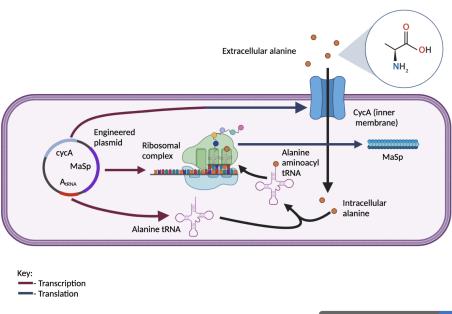
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Quantities modelled

- \bullet A_{intra} Intracellular alanine
- tRNA Alanine tRNA
- A-tRNA Alanyl aminoacyl tRNA
- Synthetase Alanyl-tRNA synthetase catalysing binding of alanine to tRNA
- MaSp Recombinant spider silk protein construct i.e. target protein for synthesis

• CycA - Channel protein which enables alanine uptake into the cell via active transport

2 Parameters

- $N_p = \text{No. plasmids per cell} = 20$
 - Derived from medium copy number of plasmid backbone
- L_{RNA} = Nucleotide base pair length of the mRNA transcript of a gene (or a tRNA itself)
 - $-L_{cycA} = 1413 \text{ bp } [1]$
 - $-L_{tRNA} = 76 \text{ bp } [2]$
 - $-L_{synth} = 2628 \text{ bp } [3]$
- Base transcription rate $k_0 = 45$ base pairs per second[4]
- - $-\ k_{transc}^{cycA} = 0.6369\ s^{-1}$
 - $-\ k_{transc}^{tRNA} = 11.84\ s^{-1}$
 - $-k_{transc}^{synth} = 0.3424 \ s^{-1}$
- \bullet k_{deg} Rate constant for degradation
 - Assume all degradation steps follow first-order kinetics, therefore

$$* k_{deg} = \frac{ln(2)}{\tau_{1/2}}$$

- Protein
 - * Mean $\tau_{1/2} = 20$ hours [5]

*
$$k_{deg}^{CycA} = k_{deg}^{MaSp} = k_{deg}^{Synth} = 9.6 \text{ x } 10^{-6} \text{ s}^{-1}$$

- tRNA
 - * tRNA degradation is only non-negligible for the case of amino acid starvation [6]
 - * $\tau_{1/2} = 10 \text{ minutes}$
 - * $k_{deg}^{tRNA} = 1.2 \times 10^{-3} \ s^{-1}$
- Here we assume alanyl-tRNA complexes are used up sufficiently quickly that they are unlikely to be degraded (by a tRNA nuclease)
- N_k No. alanine residues present within a particular protein k
 - $-N_{CucA} = 47 \text{ residues } [1]$
 - $-N_{MaSp} = 51 \text{ residues } [7]$
 - $-N_{synth} = 91 \text{ residues } [3]$

- Other rate constants
 - k_{cat} Rate constant for alanine uptake through CycA (determined using ML tool DLKCat [8])
 - * $k_{cat} = 0.9953 \ s^{-1}$
 - $-k_{synth}$ = Rate constant for rate-determining aminoacylation step = $2.0s^{-1}$ [9]
- U_0 Base alanine uptake rate
 - $-U_0 = 1.17 \text{ mmol/}30 \text{ seconds/kg wet weight of } E. \text{ coli } [10]$
 - E. coli wet cell weight = 10^{-12} g/cell [11]
 - $: U_0 = 23500 \text{ molecules/cell/second}$
- Initial values of quantities (if non-zero)
 - Equilibrium population of alanine tRNAs per cell = $[D]_0 = 4000$ [12]
 - Equilibrium population of alanyl-tRNA synthetases per cell = $[I]_0$ = 6695 [12]
 - * Uses known equilibrium rate constant (i.e. turnover rate) for the synthetase from [9]

3 Governing Equations

3.1 Alanine import

$$\frac{d[A_{intra}]}{dt} = U_0 + k_{cat}[CycA] \tag{1}$$

3.2 Aminoacylation

If tRNA availability is the limiting factor:

$$\frac{d[A - tRNA]}{dt} = [tRNA] \tag{2}$$

$$\frac{d[A_{intra}]}{dt} = -[tRNA] \tag{3}$$

$$\frac{d[tRNA]}{dt} = -[tRNA] \tag{4}$$

If intracellular alanine availability is the limiting factor:

$$\frac{d[A - tRNA]}{dt} = [A_{intra}] \tag{5}$$

$$\frac{d[tRNA]}{dt} = -[A_{intra}] \tag{6}$$

$$\frac{d[A_{intra}]}{dt} = -[A_{intra}] \tag{7}$$

If synthetase activity is the limiting factor:

$$\frac{d[A - tRNA]}{dt} = k_{synth}[Synthetase] \tag{8}$$

$$\frac{d[tRNA]}{dt} = -k_{synth}[Synthetase] \tag{9}$$

$$\frac{d[A_{intra}]}{dt} = -k_{synth}[Synthetase] \tag{10}$$

3.3 Transcription + translation

 $\label{eq:demand} \mbox{Demand} = \mbox{Alanyl} \mbox{ tRNA demand for translation of CycA and alanyl-tRNA synthetase}$

$$Demand = k_{transc}^{CycA} N_{CycA} + k_{transc}^{Synth} N_{Synth}$$
 (11)

If $[A-tRNA] \ge Demand$:

$$\frac{d[CycA]}{dt} = k_{transc}^{CycA} \tag{12}$$

$$\frac{d[Synthetase]}{dt} = k_{transc}^{Synth} \tag{13}$$

$$\frac{d[MaSp]}{dt} = \frac{[A - tRNA] - Demand}{N_{MaSp}}$$
 (14)

Else:

$$\frac{d[CycA]}{dt} = \frac{[A - tRNA]}{Demand} k_{transc}^{CycA}$$
(15)

$$\frac{d[Synthetase]}{dt} = \frac{[A - tRNA]}{Demand} k_{transc}^{Synth}$$
 (16)

3.4 Degradation

$$\frac{d[CycA]}{dt} = -k_{deg}^{CycA}[CycA] \tag{17}$$

$$\frac{d[Synthetase]}{dt} = -k_{deg}^{Synth}[Synthetase] \tag{18}$$

$$\frac{d[MaSp]}{dt} = -k_{deg}^{MaSp}[MaSp] \tag{19}$$

If alanine availability is the limiting factor for aminoacylation (i.e. under amino acid starvation conditions):

$$\frac{d[tRNA]}{dt} = -k_{deg}^{tRNA}[tRNA] \tag{20}$$

References

- [1] https://biocyc.org/gene?orgid=ECOLI&id=EG12504#
- [2] http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/bacteria/Esch_coli_BL21DE3/genes/tRNA-Ala-GGC-1-1.html
- [3] https://www.uniprot.org/uniprotkb/P00957/entry#sequences
- [4] https://bionumbers.hms.harvard.edu/bionumber.aspx?id=109043&ver=3&trm=transcription&org=
- [5] https://bionumbers.hms.harvard.edu/bionumber.aspx?s=n&v=2&id=111930
- [6] https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5314770/
- [7] Link registry page
- [8] https://www.nature.com/articles/s41929-022-00798-z
- [9] https://doi.org/10.1016/j.jmb.2006.06.015
- [10] https://www.sciencedirect.com/science/article/pii/ S0021925818945072
- [11] https://ecmdb.ca/e_coli_stats
- [12] https://doi.org/10.1128/jb.158.3.769-776.1984