

The 16S ribosomal RNA mutation database (16SMDB)

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ABSTRACT

The 16S ribosomal RNA mutation database (16SMDB) provides a list of mutated positions in 16S ribosomal RNA from *Escherichia coli* and the identity of each alteration. Information provided for each mutation includes: (i) a brief description of the phenotype(s) associated with each mutation; (ii) whether a mutant phenotype has been detected by *in vivo* or *in vitro* methods; (iii) relevant literature citations. The database is available via ftp and on the World Wide Web.

DESCRIPTION

The 16S ribosomal RNA mutation database (16SMDB), currently at Franklin and Marshall College, consists of an annotated list

of 223 alterations distributed over 126 positions in 16S ribosomal RNA from *Escherichia coli*. Table 1 illustrates the format for presentation of the data and provides a list of new alterations added to the database since the previous announcement (1). Mutated positions are arranged in order beginning with the 5'-end of 16S rRNA and ending with the 3'-end. Phenotypes associated with each alteration are briefly described and designated as to whether the phenotypes were detected *in vivo* or *in vitro*. Appropriate references are provided for each alteration. A review of the data and genetic methods employed in the detection of 16S rRNA mutant phenotypes has been published elsewhere (2). A related database of mutated positions in 23S ribosomal RNA from *E. coli* is described in a separate announcement (3).

Table 1. New single and double mutations in 16S ribosomal RNA

Position ^a	Alteration	Phenotype ^{b,c}	Reference(s)
52	C52U/G359A	(With U1192) Restores Spc ^r growth abolished by G359A alone. ^b	4
146	G146A/C176U	(With U1192) Spc ^s . ^b	4
153	C153U/G168A	(With U1192) Spc ^{ts} . ^b	4
168	G168A/C153U	(With U1192) Spc ^{ts} . ^b	4
176	C176U/G146A	(With U1192) Spc ^s . ^b	4
339	C339U/G350A	(With U1192) Spc ^{ts} . ^b	4
350	G350A/C339U	(With U1192) Spc ^{ts} . ^b	4
359	G359A/C52U	(With U1192) Restores Spc ^r growth abolished by G359A	4
517 ^a	G→A, C or U	Increased translational error rate. ^b Increased level of chemical modification at positions 530, 531 and 532 in 70S ribosomes. ^c	5-7
529 ^a	G→U	Lethal; severe reduction of translational accuracy. ^b	8
571 ^a	U→A	Impaired structural stability and function of 30S subunit. ^{b,c}	9
	U571A/A865U	Restores both structure and function to wild-type. ^{b,c}	9
598	U598A/A640U	Partial restoration of S8 binding, with 5-fold reduced binding strength. ^c	10
640	A640U/U598A	Partial restoration of S8 binding, with 5-fold reduced binding strength. ^c	10
726	C→G	Suppressed requirement for 4.5S RNA in translation of natural mRNAs by cell extracts. ^c	6
732	C→U	Suppressed requirement for 4.5S RNA in translation of natural mRNAs by cell extracts. ^c	6
865 ^a	A→U	Impaired structural stability and function of 30S subunit. ^{b,c}	9
	A865U/U571A	Restores both structure and function to wild-type. ^{b,c}	9
885 ^a	G885C/C912G	(With U1192) Restores normal growth and streptomycin sensitivity to G912 mutant. ^b	11
	G885U/C912G	(With U1192) Reduced growth rate; streptomycin ^s . ^b	11
	G885C	(With U1192) Lethal at high expression levels. ^b	11
912	C912G/G885C	(With U1192) Restores normal growth and streptomycin sensitivity to G912 mutant. ^b	6,11
	C912G/G885U	(With U1192) Reduced growth rate; streptomycin ^s . ^b	6,11
981 ^a	U→A or G	Lethal under natural promoter; partially excluded from polysomes. ^b	12
	U→C	(With U1192) Recessive lethal; Spc ^s . ^b	12
1054 ^a	C→A or G	Nonsense suppressors. ^b	13

Table 1. continued

Position ^a	Alteration	Phenotype ^{b,c}	Reference(s)
	ΔC	No effect on translational fidelity. ^b	13
1057 ^a	G1057C/G1058U	Severe effects on growth rate, mutant ribosome incorporation into polysomes and translational fidelity. ^{b,c}	6,14
1058 ^a	G1058U/G1057C	Severe effects on growth rate, mutant ribosome incorporation into polysomes and translational fidelity. ^{b,c}	6,14
1064	G→A, C or U	Spc ^r . ^{b,c}	15
	G1064A/C1192U	Spc ^r . ^{b,c}	15
	G1064C/C1192G	Spc ^r ; 5-fold lower translational activity. ^{b,c}	15
	G1064U/C1192A	Spc ^r . ^{b,c}	15
1066	C→U	Spc ^r ; increased sensitivity to fusidic acid. ^b Suppressed requirement for 4.5S RNA in translation of natural mRNAs by cell extracts. ^c	6,16
1192	C1192U/G1064A	Spc ^r . ^{b,c}	15
	C1192G/G1064C	Spc ^r ; 5-fold lower translational activity. ^{b,c}	15
	C1192A/G1064U	Spc ^r . ^{b,c}	15
1199 ^a	U1199C/C1200U	Severely retarded growth rate. ^{b,c}	6,14
	U1199G/C1200G	Severely retarded growth rate. ^{b,c}	6,14
	U1199G/C1203G	Severely retarded growth rate. ^{b,c}	6,14
1200	C→U	No effect on growth rate; effect on translational fidelity. ^{b,c}	6,13,14
	C1200U/U1199C	Severe effects on growth rate, mutant ribosome incorporation into polysomes and translational fidelity. ^{b,c}	6,13,14
	C1200G/U1199G	Severe effects on growth rate, mutant ribosome incorporation into polysomes and translational fidelity. ^{b,c}	6,13,14
1202	U1202G/C1203G	No effect on growth rate or translational accuracy. ^{b,c}	6,13,14
	U1202C/C1203U	No effect on growth rate or translational accuracy. ^{b,c}	6,13,14
1203	C→U	No effect on growth rate or translational accuracy. ^{b,c}	6,13,14
	C1203G/U1202G	No effect on growth rate or translational accuracy. ^{b,c}	6,13,14
	C1203G/U1199G	No effect on growth rate or translational accuracy. ^{b,c}	6,13,14
1244	G1244A/C1293U	(With U1192) Spc ^s . ^b	4
1245	C1245U/G1292A	(With U1192) Restores Spc ^r abolished by G1292A alone. ^b	4
1292	G1292A/C1245U	(With U1192) Restores Spc ^r abolished by G1292A alone. ^b	4
1293	C1293U/G1244A	(With U1192) Spc ^s . ^b	4
1341 ^a	U→C	Increased S7 affinity. ^c	17
1351	U→C	Reduced S7 affinity. ^c	17
1357	A→C	No effect on S7 binding. ^c	17
1395 ^a	C→U	Increased levels of stop codon read-through and frame-shifting. ^b	6
1400 ^a	Δ1400	Increased levels of stop codon read-through and frame-shifting. ^b	6
1407 ^a	C→U	Increased levels of stop codon read-through and frame-shifting. ^b	6
1409	C→G or A	Increased levels of stop codon read-through and frame-shifting. ^b	6
	C1409A/G1491A		6
	C1409G/G1491C	Increased accuracy; small decreases in stop codon read-through and frame-shifting. ^b	6
	C1409U/G1491A	Increased accuracy; small decreases in stop codon read-through and frame-shifting. ^b	6
1431	A→G	Nonsense suppressor. ^b	13
1483 ^a	A→G	Nonsense suppressor. ^b	13
1491	G→C, A or U	Increased levels of stop codon read-through and frame-shifting. ^b	6
	G1491A/C1409A	Increased levels of stop codon read-through and frame-shifting. ^b	6
	G1491C/C1409G	Increased accuracy; small decreases in stop codon read-through and frame-shifting. ^b	6
	G1491A/C1409U	Increased accuracy; small decreases in stop codon read-through and frame-shifting. ^b	6
1492 ^a	A→C or G	Lethal; incorporated into polysomes. ^b	18
1493 ^a	A→C or U	Lethal; incorporated into polysomes. ^b	18
	A→G	Nonsense suppressor. ^b	13
1505 ^a	G→U	Increased levels of stop codon read-through and frame-shifting. ^b	6

^aHighly conserved among the 16S-like rRNAs in all three primary kingdoms (see fig. 1 in 19,20). ^b*In vivo*. ^c*In vitro*.

AVAILABILITY

Individuals with access to the Internet telecommunications network may obtain text files of 16SMDB by anonymous file transfer protocol. The ftp site is Acad.FandM.edu, the directory is /NAR. The database is also available on the World Wide Web at URL <http://www.fandm.edu/Departments/Biology/Databases/RNA.html>. Email inquiries should be addressed as follows, K_Triman@Acad.FandM.edu. Inquiries may also be directed to K.Triman by fax at (717) 291-4143. I would welcome any suggested revisions to the database, as well as information about newly characterized 16S rRNA mutations.

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