

Modeling of the engineered production of curcumin in *Escherichia coli*

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Introduction

- Curcumin is the major bioactive natural product in turmeric (*Curcuma longa*), which is commonly used as a food additive (flavor and colorant) and traditional medicine for thousands of years.
- Antioxidant[1], anti-cancer[2], anti-allergic[3], anti-inflammatory[4], and anti-Alzheimer's[5] effects
- Current production relies on extraction of producing plants: requires large quantities of farmland and organic solvents[6]
- Microbial production represents a great alternative: saves time and materials.
- Microorganisms can be engineered to produce curcumin by incorporating curcumin biosynthetic enzymes.
- Testing various parameters in lab experiments is time-consuming and labor-intensive.
- This work aims to establish a computer model to simulate the production of curcumin in *Escherichia coli*.

Enzyme Kinetics Data

Enzyme	Substrate	K_m (μ M)	k_{cat} (1/s)	Source
TAL	L-tyrosine	1492.2	155	[7]
4CL	<i>p</i> -coumaric acid	26	88.68	[8]
4CL	caffeic acid	44	31.4	[8]
4CL	ferulic acid	27	126	[8]
C3H	<i>p</i> -coumaric acid	8	10.2	[9]
C3H	<i>p</i> -coumaroyl-CoA	8	10.2	[9]
COMT	caffeic acid	68.75	0.092	[10]
COMT	caffeoyl-CoA	83.04	51.22	[10]
DCS	feruloyl-CoA	46	0.02 (n=1.8)	[11]
CURS	feruloyl-CoA	18	0.018333	[11]

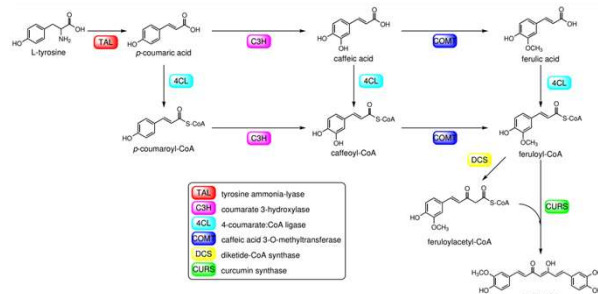


Figure 1: Full pathway from TAL to curcumin

Probabilistic Model Construction

- The PRISM Probabilistic Model Checking language
 - Continuous-time Markov chain (CTMC).
- Two assumptions made
 - The model is unaffected by the cell's central metabolism
 - Byproducts of DCS and CURS are negligible
- Each reaction is a probabilistic transition
 - The ratio of rates determines the probability a reaction will occur
 - A reaction being chosen causes an update in concentration
- Rates are calculating with the Michaelis-Menten and Hill equations

Michaelis-Menten Equation

$$rate = \frac{K_{cat} * [E] * [S]}{K_m + [S]}$$

Hill Equation

$$rate = \frac{K_{cat} * [E] * [S]^n}{K_m^n + [S]^n}$$

- Code snippet
module partial_pathway
[] fcoa > 0 -> v1: (fcoa' = fcoa + 1) & (fcoa' = fcoa - 1);
[] fcoa > 0 & fcoa > 0 -> v2: (cur' = cur + 1) & (fcoa' = fcoa - 1) &
(fcoa' = fcoa - 1);
endmodule

Results

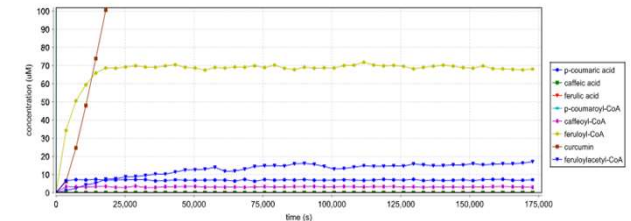


Figure 2: Concentrations of all substrates/products over a 48 hour period

- An average of 100 simulations resulted in 486.565 mg/L curcumin yield.
- C3H may be the limiting enzyme due to rate of *p*-coumaroyl-CoA production
- Overexpression modeling analysis was done to test C3H hypothesis: overexpressing C3H to 50 mg/L increased the curcumin yield 32.7%.
- All combinations of two or three enzymes changed to 10 mg/L or 50 mg/L were simulated to determine the optimum concentration of enzymes (See table below)

Enzyme_concentration (mg/L)	Curcumin yield (mg/L)
C3H_50, DCS_50, CURS_50	957.7
4CL_10, C3H_50, CURS_50	733.2
All at 25	486.6
C3H_10, DCS_50, CURS_10	140

- This data shows that C3H, DCS, and CURS are the three most limiting enzymes and increasing them will increase the final curcumin yield.
- C3H, DCS, and CURS have been marked as further optimization targets

Conclusions and Future Work

- More work is to be done to determine more accurate kinetic parameters for all reactions
- More products will be added to the model (curcuminoids)
- Using the information from our representative model, we will validate the model in the lab.

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GitHub code

