A genetic and bioinformatic analysis of Streptomyces coelicolor genes containing TTA codons, possible targets for regulation by a developmentally significant tRNA

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Abstract

... Streptomyces coelicolor ... bldA ... S. coelicolor ... Streptomyces avermitilis ... S. coelicolor ... S. avermitilis ... S. coelicolor ... Streptomyces ...

Introduction

Streptomyces

et al.

et al.
Streptomyces
S. coelicolor *et al.* *Streptomyces avermitilis* *et al.*

S. coelicolor

Materials and methods

Sequences

S. coelicolor

S. avermitilis

S. coelicolor

S. coelicolor
et al.

Finding orthologues of TTA-containing genes of *S. coelicolor* in *S. avermitilis*

et al.

S. coelicolor *S. avermitilis*
S. avermitilis *S. coelicolor*
S. coelicolor *S. avermitilis*

Expression prediction

S. coelicolor *S. avermitilis* *et al.*

Distribution of some TTA-containing genes in *S. coelicolor*

Escherichia coli

et al.
et al.
E. coli
S. coelicolor
et al.

et al.

Results

TTA codons in *Streptomyces* genes are rarer than expected

S. coelicolor %

%.
%. %.
% %

et al.

%

Table 1. TTA-containing genes in the *Streptomyces coelicolor* genome

Genome segment (by gene number)	TTA-containing genes*
SCO0001 to 1000	(0010, 0014, **00 0**), 0075, 0101, 0124, 0145, 0182, **0** , 0308, 0383, 0399, 0588, **0** , 0856, 0992
SCO1001 to 2000	1004, **10** , **11** , 1227, **1** , 1273, 1331, **1 0,1** , **1** , 1604, **1– 0,** 1983
SCO2001 to 3000	2320, 2426, 2524, 2603, 2604, **0** ,
SCO3001 to 4000	, 3262, 3265, 3268, 3294, , 3468, 3469, 3487, 3490, 3496, 3498, 3570, 3682, 3693, , **0**, 3776, 3897, 3929, 3930, 3934, , 3982, 3983
SCO4001 to 5000	**01** , 4060, 4063, **11** , **1** , 4213, 4262, 4263, 4301, **1** , 4346, 4349, , 4431, 4464, 4481, , 4615, , 4642, 4671, , **0**, 4823
SCO5001 to 6000	5007, 5017, **0 0**, 5083, 5085, **0** , 5276, 5345, 5350, 5411, , **0** , , 5606, 5633, 5786, 5799, 5881, 5913, –, **0**, 5995
SCO6001 to 7000	6034, 6075, **0** , , 6315, 6324, – , 6386, 6387, 6401, 6595, , 6638, **1–** , **1**, 6925, 6930, 6936
SCO7001 to 7845	7070, 7080, 7091, 7092, 7137, 7212, , , **1**, , **1**, 7465, 7614, 7798, 7801, 7802, 7807, 7812, 7814, (7827, 7833, 7837)

* indicates that there is an orthologue in *S. avermitilis*; *italics* indicates that the annotated gene has an inappropriate start or stop codon; underlining indicates that the genes fall within putative laterally acquired gene islands; and (brackets) indicates that the genes are part of the repeated ends of the chromosome.

S. avermitilis … *S. coelicolor* …

… *S. avermitilis-E. coli Bacillus subtilis* …

… *Deinococcus radiodurans* … *Halobacterium* …

… *Mycobacterium tuberculosis Streptomyces* …

S. coelicolor … *S. avermitilis-*
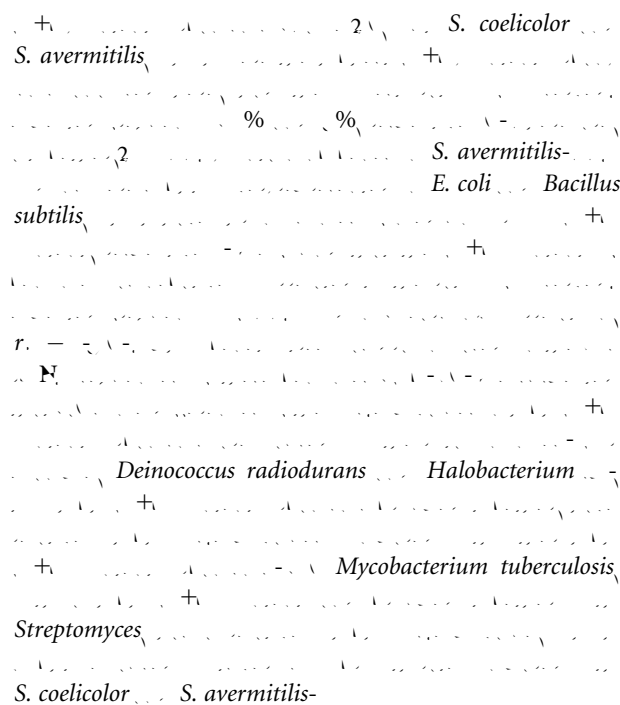
The functional classification of TTA-containing genes in *S. coelicolor*

… *et al.* … *actII-2* … *actII-4* … *redZ* … *SCO0124* … *SCO0383 SCO0399* … *SCO1273* … *SCO5222* … *SCO5799* …

S. avermitilis orthologues of TTA-containing genes of *S. coelicolor*

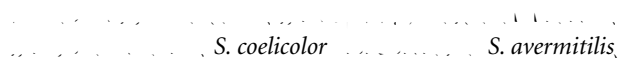… *S. coelicolor* … *S. avermitilis* …
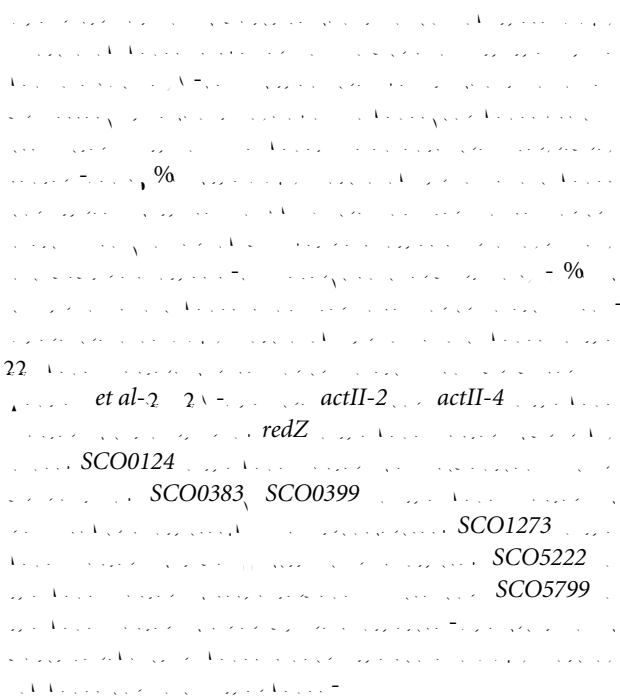
Table. The frequency of TTA codons in some bacterial genomes

Organism*	Accession number	G+C content (%)	Observed frequency (%)	Expected frequency (%)	Ratio of observed/ expected
Bacillus subtilis	NC_000964	43.5	1.9	1.5	1.33
Escherichia coli	NC_000913	50.8	1.4	0.84	1.66
Mycobacterium tuberculosis	NC_002755	65.6	0.16	0.32	0.51
Pseudomonas aeruginosa	NC_002516	66.6	0.029	0.20	0.14
Deinococcus radiodurans	NC_001263, NC_001264	67	0.070	0.19	0.36
Ralstonia solanacearum	NC_003295	67	0.025	0.17	0.15
Caulobacter crescentus	NC_002696	67.2	0.035	0.14	0.25
Bordetella pertussis	NC_002929	67.7	0.022	0.17	0.13
Halobacterium sp.	NC_002607	67.9	0.068	0.18	0.39
S. avermitilis	NC_003155	70.7	0.011	0.12	0.09
S. coelicolor	NC_003888	72.1	0.006	0.095	0.06

*Some genomes with G+C content > 65% are included. *Bacillus subtilis* and *Escherichia coli* genomes are also chosen to represent well-studied bacteria with low or medium G+C content, respectively.
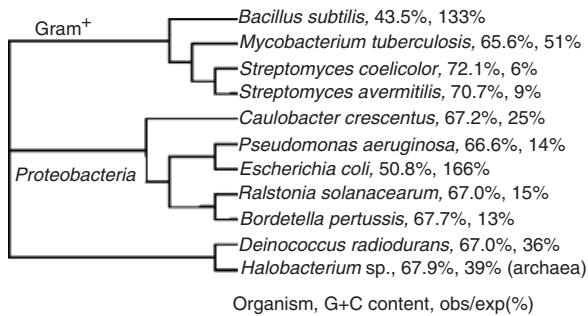
Fig. 1. Phylogenetic tree of microorganisms in Table 3. Their G+C content and the ratio of observed/expected frequency of TTA codon (obs/exp) are also shown.

Table. Function classification of all chromosomal genes and of TTA-containing chromosomal genes in *Streptomyces coelicolor*

Function classification	n (% in all genes)	n (% in TTA-containing genes)
Unknown function	2371 (30.3)	59 (40.7)
Cell processes	802 (10.2)	3 (2.1)
Macromolecule metabolism	496 (6.3)	6 (4.1)
Metabolism of small molecules	1104 (14.1)	15 (10.3)
Cell envelope	1383 (17.7)	21 (14.5)
Extrachromosomal*	139 (1.8)	14 (9.7)
Regulation	965 (12.3)	17 (11.7)
Not classified	565 (7.2)	10 (6.9)
Total	7825 (100.0)	145 (100.0)

*'Extrachromosomal' includes laterally acquired elements, phage-related genes, plasmid-related genes, transposon/insertion element-related genes.

Streptomyces

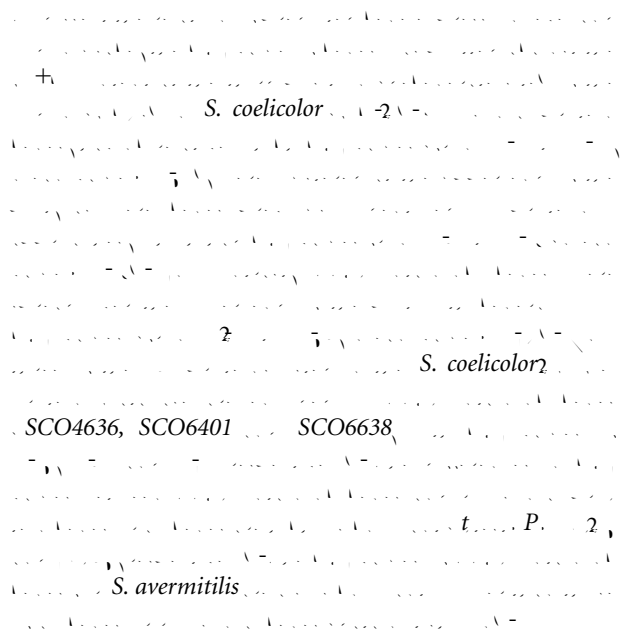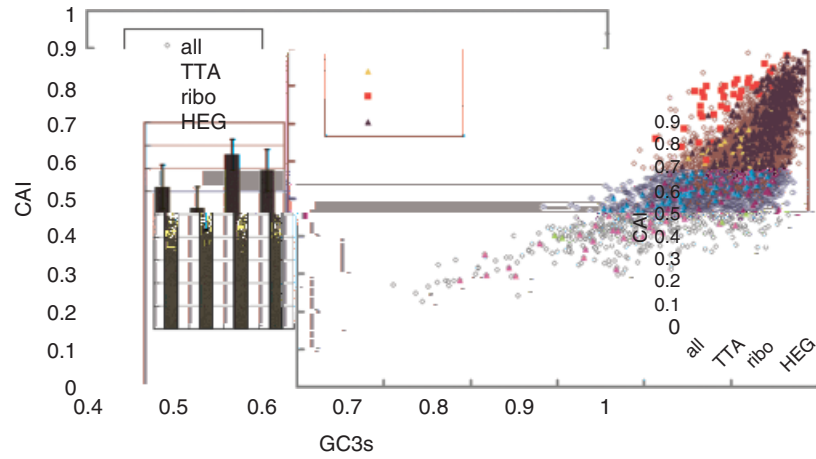### Distribution of 21 TTA-containing genes in *S. coelicolor*
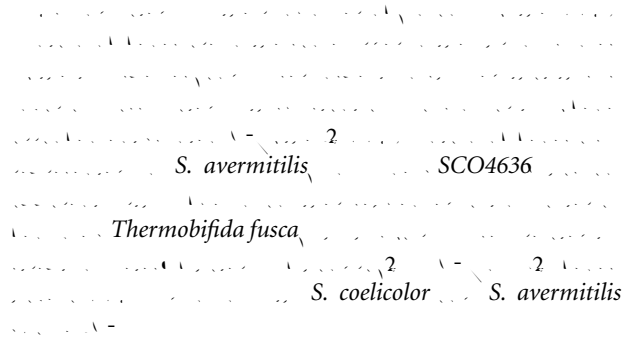
bldA ... *S. coelicolor*

. . . . The codon adaptation index (CAI) values of genes in *S. coelicolor*. (a) CAI plotted against GC3s (G+C content at the 3rd

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act ...

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Author contributions

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bldA

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bldA

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