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Expanded versions of the 16S and 23S Ribosomal RNA Mutation Databases (16SMDBexp and 23SMDBexp)

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ABSTRACT

Expanded versions of the Ribosomal RNA Mutation Databases provide lists of mutated positions in 16S and 16S-like ribosomal RNA (16SMDBexp) and 23S and 23S-like ribosomal RNA (23SMDBexp) and the identity of each alteration. Alterations from organisms other than *Escherichia coli* are reported at positions according to the *E.coli* numbering system. 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, and (iii) relevant literature citations. The databases are available via ftp and on the World Wide Web at the following URL:
http://www.fandm.edu/Departments/Biology/Databases/RNA.html

DESCRIPTION

The expanded version of the 16S Ribosomal RNA Mutation Database (16SMDBexp), currently at Franklin and Marshall College, consists of an annotated list of 295 alterations distributed over 157 positions in 16S ribosomal RNA from *Escherichia coli* and in 16S-like rRNA from other organisms. Table 1 illustrates the format for presentation of the data and includes 62 new alterations added to the 16SMDBexp database since the previous announcement (32). 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 (29).

The 23S Ribosomal RNA Mutation Database (23SMDB), currently at Franklin and Marshall College, consists of an annotated list of 271 alterations distributed over 143 positions in 23S ribosomal RNA from *E.coli* and in 23S-like rRNA from other organisms. Table 2 includes 36 new alterations added to the 23SMDBexp database since the previous announcement (32). A review of the data and genetic methods employed in the detection of 23S rRNA mutant phenotypes will be published elsewhere (33).

There are currently six text files of ribosomal RNA mutations available: (i) 16SMDBexp and (ii) 23SMDBexp, both described above, (iii) 16SMDB and (iv) 23SMDB, files containing only the data from *E.coli*, and (v) 16S-likeMDB and (vi) 23S-likeMDB, files containing only the data from organisms other than *E.coli* (28,30–32). Ultimately the goal of this work is to provide a database that can be queried for specific kinds of information. Our plan is to organize the data, so that one can access, for example: (i) all the data from one specific organism, (ii) all the data for one specific nucleotide position, or (iii) all the data for one specific phenotype.

AVAILABILITY

Individuals with access to the Internet telecommunications network may obtain text files of the ribosomal RNA mutation databases by anonymous file transfer protocol. The ftp site is: Acad.FandM.edu; the directory is: /NAR .

The databases are also available on the World Wide Web at the following 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 at Fax: (717) 399 4548. The authors welcome any suggested revisions to the database, as well as information about newly characterized 16S or 23S rRNA mutations.

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Table 1. 16SMDBexp: single and double mutations in 16S and 16S-like ribosomal RNA

Position	Alteration	Phenotype	Ref(s)
13	U→9A	Impaired growth	17
13	U13A/A914U	Impaired growth	17
18	C18A	Inhibits translation. Mutant 30S particles are impaired in forming 70S tight couples	17
23	C23U	Dominant cold-sensitive phenotype and a defective maturation of the 16S rRNA 5′ end	18
517	G→A	Increased sensitivity to streptomycin in *S.cerevisiae*	3
517	U→A	Polysome formation severely inhibited while tight couple formation was not disturbed	17
526	C→U	Extra *Pvu*II site in region coding for 530-loop in *N.plumbaginifolia*	37
527	G→U	Lethal, found in all ribosome fractions	21
527	G527U/A1492C	Lethal, found in polysome	21
527	G527U/A1492G	Like G527U	21
527	G527U/A1492U	Lethal, found in polysome	21
527	G527U/A1493C	Like G527U	21
527	G527U/A1493G	Lethal, found in polysome	21
527	G527U/A1493U	Like G527U	21
529	G→U	Stimulates initiation from a non-AUG initiation codon	14
530	G530A/A531G	No increase in initiation from non-AUG codons	14
597	G597A/C643U	Slightly decreased affinity for S8 binding	13
597	G597C/U641A/ C643G	No effect on S8 binding	13
597	G597U/C643G	No binding of S8	13
597	G597U/U641A/C643G	No binding of S8	13
597	G597U/U641C/C643G	No effect on S8 binding	13
653	ΔU	No effect on *B.stearothermophilus* S15 binding	1
665	A665C/A668C	No effect on *B.stearothermophilus* S15 binding	1
740	U→C	Slight reduction in S15 binding	1
748	ΔA	30-fold reduction in S15 affinity	1
749	C→A	Little effect on S15 binding	1
752	G→C	Severely reduced affinity for S15	1
787	A→C	Produces ribosomes that are highly functional	8
787	A→G	Strongly inhibits ribosome function	8
787	A→U	Moderately inhibits ribosome function	8
787	A787C/C795A	Moderately inhibits ribosome function	8
787	A787C/C795G	Strongly inhibits ribosome function	8
787	A787C/C795U	Produces ribosomes that are highly functional	8
787	A787G/C795A	Moderately inhibits ribosome function	8
787	A787G/C795G	Moderately inhibits ribosome function	8
787	A787G/C795U	Produces ribosomes that are highly functional	8
787	A787U/C795A	Strongly inhibits ribosome function	8
787	A787U/C795G	Strongly inhibits ribosome function	8
787	A787U/C795U	Produces ribosomes that are highly functional	8
795	C→A	Produces ribosomes that are highly functional	8
795	C→G	Moderately inhibits ribosome function	8
795	C→U	Produces ribosomes that are highly functional	8
885	G→C	Interfere with 912·885 base pair and favored 912·888 conformation	10
885	G→A	Novel mutation for streptomycin resistance. Creates a *Sty*I recognition sequence. Affects binding of S12. In *N.plumbaginifolia*	37
885	G→U	Favored the 912·885 conformation. Increases rates of readthrough errors and in-frame stop codons	10
888	G→A	Antisuppressor phenotype in Yeast. Increased base pairing in the 912·888 conformation	10
910	C→G	Favored the 912·888 conformation, but without cold-sensitivity. Lowers stop codon read-through rates, and elevated rate of frame-shifting.	10
910	C910G/G887C	Favored the 912·885 conformation. Increases rates of readthrough errors and in-frame stop codons	10
911	U→C	Favored the 912·885 conformation. Increases rates of readthrough errors and in-frame stop codons	10
912	C→G	Favored the 912·888 conformation, but without cold-sensitivity. Lowers stop codon read-through rates, and elevated rate of frame-shifting.	10
912	C→U	High-level streptomycin resistance in *N.plumbaginifolia*	37
912	C912G/G885C	Favored the 912·885 conformation. Increases rates of readthrough errors and in-frame stop codons	10

Table 1. *continued*

Position	Alteration	Phenotype	Ref(s)
912	C912G/G885C	Favored the 912·885 conformation. Increases rates of readthrough errors and in-frame stop codons	10
912	C912G/G885U	Allowed base pairing at 912·885 but interfered with 912·888 base pairing	10
912	C912G/G888C	Favored the 912·888 conformation and cold sensitivity, but does not increase reactivity to kethoxal	10
912	C912G/G888U	Favored 912·888 conformation but cold-sensitive	10
912	U→C	Decreases resistance to streptomycin and increases resistance to paromomycin and inhibits nonsense suppression induced by paromomycin in *S.cerevisiae*	3
913	A→G	Moderate effect of streptomycin binding in *N.plumbaginifolia*	37
914	A→U	Impaired growth	17
915	A→G	Increased streptomycin binding in *N.plumbaginifolia*	37
1054	C→A	Lethal above 37°C or high expression. UGA suppression	15
1054	C→G	Slight defect in subunit association. Suppresses all three termination codons	15
1054	C→U	Temperature sensitive lethality; slow growth rate at 37°C and when highly expressed. Defective ability to enter polysome	15
1054	ΔC	Lethal at 31°C, No suppression of trpA nonsense mutation. Affects 30S subunit assembly and subunit association	15
1065	U1065C/A1191G	Inhibits translation, increased level of acetylation, and does not allow S5 to bind. Causes an accumulation of free 30S subunits	18
1192	C→G	Gain resistance to spectinomycin and macrolides in *Mycobacterium smegmatis*	20
1192	C→U	Spectinomycin resistance, but no effect on stop codon, readthrough, frameshifting, or initiation events	14
1199	U1199C/C1200U	Stimulates initiation from a non-AUG initiation codon	14
1199	U1199G/C1200G	Stimulates initiation from a non-AUG initiation codon	14
1341	U→C	No effect on growth rate	4
1341	U1341C/C1192U	No effect on growth rate	4
1351	A1351C/C1192U	Counteracts mutation C1192U and restores spectinomycin binding. No cell growth	4
1351	U→C	No effect on growth rate	4
1357	A→C	No effect on growth rate	4
1357	A1357C/C1192U	Severely decreased growth rate due to defect in elongation	4
1386	G→A	Spectinomycin resistance in *N.tabacum*	25
1395	C1395U/G1505U	Viable cells, suppresses lethality. Stimulates initiation from a non-AUG initiation codon. Increased growth rate over C1395U alone	14
1400	ΔC1400/G1505U	Viable cells, suppresses lethality. Stimulates initiation from a non-AUG initiation codon. Increased growth rate over ΔC1400 alone	14
1405	G→C	Significantly reduced interaction with Paromomycin at positions 1491 and 1494	12
1405	G1405C/C1496G	No affect on Paromomycin binding	12
1406	U→A or C	No affect on Paromomycin binding	12
1406	U1406G/U1495G	No effect on Paromomycin binding	12
1407	C→G	Severely impaired Paromomycin binding	12
1407	C1407G/G1494C	Severely impaired Paromomycin binding	12
1407	C1407U/G1494G	Severely impaired Paromomycin binding	12
1407	C1407U/G1494A	Severely impaired Paromomycin binding	12
1407	C1407U/G1505U	Viable cells, suppresses lethality. Stimulates initiation from a non-AUG initiation codon. Increased growth rate over C1407U alone	14
1408	A→C	Moderate reduction of Paromomycin binding	12
1408	A→G	Gain resistance to gentamicin, amikacin, or tobramycin in *Mycobacterium smegmatis*	20
1408	A→G	High level neamine and kanamycin resistance in *C.reinhardtii*	6
1408	A→G	Weak reduction of Paromomycin binding	12
1408	A→U	Large reduction of Paromomycin binding	12
1409	C→U	Low level neamine and kanamycin resistance in *C.reinhardtii*	6
1409	C1409A/G1491U	Slightly reduced interaction with Paromomycin	12
1409	C1409G/G1491C	Slightly reduced interaction with Paromomycin	12
1491	G→U	Weakened interaction with Paromomycin	12
1492	A1492C/A1493C	No effect on Paromomycin binding	12
1494	G→C	Severely impaired Paromomycin binding	12
1495	U→A or C	Greatly reduced affinity for Paromomycin binding	12
1495	U→G	No effect on Paromomycin binding	12
1495	U1495G/U1406G	No effect on Paromomycin binding	12
1496	C→G	Significant reduction of paromomycin binding at positions 1405 and 1491. Slight reduction of Paromomycin binding at position 1494	12
1505	G1505U/G791A	Slower growth rate than G791A alone	14

Table 2. 23SMDBexp: single and double mutations in 23S and 23S-like ribosomal RNA

Position	Alteration	Phenotype	Ref(s)
1067	A1067U	Normal growth	22,23
1093	G→U	*trpA* UGA suppressor; temperature sensitive	36
	G→C	*trpA* UGA suppressor; temperature sensitive	36
	G→A	*trpA* UGA suppressor; temperature sensitive	36
	G1093A/A1098G	*trpA* UGA suppressor; temperature sensitive	36
1098	A→U	Normal growth phenotpye	36
	A→G	Normal growth phenotpye	36
	A→C	*trpA* UGA suppressor; temperature sensitive	36
	A1098G/G1093A	*trpA* UGA suppressor; temperature sensitive	36
2057	G→A	Ery^r in *Chlamydomonas* chloroplasts	6
2058	A→G	Ery^r, Lincomycin and clindamycin resistance in *Chlamydomonas* chloroplasts	6
	A→G	Lincomycin resistance in *Solanum nigrum* chloroplasts	7
	A→G	Clarithromycin resistance in *Helicobacter pylori*	34
2059	A→G	Clarithromycin resistance in *H.pylori*	34
2061	G→A	Chloramphenicol resistance in rat mitochondria	35
2062	A→C	Chloramphenicol resistance in *Halobacterium halobium*	11
2249	U2249C	Normal growth	22,23
2250	G2250A	Normal growth	22,23
	G2250A/C2254U	Normal growth	22,23
2251	G→A	Dominant lethal; Abolished both binding of tRNA and peptidyl transferase activity	5
	G→U	Dominant lethal; Abolished both binding of tRNA and peptidyl transferase activity	5
2252	G→A, C or U	Less than 5% of control level peptidyl transferase activity	19
2253	G2253A	19% of control level peptidyl transferase activity	19
	G2253C	42% control level peptidyl transferase activity	19
	G2253U	Less than 5% control level peptidyl transferase activity	19
2254	C2254U	Normal growth	22,23
2438	U→C	Amicetin resistance in *H.halobium*	9
	U→A	Amicetin resistance and reduced growth rate in *H.halobium*	9
	U→G	Unstable in presence or absence of amicetin in *H.halobium*	9
2452	C→A	Chloramphenicol resistance in human mitochondria	2
	C→U	Anisomycin resistance in *Tetrahymena thermophila*	26
	C→U	Chloramphenicol resistance in *H.halobium*	
	C→U	Low level sparsomycin resistance in *H.halobium*	27
2499	C→U	Sparsomycin resistance in *H.halobium*	27
2505	G→A	14% activity of 70S ribosomes	19
	G→C	Excluded from 70S ribosomes; 17% activity of 70S ribosomes	19
	G→U	<5% activity of 70S ribosomes	19
2506	U→A	Dominant lethal; 5% activity of 70S ribosomes	19
	U→C	20% activity of 70S ribosomes	19
	U→G	<5% activity of 70S ribosomes	19
2507	C2507U	Dominant lethal	22,23
	C2507U/G2581A	Dominant lethal; Inhibition of puromycin in reaction	22,23
	Δ507/G2581A	Dominant lethal; Inhibition of puromycin in reaction	22,23
2508	G2508U	Control level peptidyl transferase activity	18,19
2580	U2580A	Deleterious; <5% activity of 70S ribosomes	19
	U2580C	Dominant lethal; 12% activity of 70S ribosomes	19
	U2580G	Deleterious; 6% activity of 70S ribosomes	19

Table 2. *continued*

Position	Alteration	Phenotype	Ref(s)
	U2580C	Reduced growth	22,23
2581	G2581A	Deleterious; 22% activity of 70S ribosomes	22,23
	G2581A	Dominant lethal inhibition of puromycin in reaction	22,23
	G2581C	Deleterious; 13% activity of 70S ribosomes	22,23
	G2581U	Deleterious; 18% activity of 70S ribosomes	22,23
2582	G2582A	<5% of control level peptidyl transferase activity	22,23
	G2582C	<5% of control level peptidyl transferase activity	22,23
	G2582U	<5% of control level peptidyl transferase activity	22,23
2583	G→A	<5% of control level peptidyl transferase activity	19
	G→C	<5% of control level peptidyl transferase activity	19
	G→U	Dominant lethal; <5% of control level peptidyl transferase activity	19
2584	U→A	Deleterious; 20% activity of 70S ribosomes	19
	U→C	Deleterious; 20% activity of 70S ribosomes	19
	U→G	Dominant lethal	19
2585	U→A	Dominant lethal; <6% of control level peptidyl transferase activity; disrupted binding of tRNA fragment, Decreased peptidyl transferase activity	19, 5
	U→C	Dominant lethal; <6% of control level peptidyl transferase activity; disrupted binding of tRNA fragment, Decreased peptidyl transferase activity	19, 5
	U→G	Dominant lethal; 36% of control level peptidyl transferase activity; disrupted binding of tRNA fragment, Decreased peptidyl transferase activity	19, 5
2611	C→U or G	Ery^r and low level lincomycin and clindamycin resistance in *Chlamydomonas* chloroplasts	6

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