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The 16S ribosomal RNA mutation database (16SMDB)

Kathleen L.Triman
Department of Biology, Franklin and Marshall College, PO Box 3003, Lancaster, PA 17604, USA

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: (1) a brief description of the phenotype(s) associated with each mutation, (2) whether a mutant phenotype has been detected by *in vivo* or *in vitro* methods, and (3) relevant literature citations. The database is available via ftp.

DESCRIPTION

The 16S Ribosomal RNA Mutation Database (16SMDB), currently at Franklin and Marshall College, consists of an annotated list of 172 alterations distributed over 98 positions in 16S ribosomal RNA from *Escherichia coli.* Table I illustrates the format for presentation of the data (as shown for positions 11 through 146) and provides a list of the alterations and positions currently included in the database. 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 (Triman, 1994).

AVAILABILITY

Individuals with access to the Internet telecommunications network may obtain text files of 16SMDB by anonymous file transfer protocol. A Readme-file contains instructions about the use of the database.
The ftp site is: Acad.FandM.edu
The directory is: /NAR
Email inquiries should be addressed as follows: K_Triman@Acad.FandM.edu. Inquiries may also be directed to K. Triman at FAX (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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Table I. Single and double mutations in 16S ribosomal RNA

Position[a]	Alteration	Phenotype[b,c]	Reference(s)
11	G to A	U23 suppressor.[b]	Dammel and Noller, 1993
13[a]	U to A or C	Reduction of both streptomycin-induced misreading and streptomycin binding.[c]	Pinard *et al.*, 1993.
	U13A/A914U	No suppression of U13 effects.[c]	"
	U13C/A914G	No suppression of U13 effects.[c]	"
15[a]	G to A	Moderate U23 suppressor.[b]	Dammel and Noller, 1993
18	C to A, G or U	Dramatic reduction in translational activity.[b]	Brink *et al.*, 1993a, b.
	C18A/G917U	Translational activity restored.[b]	"
	C18G/G917C	Translational activity restored.[b]	"
	C18U/G917A	Translational activity restored.[b]	"
23	C to U	Cold-sensitive dominant.[b]	Dammel and Noller, 1993.
146	G to A	(With U1192) Spc[s] recessive.[b]	Triman *et al.*, 1989.
153	C to U	352	C352U/A353G
189	A189G/A190G	353	A353G/C352U
190	A190G/A189G	359	G to A
250	A250G/G251A	505	G to U
			G505C/G506C
251	G251A/A250G	506	G to A
321	A to C or G		G506C/G505C
	A321C/G322U		G506A/C525U
	A321G/G322A	507	C to U
322	C to A		C507U/G524A
	G322A/A321G	517[a]	ΔG
	G322U/A321C		G to A, C, or U
323	U to G		G517U/U534G
332	G to A	523	A to C
350	G to A	524	G to A
524	G524A/C507U		
525	C to U	792[a]	A to G,C or U
	C5252U/G506A	814[a]	A to G, C or U
	C525G/C526G	888	G888A/C912U
912			ΔC
526	C to A		C to A
	C526A/G505U		C to G
	C526G/C525G		C to U
527[a]	G to U		C912U/G888A
528[a]	C to G	913	A to G
529[a]	G to U	914[a]	A to C
530[a]	G to A		A to G or U
	G to U		A914G/U13A
531	U to G		A914U/U13C
534	U to G or C	915[a]	A to G
	U534G/G517U	917	G917A/C18U
538	G to A		G917C/C18G
595	ΔA		G917U/C18A
	A to U	966	G to A, C or U
597	G597C/C643G	967	ΔC
598	U to A		C to A, G or U
	U598A/A642U	980	C to A or G
599	C to G	1054[a]	ΔC
	C599G/G639C	C to A, G or U	
618	C to U	1192	C to A, G or U
624	C to U	1199[a]	U to C
627	G to A		U1199C/U1202C
631	C to U	1202	U to C
634	C to U		U1202C/U1199C
639	G639C/C599G	1207	G to C or U
640	ΔA	1292	G to A
		1293	C to U
	A to U	1388	C to U
641	U to C	1389	C to U
	U to A	1395[a]	C to U
642	ΔA	1397[a]	C to U
	A to U		ΔC
	A642U/U598A	1398[a]	ΔA
643	C to U	1399[a]	C to A
	C to G		C to U
	C643G/G597C		C1399A/G1401C

Table I. (*cont.*)

Position[a]	Alteration	Phenotype[b,c]	Reference(s)
645	G to A		C1399A/G1401U
651	C to U	1400[a]	ΔC
726	C to G		C to A
791[a]	G to A		C to G
1400[a]	C to U	1518	A to C,G or U
1401[a]	ΔG	1519	A to C, G or U
	G to A	1523	G to A
	G to C or U	1524	C1524U/U1512C
	G1401C/C1399A	1535–1540	CCTCC to CACAC
	G1401U/C1399A		CCTCC to GGAGG
	G1401C/C1501G	1538	C to U
1402[a]	C to U		C to G
	ΔC		
1404[a]	C to U or G		
	C1404G/C1496G		
	C1404G/G1497C		
1405[a]	G to C		
	G1405C/C1496G		
	G1405C/G1497C		
1407[a]	C to U		
1409	C to G or A		
	C to U		
	C1409A/C1411G		
	C1409A/G1491U		
	C1409G/G1491C		
	C1409U/G1491A		
1411	C1411G/C1409A		
1416	G to U		
1469	C to U		
1489	G1489C/G1491U		
1491	G to A		
	G to C or U		
	G1491A/C1409G		
	G1491C/C1409G		
	G1491U/C1409A		
	G1491U/G1489C		
1496[a]	C to G		
	C1496G/C1404G		
	C1496G/G1405C		
1497[a]	G to C		
	G1497C/C1404G		
	G1497C/G1405C		
1498[a]	U to G, C or A		
1501[a]	C to G		
	C1501G/G1401C		
1505[a]	G to A, C or U		
1512[a]	U to C or G		
	U1512C/C1524U		

[a]highly conserved among the 16S-like rRNAs in all three primary kingdoms (see Figure 1 in Noller, 1993; Gutell, 1992); [b]*in vivo*; [c]*in vitro*.