cgca     4  Ltaa  265  Lcaa ->  B6-1-1-1-1   Bacillus subtilis subsp. subtilis str. 168            [Z99108]
 22 Ygta     5  Wcca    24 @Hgtg     9  Qttg    49  Ggcc     5  Cgca     7  Ltaa  265  Lcaa --- B6-1-1-1-1   Bacillus subtilis                                     [K01389]
 22 Ygta     5  Wcca    24 @Hgtg     9  Qttg    49  Ggcc     5  Cgca     7  Ltaa  265  Lcaa ->  B6-1-1-1-1   Bacillus subtilis                                     [AL009126]
 22 Ygta     5  Wcca    24 @Hgtg     9  Qttg    49  Ggcc     5  Cgca     7  Ltaa  265  Lcaa ->  B6-1-1-1-1   Bacillus subtilis                                     [Z82044]
 54 Ygta    11  Wcca    18 @Hgtg    13  Qttg     4  Ggcc     7  Cgca    26  Ltaa   15  Racg ->  B6-1-1-1-1   Bacillus halodurans C-125                             [AP001510]
154 Atgc   363  Ygta    12 @Hgtg    15  Qttg     4  Ggcc     1  Racg ---    ---- ---    ---- --- B6-1-1-1-1   Bacillus halodurans                                   [AB013377]
171 Mcat     5  Ygta    12 @Hgtg    15  Qttg     4  Ggcc     1  Racg   185  Gtcc    41 ~BH28 --- B6-1-1-1-1   Bacillus halodurans C-125                             [AP001516*]
 54 Ygta    11  Wcca    18 @Hgtg    13  Qttg     4  Ggcc   464 ~TnpA ---    ---- ---    ---- --- B6-1-1-1-1   Bacillus halodurans                                   [AB031215]
  7 Gtcc    82  Rtct     7 @Hgtg     6  Qttg     9  Kttt    22  Kttt    13  Ltag   29  Ggcc ->  B6-1-4-1-2-1 Clostridium perfringens str. 13                       [AP003193*]
  7 Gtcc    82  Rtct     7 @Hgtg     6  Qttg     9  Kttt    22  Kttt    13  Ltag   29  Ggcc ->  B6-1-4-1-2-1 Clostridium perfringens                               [BA000016*]
---  Gtcc    4  Rtct    11 @Hgtg     3  Qttg     4  Kttt    38  Lcag     5  Ggcc   25  Kctt ->  B6-1-4-1-1-1 Thermoanaerobacter tengcongensis                      [AE013030*]
198 Gtcc     4  Rtct    11 @Hgtg     3  Qttg     4  Kttt    38  Lcag     5  Ggcc   25  Kctt ->  B6-1-4-2-1-1 Thermoanaerobacter tengcongensis                      [AE008691*]
 10 Gtcc     9  Kctt    17 @Hgtg     7  Qttg    25  Kttt     6  Ltag    18  Ggcc    8  Gtcc ->  B6-1-4-1-2-1 Clostridium acetobutylicum                            [AE001437*]
 10 Gtcc     9  Kctt    17 @Hgtg     7  Qttg    25  Kttt     6  Ltag    18  Ggcc    8  Gtcc ->  B6-1-4-1-2-1 Clostridium acetobutylicum                            [AE007764*]
  4 Rtct     4  Kctt    11 @Hgtg     9  Qttg     3  Kttt    23  Ltag    19  Ggcc   11  Gtcc ->  B6-1-4-1-2-1 Clostridium tetani E88                                [AE015944*]
  4 Rtct     4  Kctt    11 @Hgtg     9  Qttg     3  Kttt    23  Ltag    19  Ggcc   11  Gtcc ->  B6-1-4-1-2-1 Clostridium tetani E88                                [AE015927*]
  6 Gtcc    38  Rtct     7 @Hgtg     8  Qttg    10  Kttt    13  Ltag    26  Ggcc    6  Gtcc ->  B6-1-4-1-2-1 Clostridium perfringens str. 13                       [AP003193*]
  6 Gtcc    38  Rtct     7 @Hgtg     8  Qttg    10  Kttt    13  Ltag    26  Ggcc    6  Gtcc ->  B6-1-4-1-2-1 Clostridium perfringens                               [BA000016*]
  9 Gtcc     9  Rtct    16 @Hgtg     7  Qttg    25  Kttt     6  Ltag    18  Ggcc    8  Gtcc ->  B6-1-4-1-2-1 Clostridium acetobutylicum                            [AE007764*]
  9 Gtcc     9  Rtct    16 @Hgtg     7  Qttg    25  Kttt     6  Ltag    18  Ggcc    8  Gtcc ->  B6-1-4-1-2-1 Clostridium acetobutylicum                            [AE001437*]
  2 Fgaa    98  Wcca    18 @Hgtg     6  Qttg    -1  Lcaa ---    ---- ---    ---- ---    ---- --- B6-1-2-4-2   Streptococcus agalactiae                              [AF302130]
 11 Ygta    34  Wcca    18 @Hgtg     6  Qttg     0  Lcaa ---    ---- ---    ---- ---    ---- --- B6-1-2-4-2   Streptococcus agalactiae                              [AF302131]
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12	Ygta	6	Wcca	13	@Hgtg	16	Qttg	14	Lcaa	82	~?CDS	---	----	---	----	---	B6-1-2-4-2	Streptococcus mutans UA159	[AE014870]
11	Ygta	6	Wcca	14	@Hgtg	6	Qttg	10	Lcaa	309	SAG0	---	----	---	----	---	B6-1-2-4-2	Streptococcus agalactiae 2603V/R	[AE014202]
11	Ygta	6	Wcca	14	@Hgtg	6	Qttg	10	Lcaa	410	SAG0	---	----	---	----	---	B6-1-2-4-2	Streptococcus agalactiae 2603V/R	[AE014195]
11	Ygta	6	Wcca	14	@Hgtg	6	Qttg	10	Lcaa	410	SAG0	####	SAG0	403	16S	->	B6-1-2-4-2	Streptococcus agalactiae	[AE009948]
11	Ygta	6	Wcca	14	@Hgtg	6	Qttg	10	Lcaa	309	SAG0	####	yfiA	329	16S	->	B6-1-2-4-2	Streptococcus agalactiae	[AE009948]
12	Ygta	6	Wcca	13	@Hgtg	16	Qttg	14	Lcaa	82	~SMU.	####	SMU.	104	~Scga	->	B6-1-2-4-2	Streptococcus mutans UA159	[AE014133]
12	Ygta	4	Wcca	14	@Hgtg	10	Qttg	9	Lcaa	106	SP20	---	----	---	----	---	B6-1-2-4-2	Streptococcus pneumoniae TIGR4	[AE007495*]
12	Ygta	4	Wcca	14	@Hgtg	10	Qttg	9	Lcaa	106	SP20	####	SP20	93	Ettc	->	B6-1-2-4-2	Streptococcus pneumoniae	[AE005672*]
19	Ygta	6	Wcca	11	@Hgtg	8	Qttg	19	Lcaa	1767	SPs0	####	SPs0	1096	16S	->	B6-1-2-4-2	Streptococcus pyogenes SSI-1	[AP005141]
19	Ygta	6	Wcca	11	@Hgtg	8	Qttg	19	Lcaa	1767	SPs0	####	SPs0	1096	16S	->	B6-1-2-4-2	Streptococcus pyogenes SSI-1	[BA000034]
19	Ygta	6	Wcca	11	@Hgtg	9	Qttg	19	Lcaa	259	SPy0	---	----	---	----	---	B6-1-2-4-2	Streptococcus pyogenes M1 GAS	[AE006479]
19	Ygta	6	Wcca	11	@Hgtg	9	Qttg	19	Lcaa	259	SPy0	####	oppF	1089	16S	->	B6-1-2-4-2	Streptococcus pyogenes	[AE004092]
19	Ygta	6	Wcca	11	@Hgtg	8	Qttg	19	Lcaa	259	SpyM	---	----	---	----	---	B6-1-2-4-2	Streptococcus pyogenes MGAS315	[AE014137]
19	Ygta	6	Wcca	11	@Hgtg	8	Qttg	19	Lcaa	259	SpyM	####	oppF	1096	16S	->	B6-1-2-4-2	Streptococcus pyogenes MGAS315	[AE014074]
11	Ygta	6	Wcca	14	@Hgtg	6	Qttg	10	Lcaa	413	gbs0	---	----	---	----	---	B6-1-2-4-2	Streptococcus agalactiae NEM316	[AL766843]
11	Ygta	6	Wcca	14	@Hgtg	6	Qttg	10	Lcaa	141	gbs0	####	gbs0	369	16S	->	B6-1-2-4-2	Streptococcus agalactiae NEM316	[AL732656]
11	Ygta	6	Wcca	14	@Hgtg	6	Qttg	10	Lcaa	141	gbs0	####	gbs0	369	16S	->	B6-1-2-4-2	Streptococcus agalactiae NEM316	[AL766844]
11	Ygta	6	Wcca	14	@Hgtg	6	Qttg	10	Lcaa	413	gbs0	####	gbs0	445	16S	->	B6-1-2-4-2	Streptococcus agalactiae NEM316	[AL732656]
12	Ygta	4	Wcca	14	@Hgtg	10	Qttg	9	Lcaa	106	spr1	---	----	---	----	---	B6-1-2-4-2	Streptococcus pneumoniae R6	[AE008551*]
12	Ygta	4	Wcca	14	@Hgtg	10	Qttg	9	Lcaa	106	spr1	####	comX	93	Ettc	->	B6-1-2-4-2	Streptococcus pneumoniae	[AE007317*]
---	----	---	----	---	@Hgtg	23	Qttg	28	Ltag	---	----	---	----	---	----	---	B6-1-3-1-1-1	Acholeplasma laidlawii	[X61067]
---	ackA	46	Sgga	443	@Hgtg	88	Qttg	53	Ltag	23	Wcca	431	?CDS	####	pepP	->	B6-1-3-1-1-2	Onion yellows phytoplasma OY-M	[AP006628]
---	ackA	46	Sgga	443	@Hgtg	88	Qttg	53	Ltag	23	Wcca	431	PAM1	####	pepP	->	B6-1-3-1-1-2	Onion yellows phytoplasma	[AP006628]
---	?CDS	146	Ptgg	22	@Hgtg	20	Rtcg	44	~?CDS	####	~?CDS	25	Qttg	85	Mcat	->	B12-5-1-2-1	Helicobacter hepaticus ATCC 51449	[AE017144]
---	HH003	146	Ptgg	22	@Hgtg	20	Rtcg	44	~HH003	####	~HH02	25	Qttg	85	Mcat	->	B12-5-1-2-1	Helicobacter hepaticus ATCC 51449	[AE017125]
---	HP041	-230	Ptgg	68	@Hgtg	60	Rtcg	25	Rtct	29	HP04	---	----	---	----	---	B12-5-1-2-1	Helicobacter pylori 26695	[AE000557]
53393	HP041	-230	Ptgg	68	@Hgtg	60	Rtcg	25	Rtct	29	HP04	####	~HP04	648	23S	->	B12-5-1-2-1	Helicobacter pylori 26695	[AE000511]
34566	Cj166	42	Ptgg	24	@Hgtg	3	Rtcg	14	Rtct	4	Ltag	174	Cj16	####	~ribD	->	B12-5-1-1-1	Campylobacter jejuni	[AL111168*]
34678	Cj166	42	Ptgg	24	@Hgtg	3	Rtcg	14	Rtct	4	Ltag	174	Cj16	####	~ribD	->	B12-5-1-1-1	Campylobacter jejuni subsp. jejuni NCTC 11168	[AL139079*]
88	Gtcc	14	Rtct	14	@Hgtg	8	Rtcg	73	TM019	---	----	---	----	---	----	---	B3-1-1-1	Thermotoga maritima	[AE001704*]
88	Gtcc	14	Rtct	14	@Hgtg	8	Rtcg	73	TM019	####	~TM01	48	~5S	37	~23S	->	B3-1-1-1	Thermotoga maritima	[AE000512*]
---	----	---	~Fgaa	136	@Hgtg	14	Rtcg	80	TP063	---	----	---	----	---	----	---	B10-1-2-2	Treponema pallidum subsp. pallidum str. Nichols	[AE001239*]
1E+05	~TP063	-30	~Fgaa	136	@Hgtg	14	Rtcg	80	TP063	####	~TP05	159	Mcat	69	Dgtc	->	B10-1-2-2	Treponema pallidum	[AE000520*]
---	----	---	~?CDS	143	@Hgtg	32	Rtcg	106	rpsD	---	----	---	----	---	----	---	B10-1-2-2	Treponema denticola ATCC 35405	[AE017252*]

Table 3.(2) Candidates of characteristic tRNA-gene tandems whose headings begin with H. (for His)

Heading						Class code	bacterial name
@Hatg	Hatg					B11-2-1-1-2	Chlamydophila pneumoniae
@Hgtg	16S	Atgc	23S			A1-4-1-1-1	Methanocaldococcus jannaschii
@Hgtg	Ettc					B9-1-1-1-1	Chlorobium tepidum
@Hgtg	Ggcc					B10-1-2-1	Borrelia burgdorferi
@Hgtg	Gtcc					B6-1-1	Bacillus, Listeria
@Hgtg	Gtcc	Igat				B6-1-1	Bacillus, Listeria
@Hgtg	Gtcc	Igat	Ngtt			B6-1-1	Bacillus, Listeria
@Hgtg	Gtcc	Igat	Ngtt	Sgct		B6-1-1	Bacillus, Listeria
@Hgtg	Gtcc	Igat	Ngtt	Sgct	Ettc	B6-1-1	Bacillus, Listeria
@Hgtg	Gtcc	Ngtt				B6-1-1-4-1	Staphylococcus
@Hgtg	Gtcc	Ngtt	Ettc			B6-1-1-4-1	Staphylococcus
@Hgtg	Gtcc	Ngtt	Ettc	Sgga		B6-1-1-4-1	Staphylococcus
@Hgtg	Hgtg					B12-2-1-1-1	Chromobacterium violaceum
@Hgtg	Hgtg	Hgtg				B12-2-1-1-1	Chromobacterium violaceum
@Hgtg	Kctt					B7, B12	Fusobacterium, Xanthomonas, Xylella
@Hgtg	Kctt	Ltag				B7, B12	Fusobacterium, Xanthomonas
@Hgtg	Kttt	Ltag	Qttg			B7-1-1-1	Fusobacterium nucleatum
@Hgtg	Lcag					B12-3	Aeromonas, Blochmannia, Escherichia, Photorhabdus,Pseudomonas, Salmonella,Shigella , Yersinia
@Hgtg	Lcag	Ptgg				B12-3	Aeromonas, Blochmannia, Escherichia, Photorhabdus, Salmonella,Shigella , Yersinia
@Hgtg	Lcag	Ptgg	Lcag			B12-3-4-1-4	Escherichia coli
@Hgtg	Lcag	Ptgg	Lcag	Ptgg		B12-3-4-1-4	Escherichia coli
@Hgtg	Ltag					B4, B6,B12	Deinococcus, Thermus;Bacillus ; Geobacter, Pseudomonas
@Hgtg	Ltag	Ggcc				B6-1-1-1-1	Bacillus
@Hgtg	Ltag	Ggcc	Ltaa			B6-1-1-1-1	Bacillus
@Hgtg	Ltag	Ggcc	Ltaa	Racg		B6-1-1-1-1	Bacillus
@Hgtg	Ltag	Ggcc	Ltaa	Racg	Ptgg	B6-1-1-1-1	Bacillus
@Hgtg	Ltag	Hgtg				B12-3-8-1-1	Pseudomonas aeruginosa
@Hgtg	Mcat					B6-1-1-1-3	Oceanobacillus iheyensis
@Hgtg	Mcat	Stga				B6-1-1-1-3	Oceanobacillus iheyensis
@Hgtg	Mcat	Stga	Fgaa			B6-1-1-1-3	Oceanobacillus iheyensis
@Hgtg	Ptgg					B11, B12	Buchnera, Haemophilus,Photobacterium,Shewanella,Vibrio
@Hgtg	Ptgg	16S				B12-3-6-1-1	Haemophilus ducreyi
@Hgtg	Ptgg	16S	Ettc			B12-3-6-1-1	Haemophilus ducreyi
@Hgtg	Ptgg	16S	Ettc	23S		B12-3-6-1-1	Haemophilus ducreyi
@Hgtg	Ptgg	16S	Ettc	23S	5S	B12-3-6-1-1	Haemophilus ducreyi
@Hgtg	Ptgg	Hgtg				B12-3-10-1-4	Vibrio
@Hgtg	Ptgg	Hgtg	Ptgg			B12-3-10-1-4	Vibrio
@Hgtg	Ptgg	Ptgg				B11, B12	Photobacterium, Shewanella
@Hgtg	Ptgg	Ptgg	Hgtg			B11-2-1-1-2	Photobacterium phosphoreum
@Hgtg	Ptgg	Ptgg	Hgtg	Ptgg		B11-2-1-1-2	Photobacterium phosphoreum
@Hgtg	Qttg					B6-1	Enterococcus, Lactobacillu, Staphylococcus

@Hgtg	Qttg	Cgca				B6-1	Enterococcus, Lactobacillu, Staphylococcus
@Hgtg	Qttg	Cgca	Gtcc			B6-1-1-4-1	Staphylococcus
@Hgtg	Qttg	Cgca	Gtcc	Gtcc		B6-1-1-4-1	Staphylococcus
@Hgtg	Qttg	Cgca	Gtcc	Gtcc	Gtcc	B6-1-1-4-1	Staphylococcus epidermidis
@Hgtg	Qttg	Cgca	Gtcc	Gtcc	Gtcc	B6-1-1-4-1	Staphylococcus epidermidis
@Hgtg	Qttg	Cgca	Gtcc	Gtcc	Lcaa	B6-1-1-4-1	Staphylococcus aureus
@Hgtg	Qttg	Cgca	Lcaa			B6-1-2	Enterococcus, Lactobacillus
@Hgtg	Qttg	Ggcc				B6-1-1	Bacillus, Listeria, Oceanobacillus
@Hgtg	Qttg	Ggcc	Cgca			B6-1-1	Bacillus, Listeria, Oceanobacillus
@Hgtg	Qttg	Ggcc	Cgca	Lcaa		B6-1-1	Bacillus, Listeria, Oceanobacillus
@Hgtg	Qttg	Ggcc	Cgca	Ltaa	Lcaa	B6-1-1-1-1	Bacillus subtilis
@Hgtg	Qttg	Ggcc	Cgca	Ltaa	Racg	B6-1-1-1-1	Bacillus halodurans
@Hgtg	Qttg	Ggcc	Racg			B6-1-1-1-1	Bacillus halodurans
@Hgtg	Qttg	Ggcc	Racg	Gtcc		B6-1-1-1-1	Bacillus halodurans
@Hgtg	Qttg	Kttt				B6-1-4-1	Clostridium, Thermoanaerobacter
@Hgtg	Qttg	Kttt	Kttt			B6-1-4-1	Clostridium, Thermoanaerobacter
@Hgtg	Qttg	Kttt	Kttt	Ltag		B6-1-4-1	Clostridium, Thermoanaerobacter
@Hgtg	Qttg	Kttt	Kttt	Ltag	Ggcc	B6-1-4-1	Clostridium, Thermoanaerobacter
@Hgtg	Qttg	Kttt	Ltag			B6-1-4-1-2-1	Clostridium
@Hgtg	Qttg	Kttt	Ltag	Ggcc		B6-1-4-1-2-1	Clostridium
@Hgtg	Qttg	Kttt	Ltag	Ggcc	Gtcc	B6-1-4-1-2-1	Clostridium
@Hgtg	Qttg	Lcaa				B6-1-2-4-2	Streptococcus
@Hgtg	Qttg	Ltag				B6-1-3-1-1	Acholeplasma,Phytoplasma
@Hgtg	Qttg	Ltag	Wcca			B6-1-3-1-1-2	Onion yellows phytoplasma
@Hgtg	Rtcg					B3,B10,B12	Tehrmotoga, Treponema, Campylobacter, Helicobacter
@Hgtg	Rtcg	Rtct				B12-5-1-2-1	Campylobacter, Helicobacter
@Hgtg	Rtcg	Rtct	Ltag			B12-5-1-1-1	Campylobacter jejuni

Table 4. Examples of putative genes newly detected

Accession No.	tRNA and/or rRNA gene tandem
AB013377	AStga(1300–1388gtta)Mcat(1574–1646acca)YHQttg(1844–1914acca)GR
AB031213	NSEVDLLRPtgg(2595–2667acca)GI Σ Λ Φ
AB031215	GRacg(9668–9740gcca)
AB071783	Σ IAtgc(320–394acca) Λ [Cf. // A(455–531)//]
AE000052	CPMIcat(6625–6696)SMDF
AE000129	Atgc(5476–5547aaca), Dgtc(8906–8986gcca) [Cf. (A or B)tgc(5476–5551), (D or V)gtc(8906–8990)]
AE000406	complement Atgc(tggt5721–5792)I [Cf. //(A or B)tgc//]
AE000453	Dgtc(3233–3305gcca)W [Cf. //(D or OTHER)gtc//)]
AE001652	G(1733–1802)E(4945–5019)K(5045–5117) [Cf. complement G(1733–1803),and complement EK]
AE006473	Σ A Λ Φ(9535–9649)VDKLTGLRP
AE006474	Σ A Λ Φ(5002–5116)VGIESMFGIS
AE006479	Σ A Λ Φ(5551–5661)VGIESMFYWHQL
AE006496	Σ A Λ Φ(5937–6051)NR
AE006592	complement EITLKDV Φ(6697–6891) Λ A Σ
AE006615	complement, RN Φ(932–1046) Λ A Σ
AE007319	E Σ A Λ Φ(5764–5878)N, [Cf. // Φ(5755–5902)N(5883–// overlap(Φ & N)]]
AE008706	Igat(10816–10888)Atgc(11002–11073) [Cf. I(10826–10899)[A or B](11012–11084)]
AE014136	Σ A Λ Φ(22026–22140)VDKLTGLRP, Σ A Λ Φ(28028–28143)VDKLTGLRPMMSMFGIS,
AE014137	Σ A Λ Φ(33169–33283)VGIESMFYWHQL
AE014141	Σ A Λ Φ(5613–5717)NR
AE014162	complement EITLKDV Φ(22529–22743) Λ A Σ
AE014168	complement, RN Φ(933–1047) Λ A Σ
AE014192	Φ(10–124)VDKLTGLRP Σ A Λ Φ(5841–5955)VDKLTGLRPMMSMFGIS
AE014195	Σ A Λ Φ(178111–7925)VDKLTIE
AE014202	Σ A Λ Φ(17813–17927)VGIESMFYWHQL
AE014207	E Σ A Λ Φ(9537–9654)N [Cf. // Φ(9519–9679)N(9660–// overlap(Φ & N)]
AE014210	Σ A Λ Φ(1048810602)VGIE
AE015714	complement Kttt(869–1049) long D-loop (tgccctagctttataaaaaaag:22 n) Not a tRNA or ctttataaaaaaag to be deleted
AE016998	Σ Λ Φ(155848–155961)NTEVYQ
AE016999	Σ Λ Φ(207456–207570)NSEVMDFTYWHQGCL
AE017000	Σ Λ Φ(114882–1114995)VYQKLOGLRPASSMDFTWINE
AE017013	complement ESNIGKTFDMSMMAPLGLHTV Φ(269750–269861) Λ Σ
AE017205	complement N Φ Λ (146140–146905) Σ [Cf. // Φ(–145978) Λ (145965–149015)// overlap(Φ & Λ)]]
AE017205	complement N Φ Λ (152807–155682) Σ [Cf. // Φ(–152645) Λ (152632–155682)// overlap(Φ & Λ)]]
AE017205	complement N Φ Λ (167256–170131) Σ [Cf. // Φ(–167094) Λ (167081–170131)// overlap(Φ & Λ)]]
AE017280	complement E(GAA)(t32876–32946) S(AGC)(tggc32957–33043)N((AAC)tggc33055–33125)I(AUC)(tggt33137–33209) [Cf. E(32875–32946)S(32953–33043)N(33051–33125)I(33133–33209)]
AE017280	complement G(GGA)(a33221–33290)K(AAA)(tggt33308–33379)T(ACA)(tggt33394–33465)F(uuc)(tggt33484–33555)

[Cf. G(33220-33290)K(33304-33379)T(33390-33465)F(33480-33555)D(33568-33643)]

AE017280 complement D(GAC)(tggc33572-33643)M(AUG)(tggt33649-33721)S(UCA)(tgga33753-33841)M(AUG)(tgga33863-33935)

[Cf. M(33645-33721)S(33749-33841)M(33859-33935)]

AE017280 complement M(AUG)(tggt33944-34016)A(GCA)(t34038-34109)P(CCA)(t34126-34198)R(CGU)(c34210-34282)

[Cf. M(33940-34016)A(34037-34109))P(34125-34198)R(34209-34282)

AE017280 complement L(UUA)(tggt34290-34374)G(GGC)(tgga34395-34465)L(CUA)(t34496-34575)H(CAC)(tggg34602-34673)

[Cf. L(34286-34374)G(34391-34465)L(34495-34575)]H(34598-34673)]

AE017280 complement T(ACA)(tggt34687-34758)V(GUA)(tggt34767-34838)5(34845-34959)Λ(35061-37969)Σ(38144-39652)

[Cf. T(34683-34758)V(34763-34838)Σ(34846-34956)Λ35061-37969)Φ(38145-39652)]

AE017281 complement F(TTC)(t300444-300514)D(GAC)(tggc300561-300632)E(GAA)(t300655-300725)K(AAA)(tggt300743-300814)

[Cf. F(300443-300515)D(300557-300632)E(300654-300725)K(300739-300814)]

AF074828 A(52-123acca)Igat(136-207acca) [Cf. A(51-127)I(136-192: 57 n) I: A-arm pair 5(caccc)/4(ggtg))]

AF074829 A(52-123acca)Igat(136-207acca) [Cf. A(51-127)I(136-192:57 n) I: A-arm pair 5(cacbc)/4(ggtg)]

AF074830 A(52-123acca)Igat(136-207acca) [Cf. A(51-127)I(136-192, 57n) I: A-arm pair 5(caccc)/4(ggtg)]

AF074831 A(52-123acca)Igat(136-207acca) [Cf. A(51-127)I(136-192, 57 n) I: A-arm pair 5(caccc)/4(ggtg)]

AF074832 A(52-123acca)Igat(136-207acca) [Cf. A(51-127)I(136-192, 57 n) I: A-arm pair 5(caccc)/4(ggtg)]

AF074833 A(52-123acca)Igat(136-207acca) [Cf. A(51-127)I(136-192, 57 n) I: A-arm pair 5(caccc)/4(ggtg)]

AF074834 A(52-123acca)Igat(136-207acca) [Cf. A(51-127)I(136-192, 57 n) I: A-arm pair 5(caccc)/4(ggtg)]

AF074835 A(52-123acca)Igat(136-207acca) [Cf. A(51-127)I(136-192, 57 n) I: A-arm pair 5(caccc)/4(ggtg)]

AF074836 A(52-123acca)Igat(136-207acca) [Cf. A(51-127)I(136-192, 57 n) I: A-arm pair 5(caccc)/4(ggtg)]

AF074837 A(52-123acca)Igat(136-207acca) [Cf. A(51-127)I(136-192, 57 n) I: A-arm pair 5(caccc)/4(ggtg)]

AF074838 A(52-123acca)Igat(135-206acca) [Cf. A(51-127)I(135-191, 57 n) I: A-arm pair 5(caccc)/4(ggtg)]

AF074839 A(52-123acca)Igat(136-207acca) [Cf. A(51-127)I(136-192, 57 n) I: A-arm pair 5(caccc)/4(ggtg)]

AF074840 A(52-123acca)Igat(136-206acca) [Cf. A(51-127)I(136-192, 57 n) I: with A-arm pair 5(caccc)/4(ggtg)]

AF074841 A(52-123acca)Igat(136-207acca) [Cf. A(51-127)I(136-192, 57 n) I: with A-arm pair 5(caccc)/4(ggtg)]

AF130462 Ygta(431-512ac)TTMcat(1573-1642accg)W

AF223396 ΣIgat(252-323acca) A Λ Igat: A-arm pair 4(ccgc)/5(ccgtg)

AF223397 ΣIgat(252-323acca) A Λ Igat: A-arm pair 4(ccgc)/5(ccgtg)

AF223398 ΣIgat(252-323acca) A Λ Igat: A-arm pair 4(ccgc)/5(ccgtg)

AF223399 ΣIgat(252-323acca) Atgg Λ Igat: A-arm pair 4(ccgc)/5(ccgtg) Atgg(anticodon)

AF268429 ΣAtgc(98-174acca)Igat(200-273acca) Λ [Cf. //A(98-278, 181 n)I(200-// overlap (Atgc and Igat)]

AF302130 ΛΦ(562-676)Gtcc(757-827)Igat(865-937)Ettc(949-1019)Stag(1034-1125)Lcaa(1136-1209)

[Cf. ΛΦ(489-740)G(757-838)D(896-941)E(949-1219)S(1034-1114)M(1137-1210)]

AF302130 Fgaa(1213-1284)Ygta(1297-1376)Wcca(1384-1453)Hgtg(1470-1540)Qttg(1548-1618)Lcaa(1621->1680)

[Cf. F(1213-1284)W(1383-1451)H(1470-1451)Q(1548-1622)L(1622->1680)]

AF302131 ΛΦ(563-677)Kttt(833-904)Ltag(914-995)Ttgt(1006-1077)Igat(1108-1181)Ettc(1193-1263)

[Cf. ΛΦ(490-741)V(837-894:58n)L(961-1003: 43n)K(1012-1068:57n)D(1140-1185: 46 n)E(1193-1273)

AF302131 Mcat(1381-1455)Ygta(1542-1613)Hgtg(1715-1785) Mcat A-arm pair 5(tgggg)/6(acccga); Mcat,Ygta and Hgtg: E-loop 4n

[Cf. MY(1542-1593:52 n)H(1716-1786)]

AF312492 Σ(<1-18)Igat(342-414acca)Atgc(540-611acca) [Cf. I(166-242)A(568-643)]

AF312493 Igat(319-391acca)Atgc(517-588acca) [Cf. I(166-242)A(568-643)]

AF312494 Igat(319-392acca)Atgc(517-588acca) Igat: A-arm pair 6(cgcgca)/5(gcgtg) [Cf. I(166-242)A(568-643)]

AF312495 Σ(<1-93)?(447-512) Atgc(875-945)
AF338860 Igat(167-239acca)AΛ [Cf. //I(157-243)//]
AF338862 Igat(164-237acca)AΛ [Cf. //I(155-241)//]
AF338864 Igat(167-239acca)AΛ [Cf. //I(157-243)//]
AF375994 ΣIgat(1687-1760acca) Atgc(1785-1856acca) Λ [Cf. //I(1687-1762)A(1744-1858:115 n)//]
AF397709 ΣIgat Atgg Λ Atgg (anticodon?)
AF397714 ΣIgat Atcc Λ Atcc(anticodon?)
AF440225 ΣIgat A Igat:A-arm pair 6(cgccgc)/5(scgtg)
AF510361 ΣIgat Atgt Λ Atgt(anticodon?)
AJ012700 ΣIgat A Λ [Cf. //Icca//]
AJ012701 ΣIgat Atgc Λ [Cf. //IataAgca//]
AJ012702 ΣIgat Atgc Λ [Cf. //IataAgca//]
AJ012703 ΣIgat Atgc Λ [Cf. //IataAgca//]
AJ012704 ΣAtgcIΛ [Cf. //Acat//]
AJ012705 ΣIgat Atgc Λ [Cf. //IataAgca//]
AJ012706 ΣIgat Atgc Λ [Cf. //IataAgca//]
AJ012707 ΣIgat Atgc Λ [Cf. //IataAgca//]
AJ248283 complement G(GCA)(tggt149923-149996)F(UUC)(aggc15008-15080) [Cf. complement G(TCC)F(UCU)]
AJ248285 complement M(AUG)N(AAC) [Cf. complement M(TTA)N(TTA)]
AJ293101 Igat(AUC)A [Cf. I(AUA)A]
AP002547 Ettc(183943-184016a)Kttt(184043-184114a) [Cf. complement E(183943-184017)K(184043-184115)]
AP003363 complement MD(GAC)F D(GAC): A-arm pair 5(cctgc)/6(ggcagg) [Cf. M?D]
AP003604 complement ARVG(GGA)TMLKLLPLQQNFRY?X G(GGA) :E-loop 4 n; [Cf. //QQNFRYS(TCG)X//]
AP005141 ΣAΛΦ(22026-22140)VDKLTGLRPMMSMFGIS, ΣAΛΦ(79005-79119)VGIESMFYWHQL, ΣAΛΦ(255060-255174)NR
AP005142 ΣAΛΦ(230646-230760)VDKLTIE
AP005146 complement NRΦ(65033-65147)ΛΣ
AP005274 Igat(14851-14923acca)Atgc(14939-15007tcca), Atgc(23500-23568tcca)Igat(23903-23975acca)Atgc(23991-24059tcca)
[Cf. I(GAT)A(TGC), A(TGC)I(GAT)A(TGC)]
AP005274 Lcag(49705-49787acca), Stga(221750-221833gca), Sgct(233409-233496g)Racg(233527-233598acaa)
[Cf. L(CAG), S(TGA), S(GCT)R(ACG)]
AP005274 Scga(244294-244380acca), complement S(UCC)(ttgc256226-256309), complement P(CCG)(ttgc292470-295442)
[Cf. S(CGA), complement S(GGA), complement P(CGG)
AP005274 Tcgt(329629-329700tcca) [Cf. T(CGT)]
AP005275 Ygta(155249-155330aaca)Tggt(155954-156020)Tggt(156279-156351)Mcat(156390-156460accg)Wcca(1565558-156629gcaa)
[Cf. Y(GTA)T(GGT)T(GGT)M(CAT)W(CCA)]
AP005278 Qctg(32543-32613a)Ectc(32653-32724a)Qctg(32792-32862a)Ectc(32901-32872a), Ectc(34523-34598acaa),
[Cf. Q(CTG)E(CTC)Q(CTG)E(CTG), E(CTC)]
AP005278 complement L(TTG)(tggt80519-80591), complement P(CCC)(ttgt187177-182249),
[Cf. comolenent L(CAA), complenent P(GGG)]
AP005278 Lgag(276372-276456ac)Lgag(276544-276628acaa) [Cf. L(GAG)L(GAG)]
AP005279 complemet G(GGC)(ttga104527-104598)V(GUC)(tggt104636-104706)C(UGG)(aggt104721-104787)
[Cf. G(GCC)V(GAC)C(GCA)G(GCC)]
AP005279 complement G(GGC)(acca104833-104901)V(GUC)(tggt104939-105059)G(GGC)(a105044-105115),

[Cf. complement G(GCC)V(GAC)G(GCC)]
AP005279 V(GUG)(105463-105520acca) [Cf. V(CAC)]
AY190662 ΣIgat (235-307acca)Atgc(341-413acca) Λ [Cf. //I(255-329)A(359-434)//]
AY224382 ΣΛΦNTEttc(5985-6055acca) VYQKGA [Cf. //Q(CAA)(5985-6059)//]
AY277896 ΣIgat (524-596acca)Atgc(936-1007acca) Λ [Cf. //I(AUU)//]
AY531069 Igat(67-139acca)Atgc(185-256)Vtac(274-356acca) [Cf. //I(AUC)A(GCA)V(GUA)//]
AY591324 ΣIgat (144-216acca)Atgc(275-346acca) Λ [Cf. ΣA(161-217: 57 n)I(275-347) Λ] Inversion (I & A)
AY591325 ΣIgat (140-212acca)Atgc(271-343acca) Λ [Cf. ΣA(157-213: 57 n)I(271-343) Λ] Inversion (I & A)
AY591326 ΣIgat (132-204acca)Atgc(263-334acca) Λ [Cf. ΣA(149-205: 57 n)I(263-335) Λ] Inversion (I & A)
AY591327 ΣIgat (140-212acca)Atgc(271-342acca) Λ [Cf. ΣA(571-213: 57 n)I(271-343) Λ] Inversion (I & A)
AY591328 ΣIgat (140-212acca)Atgc(271-343acca) Λ [Cf. ΣA(571-213: 57 n)I(271-344) Λ] Inversion (I & A)
BX248585 Kctt(206786-206853acca), complement S(206999-207082) [Cf. complement K(206786-206853)S]
BX248585 Scga(255174--255257acca), complement S(a255635-255722), Ngtt(255897-255969g)]
[Cf. Complement Scga(255174-255261) S(255635-255722), Ngtt(255896-255968)]
BX248586 Vtac(44868-44939a)Kttt(44984-44056) [Cf. complement V(44868-44940)K(44984-44056)]
CR378668 complement G(GGA)(tgga182119-182189)T(ACA)(tggt-182203-182283) [Cf. complement G(TCC)T(TGT)]
CR378674 complement T(ACC)(tggt597225-59801)G(GCA)(tgga59818-59888) T(ACC) A-arm pair 6(cacccc)/5(gggtg)
[Cf. complement T(CAC)G(CAG)]
D88802 Dgtc(26423-26495gcca) [Cf. D(26423-26989: 567 n)]
J01713 MLQQttg(487-557gcca)Mcat(577-647acca)QQctg(813-883gcca) [Cf. //Q(CCU)M(CUA)QQ(AAU)]
K01983 ΣIgat (324-396a)A [Cf. //I(UCA)//]
L00194 ΣIgat (552-626acca)Atgc(685-755acca) Λ [Cf. ΣIgccAgca Λ]
L08236 ΛΦMcat(265-337acca)Dgtc(402-474) [Cf. ΛΦM(ACC)D(AAC)]
L26364 ΣIgat (386-458acca)A Λ [Cf. ΣI(CUG)A Λ]
L28159 ΣIgatAtgcΛ Igat: A-arm pair 5(caccc)/4(ggtg)
L28159 ΣIgatAtgcΛ Igat: A-arm pair 5(caccc)/4(ggtg)
L28154 ΣIA(321-391acca) Λ [Cf. ΣIA(324-399) Λ]
L28156 ΣIgatAtgcΛ [Cf. ΣIataAgcaΛ]
L28157 ΣIgatAtgcΛ [Cf. ΣItgaAcaaΛ]
L28159 ΣIgatAtgcΛ Igat: A-arm pair 5(caccc)/4(ggtg)
L28160 ΣIgatAtgcΛ Igat: A-arm pair 5(caccc)/4(ggtg)
L28161 ΣIgatAtgcΛ Igat: A-arm pair 5(caccc)/4(ggtg)
L28162 ΣIgatAtgcΛ Igat: A-arm pair 5(caccc)/4(ggtg)
L35100 ΣIgatAtgcΛ [Cf. ΣI(ATT)A(TTG)Λ]
L35101 ΣIgatAtgcΛ [Cf. GenBank ΣI(AUU)A(AGCU)Λ; EMBL ΣI(UUA)A(GCU)Λ]
L35102 ΣIAtgcΛ [Cf. ΣI(ATC)A(TTG)Λ]
L35103 ΣIgatAΛ [Cf. ΣI(UUA)AΛ]
L36472 Λ(5208-8130) [Cf. Λ or Φ]
L42976 A Igat(77->133) [Cf. //I or A//]
M13687 complement Kttt(tggt1225-1296)VtacVtacVtacVtac [Cf. K(GAT)V(CCT)V(CCT)V(CCT)]
In early days, description of position of the anticodon for Kttt was 1-3.
M23210 Vtac(22-93acca)Ttgt(130-201acca)Kttt(243-314acca)Lcag(329-411acca)Ggcc(421-491tcca)Ltaa(510-59a)R

[Cf. V(ACG)T(UUA)K(AUU)L(AUU)G(ACG)G(ACG)L(AUU)R
M65195 Gtcc(22-82a)P [Cf. G(GTT)P]
M91385 Wtca(1046-1117gcca)WS [Cf. W(AAA)WS]
U15182 Ettc(37225-37296)Egtc(37328-37400)Fgaa(37342-37509) [Cf. D(ATC)(37219-372919)F(GGC)(37596-37845)
U60278 Σ Igat (71-143acca)A [Cf. //I(UCA)//]
U60279 Σ Igat (71-143acca)A [Cf. //I(UCA)//]
U60280 Σ Igat (71-143acca)A [Cf. //I(UCA)//]
U60281 Σ Igat (71-143acca)A [Cf. //I(UCA)//]
X04108 Σ ?? [Cf. Σ (<1-42) A(GCA)(144-219)L(CUA)(228-304)]
X06727 Kttt(94-165acca)Ltag(172-251-acca) [Cf. K(UUU)L(AUG)]

tRNA and/or rRNA genes that we discovered or whose description we modified
[Cf. Original relevant data]
Note : Λ : Large subunit (23S) rRNA, Σ : Small subunit rRNA (16S) rRNA, and Φ : 5S rRNA

Accesion Number index

Accession No(s).	Bacterial name
[AB013377]to [AB031215]	*Bacillus halodurans C-125*
[AB071783]	*Saprospira sp. SS91-40*
[AE000052]	*Mycoplasma pneumoniae M129*
[AE000129] to[AE000453]	*Escherichia coli K12 MG1655*
[AE001652]	*Chlamydophila pneumoniae CWL029*
[AE006473] to [AE006615]	*Streptococcus pyogenes M1 GAS*
[AE007319]	*Streptococcus pneumoniae TIGR4*
[AE008706]	*Salmonella thphimurium LT2*
[AE014136] to [AE014168]	*Streptcoccus pytogenes MGAS315*
[AE014192]to [AE014210]	*Streptcoccus agalactiae 2603V/R*
[AE015714]	*Shewanella oneidensis MR-1*
[AE016998] to [AE017013]	*Bacillus cereus ATCC 14579*
[AE017205]	*Lactobacillus johnsonii NCC533*
[AE017280] to[AE017281]	*Bacillus cereus ATCC 10987*
[AF074828]	*Campylobacter jejuni NCTC11168*
[AF074829]	*Campylobacter jejuni NCTC11392*
[AF074830]	*Campylobacter jejuni KJ7*
[AF074831]	*Campylobacter jejuni JEO2677(3-1 a)*
[AF074832]	*Campylobacter jejuni JEO2677(3-1 a)*
[AF074833]	*Campylobacter jejuni JEO2693(125883/87)*
[AF074834]	*Campylobacter jejuni JEO2759(16-1 b)*
[AF074835]	*Campylobacter jejuni JEO2762(22-5 b)*
[AF074836]	*Campylobacter jejuni NCTC11951 T*
[AF074837]	*Campylobacter coli NCTC11366 T*
[AF074838]	*Campylobacter coli NCTC11353*
[AF074839]	*Campylobacter coli JEO2772(11-8)*
[AF074840]	*Campylobacter coli JEO2777 (783)*
[AF074841]	*Campylobacter lari CCUG29406*
[AF130462]	*Corynebacterium glutamicum ATCC 13032*
[AF223396]	*Neisseria gonorrhoeae 1245-1*
[AF223397]	*Neisseria gonorrhoeae 1199-1*
[AF223398]	*Neisseria gonorrhoeae 1021-1*
[AF223399]	*Neisseria gonorrhoeae 1231-1*
[AF268429]	*uncultured bacterium NAZ4*
[AF302130]	*Streptococcus agalactiae L41*
[AF302131]	*Streptococcus agalactiae L48*
[AF312492]	*Bartonella bacilliformis isolate Cuzco 14*
[AF312493]	*Bartonella bacilliformis isolate MONZON 269*
[AF312494]	*Bartonella bacilliformis isolate MONZON 812*

[AF312495]	*Bartonella bacilliformis isolate URBHLLY 8*
[AF338860]	*Bradyrhizobium sp. MSDJ 5493*
[AF338862]	*Bradyrhizobium sp. MSDJ 5730*
[AF338864]	*Bradyrhizobium sp. MSDJ 5726*
[AF375994]	*Candidatus Brocadia anammoxidans*
[AF397709]	*Synechococcus sp.WH 8012*
[AF397714]	*Synechococcus sp.WH 8112*
[AF440225]	*Bartonella sp.N40*
[AF510361]	*Mesorhizobium sp. vgn-4*
[AJ012700]	*Roseovarious tolerans EL-172*
[AJ012701]	*Roseovarious tolerans EL-164*
[AJ012702]	*Roseovarious tolerans EL-171*
[AJ012703]	*Roseovarious tolerans EL-222*
[AJ012704]	*Antarctobacter heliothermus EL-219*
[AJ012705]	*Rosenbacter algicola DSM 10251*
[AJ012706]	*Roseovarius denitrificans DSM 7001*
[AJ012707]	*Rosenbacter litoralis DSM 6996*
[AJ248283]	*Pyrococcus abyssi Orsay*
[AJ248285]	*Pyrococcus abyssi Orsay*
[AJ293101]	*Anabaena lemmermannii 262*
[AP002547]	*Chlamydophila pneumoniae J138*
[AP003363]	*Staphylococcus aureus substr. aures Mu 50*
[AP003604]	*Nostoc sp.PCC 7120*
[AP005141] to [AP005146]	*Streptococcus pyogenes SSI-1*
[AP005274]to [AP005279]	*Corynebacterium glutamicum ATCC 13032*
[AY190662]	*Polyangium cellulosum So9881*
[AY224382]	*Bacillus cereus BGSC 6A5*
[AY277896]	*Bartonella sp. Rt222sm*
[AY531069]	*Vibrio parahaemolytics RIMD2210856*
[AY591324] to [AY591328]	*Enterococcus faecium*
[BX248585]to [EX148586]	*Canditus Blochjmannia floridanus*
[CR378668]to [CR378674]	*Photobacterium profundum SS9*
[D88802]	*Batillis subtilis 168*
[J01713]	*Escherichia coli*
[K01983]	*Synechococcus sp. PCC 6301*
[L00194]	*Caulobacter vibrioides CB13*
[L08236]	*Bacillus subtilis 168T*
[L26364]	*Bartonella baciliformis KC584*
[L28154]	*Burkholderia cepacia*
[L28148]to [L28149]	*Pseudomanas aeruginosa*
[L28156] to [L28158]	*Burkholderia gladioli*
[L28159] to [L18162]	*Psuedmonas mendocina*
[L35100]	*Bartonella quintana Fuller*

[L35101]	*Bartonella henselae Houston*
[L35102]	*Bartonella vinsonii Baker*
[L35103]	*Bartonella elizabethae F9251*
[L36472]	*Staphylococcus aureus*
[L42976]	*Xanthomonas albilineans*
[M13687]	*Escherichia coli K12*
[M23210]	*Bacillus subtilis*
[M65195]	*Mycobacterium smegmatis*
[M91385]	*Spiroplasma citri R8A2*
[U15182]	*Mycobacterium leprae*
[U60278]	*Acinetobacter calcoaceticus ATCC 23055*
[U60279]	*Acinetobacter baumannii ATCC 19606*
[U60280]	*Acinetobacter genomosp. 3 ATCC 19004*
[U60281]	*Acinetobacter genomosp. 13 ATCC 17903*
[X04108]	*Campylobacter jejuni N941*
[X06727]	*Mycoplasma capricolum Carifornia kid(ATCC27343)*

E(GAA)VYQK of [AE016750] (*Staphylococcus*: B6-1-1-4-1) , [AE016998] and [AE017334] (*Bacillus cereus*) and [AE017024] (*Bacillus anthracis*). We found E(GAA) just on the Q(CAA)

A clue [TTW] [AF130462] (*Corynebacterium*: B6-2-2-2-3-1-1). The clue was compared with YTTMW [AP005275] (*Corynebacterium*), and as a consequence, corresponding Y and M were found.

Two clues [GDE] and [SMFW] [AF302130] (*Streptcoccus agalagtiae* B6-1-2-4-2). The first clue was compared with GIE of [AE016947] (*Entelococcus faecalis* B6-1-2-2-1) and [AE006474] (*Streptcoccus pygenes*). We found Igat just on the site of the D. The second clue was compared with SMFYW of [AE006479] (*Streptcoccus pyogenes*). Then we found Ygta between the F and the W.

4.1.2 tRNA genes (Inverted tandems)

Sometimes “unfamiliarity” of a clue becomes a clue for detection of annotation erros.

A clue [5’ KE 3’] [AE001652] (*Chlamydophila pneumoniae* B11-2-1-1-2). The clue is popular in genera of *Bacillus* (B6-1-1-1), *Leptspira* (B10-1-1-1), and *Geobacter* (B12-4-2-1), but neither in genera of *Chlamydophila* (B11-2-1-1-2) nor *Clamydia* (B11-2-1-1-1). Therefore we examined the sequence of the annotated 5’ KE 3’, and found that it matche with the complement of 3’ KE 5’. A completment tandem 3’ EK 5’ [AP002547] (*Chlamydophila pneumoniae*) should be read as 5’ EK3’.

A clue [5’ FDEK 3’] [AE017281] (*Bacillus* B6-1-1-1-1). Unlike 3’ FDEK 5’, the clue is not familiar in many *Bacillus* species. Therefore we tried to search for its complement sequence , and found a four genes which form a tetragene tandem 3 ’ FDEK 5’. This means that each template form was interpreted as a complement one.

A clue [5’ ESNIGKTFDMSMMAPRLGLHTV ΣΛΦ 3’] [AE017280] (*Bacillus cereus* B6-1-1-1-1). In a similar process, we found twenty two genes which form a 22-gene tandem 3’ ESNIGKTFDMSMMA-PRLGLHTV 5’ and 3’ ΦΛΣ5’ just on the 5’ ΣΛΦ 3’, which is hold also in [AE017039] *Bacillus anthracis*.

There are some other examples as follows: A sequence for a complement tandem for 3’GDKT5’ [AE001652] should be read as 5’GDK3’ and 3’T5’. An apparent complete tandems 3’KS5’ and 3’SSN5’ [BX248585] (*Candidatus Blochmannia floridanus*) should be read as (5’K3’ and 3’S5’), and (5’S3’, 3’S5’ and 5’N3’), respectively. A complement tandem 3’VK5’ [BX248586] (*Candidatus Blochmannia floridanus*) shold be read as 5’VK3’.

4.1.3 Expansion to rRNA genes

The first stage: A clue [ΛΦ VLKDE] [AF302131] (*Streptcoccus agalagtiae*). The clue was compared with a template VDKLTIE of [AE014195] (the same bacterium), and we found new V (not the inherent V), new D (not the inherent D), new K (not the inherent K, instead of the inherent V to be denied), L (instead of the inherent L to be denied, but up shift about 50 b), T (instesd of the inherent K to be denied), and I (instead of the inherent D to be denied) to form a new tandem ΛΦVDKLTIE.

The second stage: A clue [ΛV] of the tandem mentioned above ΛVDKLTIE [AE014195] (*Streptcoccus agalagtiae*). The clue was compared with the hot template ΛΦV of [AF302131], and we found Φ.

A clue [ΛN] ([AE006615], [AE014141], [AE014168], [AP005141] and [AP005146]) (*Streptococcus pyogenes* B6-1-2-4-2), [AE016999] (*Bacillus cereus* B6-1-1-1-1) and [AE016998] (*Bacillus cereus* B6-1-1-1-1). The clue was compared with ΛΦN of [AE017024] (*Bacillus anthracis* B6-1-1-1-1), [AB109772] (*Finegoldia magne* B6-1-4-1-4-1), [AF007319] (*Streptococcs pneumoniae* B6-1-2-4-2) and [AJ010599] (*Listeria monocytogenes* B6-1-1-3-1) . We found Φ in each species.

A clue [ΛV] [AE016998] to [AE017000] (*Bacillus cereus* B6-1-1-1-1), [AE06474] and [AE06479] (*Streptococcus pyogenes* B6-1-2-4-2), and [AE014192] (*Streptococcus agalactiae* B6-1-2-4-2). The clue was compared with a tandem ΛΦV of [AF302131] (*Streptococcus agalatiae* B6-1-2-4-2) and [AE017205] (*Lactobacillus johnsoii* B6-1-2-3-1), and respective corresponding Φ genes were found.

Now we have found several rRNA genes (Λ, Σ and Φ) shown in Table 4.

4.5 Some problems to be dissolved

4.5.1 Arbitraliness of annotation

About ten years ago, after asking DDBJ the reason why it gave a single bacteria of [X03715] two different names, *meliferum* and *melliferum*, the former was revised and an EMBL person apologized us. Because we knew that the original paper used the two, we answered that the vender did not need to apologize. However, the true reason, maybe was misselection of a single and important keyword in database search at that time. Also today a similar case remains in [L35101]: *Bartonelle* and *Baronelle*. After asking DDBJ the original word of an amino acid “Ara” of [AB100740] to [AB100760], in summer 2003 we found it was changed to “Ala” several months later. If possible, we want to be informed that the reasons why a word was adopted and abandoned just when it was abandoned.

Generally, the Annotations appear to treat codon/anticodon of tRNA genes a little too lightly. For example, data in [L35000] to [L35003] were cited from the same pair of references. However, anticodons/codons that we can obtain by literal translation from DNA sequences of cloverleaf structures are Igat(AUC) and Atgc(GCA). On the other hand the Annotations are as follows:

	Up-date		Igat(AUC)		Atgc(GCA)	
	G	E	G	E	G	E
[L35000]	1996	1999	AUU	TTA	UUG	TTG
[L35001]	1996	2000	AUU	UUA	GCU	UCG
[L35002]	1996	1999	AUC	ATC	UUG	TTG
[L35003]	1996	2000	AUU	UUA	GCA	GCA

G: GenBank E: EMBL

This suggests that update do not always afford correct annotations.

Whereas a literal translation of a sequence of a tRNA gene yields

M(AUG)L(CUA)Q(CAA)Q(CAA)M(AUG)Q(CAG)Q(CAG),

[J01713] gives the annotation

M(AUG)L(CUA)Q(CAA) Q(CCU)M(CUA) Q(CAG)Q(AAU).

4.5.2 Arbitrariness or systematic errors

When T(175-260) of [M87888] was treated as T[75-250], it was, maybe mechanically, put upstream of V(90-170). In the present day, as seen in [AJ010599], CDS(464..>1201) is arranged after and before tRNA(139..214) and tRNA(232..314) in GenBank and EMBL, respectively. This fact may suggest difference between their policies.

Several other entries of Table 4 as well as [L35000] to [L35003] consist of I and/or A. They were yielded from investigation of the16S-23S intergenic regions,8) which were inquired from a viewpoint of phylogenetic relationship among bacterial species, where annotations of individual tRNA genes involving differentiation of codon/anticodon would be not so important. Although one8a) of the papers mentioned that by alignment of four DNA sequences from the same genera but different species, a mutation of a nucleotide of anticodon of A (c to g, namely Atgc to Atgg) was detected, it dismissed such a change as a trivial mutation which has no effect on study their bacteria. It did not discuss chage of tRNA from Atgc to Ptgg. There are some tendencies from unknown causes. For example, in a group of [AF074828] to [AF074841], Igtc was shortened about 15 b. Another group of [AF223326] to [AF322329] are of A-arm 45. In [AF312492] to [AF312495], there are both Igtc and Atgc at the positions different from those indicated by the Annotations. Whereas our literal translation gives

IgatAtgc, each of [AY591324] and [AY591325] adopt AI.

The above mentioned AI in [AY591324] to [AY591328] (*Enterococcus fecium* B6-1-2-2-1) is popular in other genera of B6 and B12: *Ethanologenbacterium (B6-1-4-1-3-1), Clostridium* (B6-1-4-1-2-1), *Campylobcter* (B12-5-1-1-1), *Xanthomonas* (B12-3-11-1-2), *Helicobacter* (B12-5-1-2-1), *Antractobactor* (B12-1-2-1-1), *Xylella* (B12-3-11-1-2), but very rare (or may be no other example) in *Enterococcus*. Actually it is not ΣAIΛ but ΣIgatAtgcΛ which is frequently investigated as a tandem of the 16S-23S intergenic region. We would like to know why the order of the genes were such inverted in every case. In addition, all tandems, " tRNA-Ile"s are very short against their true lengths. We guess it would be due to some systematic error.

In each sequence of [AE014207] *Streptcoscus agalactiae*, [AF268479] Uncultured bacterium NAZ4, and (old) [M87888] *Bacillus subtilis* , two genes overlap with each other. Our alternative and reasonable annotations are shown as follows:
T(75-250) over V(95-170)
--› T(175-250) [M87888] (corrected)
Φ(9518-9679) over Ngtt(9660-9733)
--›Φ(9537-9654) [AE014207]
A(98-278) over I(200-277)
--›A(98-178) [AF248479]

In fact, there is a problem of confliction of description as exemplified as follows:
[AE008706]
14864-14937 tRNA
/gene= "aspU"
/note="tRNA-Val"

4.5.3 Systematic error or clerical careless mistake

In addition, we cannot avoid careless mistake exemplified in Appendix 2. "Heliobacter" still survive instead of "Helicobacter" ([L25079], [M88140], [M88155], and so on).

Confusion of "Ara" with Ala ([AB100740] to [AB100760]) was dissolved in 2003, but another confusion of *Chlamydophila pneumoniae* with *Chlamydia pneumoniae* began ([AE001585] to [AE001687]). We would like to avoid such careless and severe mistakes as much as possible.

4.5.4 International mutual aid

Finally, in order to hope long continuance of the ongoing irreplaceable treasure, DDBJ/GenBank/EMBL, we cannot but say that we have to stop easy use of easy answers afforded by easy computer softwares without any discussion. Some tRNA genes were reported to be very long (in Table 4. Cf. Dgtc [D88802], Atgc[AF268429] and so others) or very short (in 46, of [AF074828]). Nevertheless, it is a kind of simple careless mistakes. More serious problem is a systematic error as exemplified in misassignment of positions of anticodon/codon, which , maybe, lead to misassignment of anticodon/codon. We indicated the same thing in the case of introns of mRNAs. We guess that most of the unbelievable and miserable results are due to such rashy behavior.We cannot and must not judge whether an unfamiliar annotation is true or false. Only person who can correct wrong data is its producer. The others only can call the producer's attention. Appendix 2 is a part of such suspects we picked up. We would like to emphasize that the present explosure of mistakes and errors also is one of the results of our systematic induction-deduction system and not causal accidents.

We recommend that all of you should begin to consider how to help to maintain and improve the quality of the DDBJ/GenBank/EMBL database. One of them is to stop easy use of easy answers produced with easy computer softwares without any discussion. Another is to establish any good ways to internationally hold a set of a question and answers, opinions, criticism, and so on resulted from this in hold.We told this also in our another paper on introns of human mRNAs⁹⁾.

5. Conclusion

We made the existence of tRNA and rRNA gene-tandems that are characteristic of a various level of bacterial classes, and proved that it can be used to deductively dig up hidden and putative tRNA and rRNA genes from genome DNA sequences. In order to maintain and improve the DDBJ/GenBank/EMBL, which is valuable and irreplaceable treasure, as effectively and efficiently much as possible, we insist some ideas.

6. References

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Appendix 1

(1) A cloverleaf structure1) and a frame

Usually, a cloverleaf structure of tRNA gene contain 73 or more (up to W76) as follows:

	0 3)	1 or less
Aminoacyl stem	1 to 7, 66 to 72	7 pairs
D-stem	10 to 13, 22 to 25	4 pairs
D-loop	14 to 21	8 or more
A-stem	27-to 31, 39 to 43	5 pairs
A-loop	32 to 38 (anticodon 34 to 36)	7
E-loop	44 to 48	5 or more
TF stem	49 to 53, 61 to 65	5 pairs
TF-loop	54 to 60	7
ACCA	73 (up to 76)	1 to 4

We define a frame. Its range is only 1 to 72.

In fact, as shown even in the 1989 compilation by Sprinzl et al.2) there have been many tRNA genes a little deviating from the “standard”. We mention them in Table 4, as exemplified as A-stem 54, which means that 1 nucleotide is missing from the standarad(A-stem 55).

(2) Description of a frame

A frame is illustrated as follows:

Ex. 1 tRNA (1002...1073): 1002ggt----acctgc1073acca

Ex.2 tRNA complement(2002..2073) : tggt 2002gcaggt-----acctg2073

(3)A tRNA gene

A tRNA gene can be described as combination of a relevant amino acis with anticodon and/or codon, as exemplified with Mcat(AUG), Mcat(ATG), or simply Mcat, and/or M(AUG), M(ATG). Three rRNA genes are mentioned as simply. A (tRNA-gene) tandem is a sequence consisting of more than one tRNA(and rRNA) gene. A DNA data (a sequence, annotation and so on) is indicated with its Accession number of the DDBJ/GenBank/EMBL.

References

1) In Transfer-RNA:Structure, Properties and Recognition, P.R. Schimmel, D. Soll, J.N.Abelson, Eds, 1979, Cold Spring Harber Labopratory, N.Y. pp.518-519 (Cited as Reference No. 1 in Ref. 3.)

2) Mathius Sprinzl et al., Nucleic Acid Res. 1989, 17,r1.

3) Sergey Steinbeg et al., ibid, 1993,21,3011.

Appendix 2

For	Read	Location (Examples)
Baronella	Bartonella	[L35101]
Heliobacter	Helicobacter	[M88156],[M88140],[M88155] and [L25079]
Chlamydia	Chlamydophila	[AE001585] to [AE001687]
n (numeral) in anticodon=(pos: n..[n+2], aa:)		
	n-1	[AJ012701] to [AJ02703], [L28150],
	n-2	[AJ012704], [L35100],
	n+1	[U60278] to[U60281]
	n+4	[L00194]
”codon recognized:GAT”	”anticodon recognaized:GAT”	[AP005275],[L08236], [M23210],[L35101](part)
(Already corrected) Ara	Ala	[AB100740] to [AB100760]
tRNA complement(1221..1296) /anticodon=(pos:1..3.aa:OTHER) /note=codon recognized=GAT” /gene=”valU” /product=”tRNA-OTHER”	tRNA complement(1221..1296) /gene=”valU” /product=”tRNA-Val”	[M13687]
tRNA 75-250 Thr	175-250 Thr	[M87888]