Electronic Supplementary Materials to the paper of Rokytskyy et al. “Decoding options and accuracy of translation of developmentally regulated UUA codon in *Streptomyces*: bioinformatic analysis”

**Supplementary Methods**

Identification of tRNA genes in genomes of *Streptomyces* coelicolor, S. albus, S. ghanaensis, S. clavuligerus, S. venezuelae and S. lividans species

Sequences of tRNA genes for genome of Streptomyces coelicolor were taken from databases GtRNA-DB (Chan and Lowe 2009) and tRNADB-CE (Abe et al. 2014). Homologous sequences in genomes of *S. albus*, *S. venezuelae*, *S. lividans*, *S. ghanaensis* and *S. clavuligerus* were searched using NCBI Nucleotide database and *Streptomyces* genome server StrepDB. Further screening of the aforementioned genomes for tRNA genes has been carried out with online tRNA search tool tRNAscan-SE (Schattner et al. 2005). Potential isoacceptor tRNA were determined according to literature data (Lim and Curran 2001; Marck and Grosjean 2002; Grosjean et al. 2010). Prediction of tRNA decoding capacities was based on work of dos Reis et al. (2004).

Mining *Streptomyces* coelicolor and *S. albus* genomes for genes involved in tRNA modification

Aminoacid sequences of enzymes for posttranscriptional tRNA modifications in bacteria were taken from MODOMICS database (Machnicka et al. 2013). Orthologs of these enzymes were identified in *Streptomyces* genomes using reciprocal best BLASTP hit strategy (Kuzniar et al. 2008).

Calculating the correlations between focal (cognate) and neighbor (near-cognate) tRNA abundances and mistranslation rates for Streptomyces

Procedure described in (Shah and Gilchrist 2010) has been followed. Equations 3 and 4 described by Shah and Gilchrist (2010) were used to calculate the rates of translation with cognate and near-cognate tRNAs. Certain parameters, such as specific protein synthesis rate and peptide chain elongation rate were taken from Shahab et al. (1996) and Cox (2004). We used fixed wobble penalties of $w_{RR/YY} = 0.61$ and $w_{RY/YR} = 0.64$. These parameters were taken from Curran JF, Yarus M (1989).
Fig. S1. Correlation between a focal tRNA's abundance tF and the abundance of its neighbors tN, across six *Streptomyces* genomes (see Table S1). Each point in panels represents a tRNA species that encodes an aminoacids with degeneracy \( D \) 2 (A), 4 (B) or 6 (C). The solid lines represent the regression lines between tF and tN for each genome. Blue lines represent positive correlation, red ones – negative correlation. The data are dependent and nonrandom (Wilcoxon test, 0.042), and weakly positively correlated (Spearman coefficient, min. 0.354) for set of codons from two-fold and six-fold degenerate groups (panels A and C).
Fig. S2. The mean of the distribution of correlation coefficient values for leucine codons differ significantly from 0 (Wilcoxon test, $p < 0.05$).
Fig. S3. A. Hypothetical secondary structures of tRNA\[^{Leu}_{\text{UAA}}\] from S. albus. Anticodon position is circled. U34 and A37 positions of anticodon are marked with arrows. Enzymes known to be involed in postranscriptonal modification of these positions in model organisms (E. coli, S. cerevisiae etc) are listed at the bottom. B. Multiple sequence alignment of tRNA\[^{Leu}_{\text{UAA}}\] genes from S. coelicolor (bldA), S. albus (XNR_1995) and S. ghanaensis (SSFG_RS20685). Anticodon position is circled
Supplementary References


Shahab N, Flett F, Oliver SG, Butler PR (1996) Growth rate control of protein and nucleic acid content in Streptomyces coelicolor A3(2) and Escherichia coli B/r. Microbiology 142 ( Pt 8):1927-35.