Bacteria-wide detection of 6S RNAs

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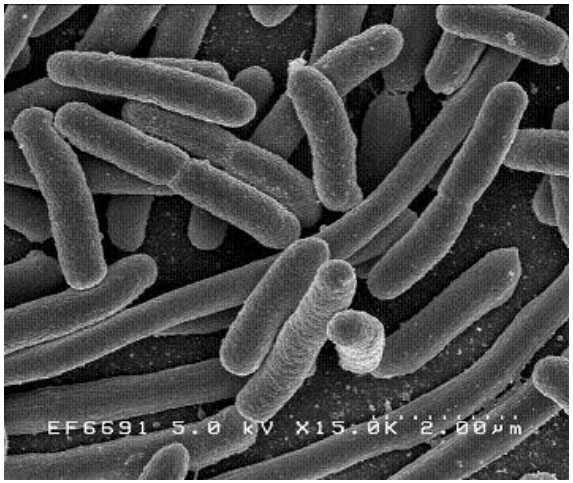
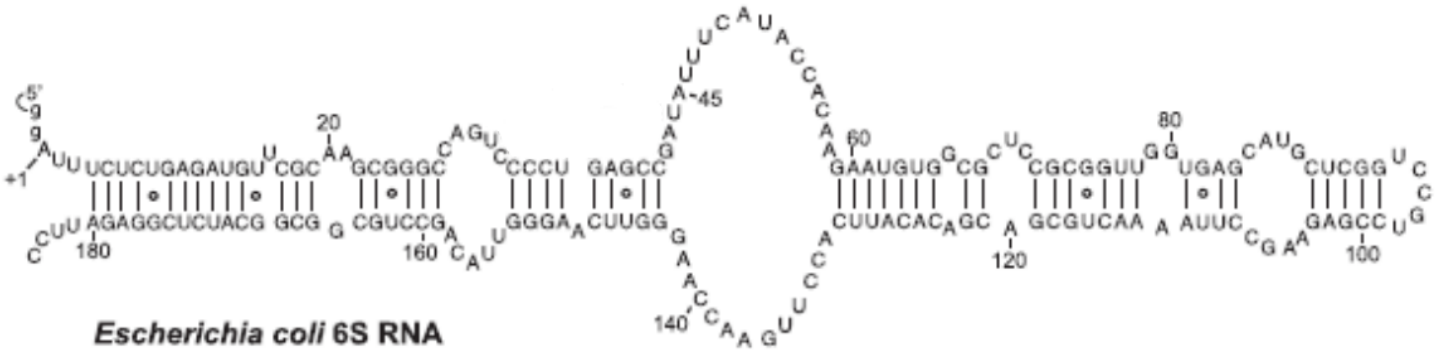
6S RNA

- Abundant small non-coding RNA in bacteria



6S RNA

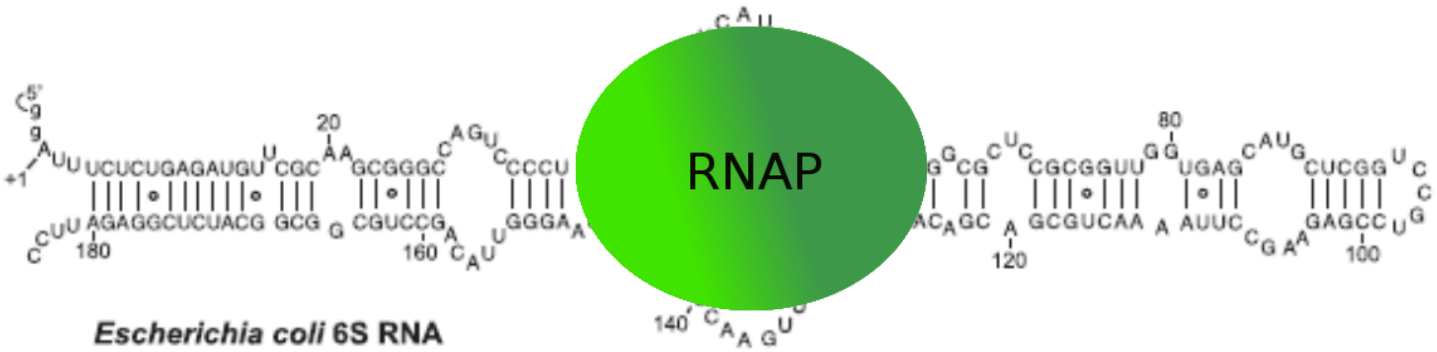
- Abundant small non-coding RNA in bacteria



***Escherichia coli* 6S RNA**

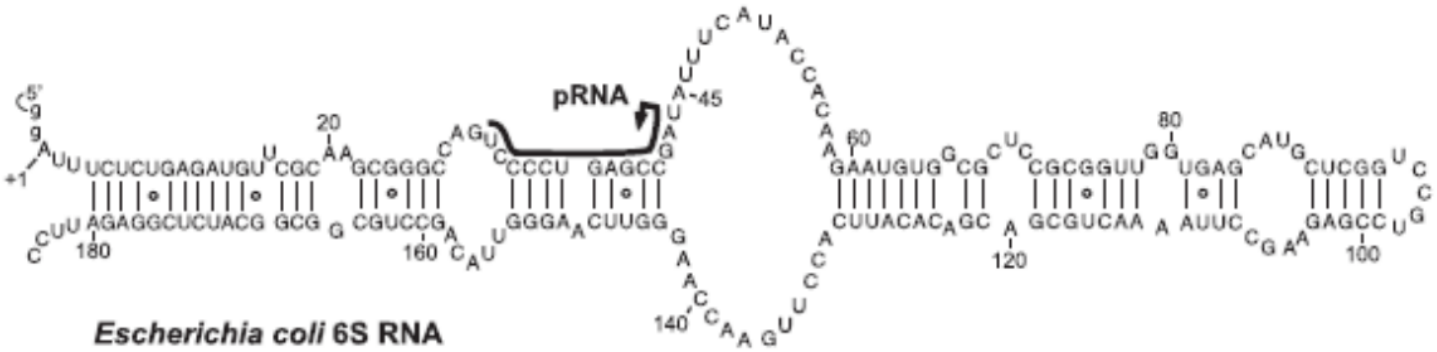
6S RNA

- Abundant small non-coding RNA in bacteria



6S RNA

- Abundant small non-coding RNA in bacteria



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Brucella_melitensis_.1 GGCGAACUGCGCUUCCCGACAGGUGUAACAGc.aUCCCCGGGGCCUUAUUGAUCUCUAA--.GGGA
E.coli.1 AUUUCUCUGAGAUGUUCGCAAGCGGGCCAGU...-CCCCUGAGCCGAUAUUUCAUACCACAaGAAU
Bacillus_subtilis_su.1 AAGAAGCUACUUUGUGCGU--AUUGUUAAUU..aAGUUUUAA-CCUUUAAGCUGUAAUA--.GGGA
#=GC SS_cons :<<<<<<<<<<<<<-<<<-----------...<<<<-<<<<<-----------------.<<<-
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Synechococcus_elonga.1 GCUCUCGCAgAGCCGACGGC-AGU.AGACCGAGCUUGACUCGGAA.ACUUAAUGUUGGCC-GCAAG
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E.coli.1 GUGGCGCUC.CGCGGUUGGUGAGC.AUGCUCGGUCCGUCCGAGAA.GCCUUAAAACUGCGACGACA
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Brucella_melitensis_.1 CGCCCACCUACUUU-GUA..GGUUCCCGGGAUCAAUCACUACCAUCGGCCG.uCGUGGU-CGCCG
E.coli.1 CAUUCACCUUGAACCAAG..GGUUCAAGGG--UUACAGCCUGCGGCGGCAU..CUCGGAGAUUCC
Bacillus_subtilis_su.1 CACCCACUUUGAGGAGUGguGGUUUAAAACUUUCUUACUUGCAUACGGCAAgaCGUAGCGAAAGC
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```
# STOCKHOLM 1.0

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Brucella_melitensis_.1  GGCGAACUGCGCUUCCCGACAGGUGUAACAGc.aUCCCCGGGGCCUUAUUGAUCUCUAA--.GGGA
E.coli.1                AUUUCUCUGAGAUGUUCGCAAGCGGGCCAGU...-CCCCUGAGCCGAUAUUUCAUACCACAaGAAU
Bacillus_subtilis_su.1  AAGAAGCUACUUUGUGCGU--AUUGUUAAUU..aAGUUUUAA-CCUUUAAGCUGUAAUA--.GGGA
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Synechococcus_elonga.1  CUCCCCCCUGGUUCUCCC..AGGUCGAAAU----CUGAGGUAAAACGGCGU..CGCGGUUAGAUC
Brucella_melitensis_.1  CGCCCACCUACUUU-GUA..GGUUCCCGGGAUCAAUCACUACCAUCGGCCG.uCGUGGU-CGCCG
E.coli.1                CAUUCACCUUGAACCAAG..GGUUCAAGGG--UUACAGCCUGCGGCGGCAU..CUCGGAGAUUCC
Bacillus_subtilis_su.1  CACCCACUUUGAGGAGUGguGGUUUAAAACUUUCUUACUUGCAUACGGCAAgaCGUAGCGAAAGC
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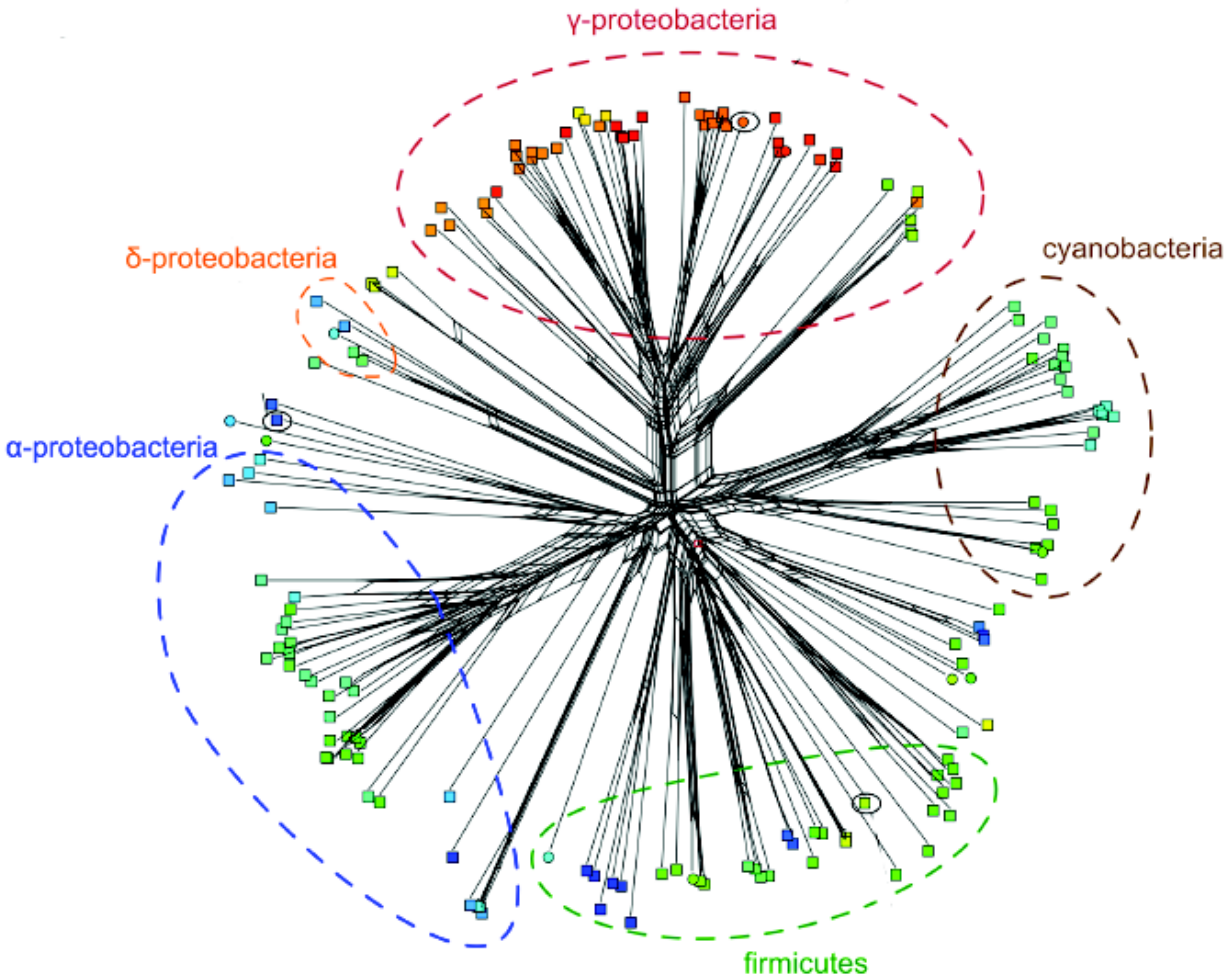
Project

- Detect 6S RNAs in all bacteria



Basic methods

cyano		
alpha		
gamma		
firmicutes		
others		
total		

Basic methods

	RFAM
cyano	
alpha	
gamma	
firmicutes	
others	
total	

Basic methods

	RFAM
cyano	24
alpha	31
gamma	42
firmicutes	41
others	16
total	**154**

Basic methods

	RFAM	Expected
cyano	24	
alpha	31	
gamma	42	
firmicutes	41	
others	16	
total	**154**	

Basic methods

	RFAM	Expected
cyano	24	40
alpha	31	126
gamma	42	266
firmicutes	41	229
others	16	439
total	**154**	**1100**

Basic methods

	RFAM	Expected	BLAST
cyano	24	40	
alpha	31	126	
gamma	42	266	
firmicutes	41	229	
others	16	439	
total	**154**	**1100**	

Basic methods

	RFAM	Expected	BLAST	
cyano	24	40	37	(1)
alpha	31	126	77	(5)
gamma	42	266	195	(16)
firmicutes	41	229	137	(10)
others	16	439	12	(22)
total	**154**	**1100**	**458**	**(54)**

Basic methods

	RFAM	Expected	BLAST		infernal	
cyano	24	40	37	(1)	39	(1)
alpha	31	126	77	(5)	101	(14)
gamma	42	266	195	(16)	234	(16)
firmicutes	41	229	137	(10)	194	(19)
others	16	439	12	(22)	117	(41)
total	**154**	**1100**	**458**	**(54)**	**685**	**(91)**

Basic methods

	RFAM	Expected	BLAST		infernal		infernal groups
cyano	24	40	37	(1)	39	(1)	
alpha	31	126	77	(5)	101	(14)	
gamma	42	266	195	(16)	234	(16)	
firmicutes	41	229	137	(10)	194	(19)	
others	16	439	12	(22)	117	(41)	
total	**154**	**1100**	**458**	**(54)**	**685**	**(91)**	

Basic methods

	RFAM	Expected	BLAST		infernal		infernal groups	
cyano	24	40	37	(1)	39	(1)	40	
alpha	31	126	77	(5)	101	(14)	114	(5)
gamma	42	266	195	(16)	234	(16)	248	(3)
firmicutes	41	229	137	(10)	194	(19)	217	(1)
others	16	439	12	(22)	117	(41)	??	
total	**154**	**1100**	**458**	**(54)**	**685**	**(91)**	**619**	**(9)**

Basic methods

	RFAM	Expected	BLAST		infernal		infernal groups		GotohScan
cyano	24	40	37	(1)	39	(1)	40		
alpha	31	126	77	(5)	101	(14)	114	(5)	
gamma	42	266	195	(16)	234	(16)	248	(3)	
firmicutes	41	229	137	(10)	194	(19)	217	(1)	
others	16	439	12	(22)	117	(41)	??		
total	**154**	**1100**	**458**	**(54)**	**685**	**(91)**	**619**	**(9)**	

Basic methods

	RFAM	Expected	BLAST		infernal		infernal groups		GotohScan	
cyano	24	40	37	(1)	39	(1)	40		39	(1)
alpha	31	126	77	(5)	101	(14)	114	(5)	117	
gamma	42	266	195	(16)	234	(16)	248	(3)	236	(6)
firmicutes	41	229	137	(10)	194	(19)	217	(1)	184	(8)
others	16	439	12	(22)	117	(41)	??		81	(71)
total	**154**	**1100**	**458**	**(54)**	**685**	**(91)**	**619**	**(9)**	**657**	**(86)**

Basic methods

	RFAM	Expected	BLAST		infernal		infernal groups		GotohScan		locarnascan
cyano	24	40	37	(1)	39	(1)	40		39	(1)	
alpha	31	126	77	(5)	101	(14)	114	(5)	117		
gamma	42	266	195	(16)	234	(16)	248	(3)	236	(6)	
firmicutes	41	229	137	(10)	194	(19)	217	(1)	184	(8)	
others	16	439	12	(22)	117	(41)	??		81	(71)	
total	**154**	**1100**	**458**	**(54)**	**685**	**(91)**	**619**	**(9)**	**657**	**(86)**	

Basic methods

	RFAM	Expected	BLAST		infernal		infernal groups		GotohScan		
cyano	24	40	37	(1)	39	(1)	40		39	(1)	??
alpha	31	126	77	(5)	101	(14)	114	(5)	117		??
gamma	42	266	195	(16)	234	(16)	248	(3)	236	(6)	??
firmicutes	41	229	137	(10)	194	(19)	217	(1)	184	(8)	??
others	16	439	12	(22)	117	(41)	??		81	(71)	??
total	**154**	**1100**	**458**	**(54)**	**685**	**(91)**	**619**	**(9)**	**657**	**(86)**	**??**

Basic methods

	RFAM	Expected	BLAST		infernal		infernal groups		GotohScan		**total**
cyano	24	40	37	(1)	39	(1)	40		39	(1)	
alpha	31	126	77	(5)	101	(14)	114	(5)	117		
gamma	42	266	195	(16)	234	(16)	248	(3)	236	(6)	
firmicutes	41	229	137	(10)	194	(19)	217	(1)	184	(8)	
others	16	439	12	(22)	117	(41)	??		81	(71)	
total	**154**	**1100**	**458**	**(54)**	**685**	**(91)**	**619**	**(9)**	**657**	**(86)**	

Basic methods

	RFAM	Expected	BLAST		infernal		infernal groups		GotohScan		**total**	
cyano	24	40	37	(1)	39	(1)	40		39	(1)	40	
alpha	31	126	77	(5)	101	(14)	114	(5)	117		119	(3)
gamma	42	266	195	(16)	234	(16)	248	(3)	236	(6)	250	(2)
firmicutes	41	229	137	(10)	194	(19)	217	(1)	184	(8)	218	(2)
others	16	439	12	(22)	117	(41)	??		81	(71)	127	(86)
total	**154**	**1100**	**458**	**(54)**	**685**	**(91)**	**619**	**(9)**	**657**	**(86)**	**754**	**(93)**

Other strategies: Synteny

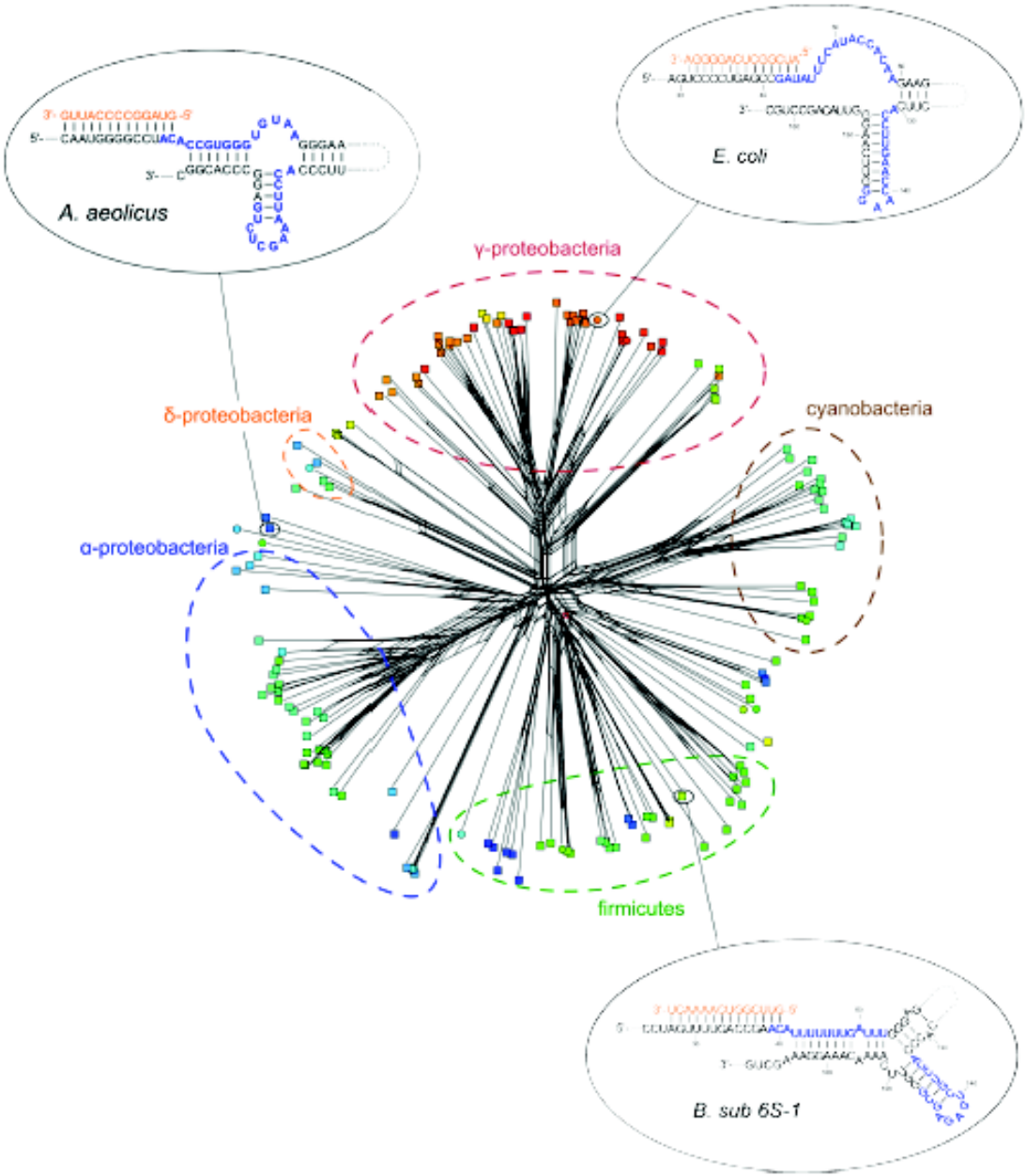
- Analysis of 10000 nt up- & downstream of 6S RNAs of the RFAM alignment

Other strategies: Synteny

- Results:
  - 40% 5-formyltetrahydrofolate cyclo-ligase $\rightarrow$ A
  - 34% Z-ring-associated protein $\rightarrow$ B
  - 28% Recombination factor protein RarA $\rightarrow$ C
  - 22% DNA-binding transcriptional activator ArgP $\rightarrow$ D

	A	B	C	D
alpha	79	41	40	2
gamma	201	235	19	121
firmicutes	8	0	157	0
others	22	76	34	3
total	**311**	**352**	**257**	**126**

Other strategies: Secondary structure rearrangements



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Thank you for your attention!