

Supplementary Information

Table S1. Production Yield $Y_{P/S}$ and Biomass Flux from Different Putrescine Producing *C. Glutamicum* Strains.

Strain	$Y_{P/S}$ (mol·mol ⁻¹)	Biomass flux (h·h ⁻¹)	Ref.
PUT3,9,6	0.00	0.99	[1]
PUT12	0.04	0.96	[1]
PUT18	0.12	0.84	[1]
PUT15	0.20	0.77	[1]
PUT21	0.33	0.46	[1]
PUT27	0.43	0.35	[1]
PUT24	0.53	0.25	[1]
NA2	0.35	0.50	This study
NA3	0.37	0.45	This study
NA4	0.37	0.46	This study
NA5	0.43	0.54	This study
NA6	0.53	0.49	This study
NA7	0.49	0.51	This study
NA8	0.47	0.53	This study

Table S2. Changes Made to the Stoichiometric Model of *Corynebacterium Glutamicum* [2].

Reaction Stoichiometry
¹ [c]CPD-217 \rightleftharpoons 24DINH2-PENTANOATE
¹ [c]CPD-299 + CO-A \rightleftharpoons D-ALANINE + ACETYL-COA
¹ [c]D-PROLINE + NADH + PROTON \rightleftharpoons 5-AMINOPENTANOATE + NAD
¹ [c]L-ORNITHINE + 2-KETOGLUTARATE \rightleftharpoons GLT + L-GLUTAMATE-GAMMA-SEMIALDEHYDE
¹ [c]L-ORNITHINE \rightleftharpoons CPD-217
¹ [c]NADP + WATER + 24DINH2-PENTANOATE \rightleftharpoons AMMONIA + NADPH + CPD-299 + PROTON
¹ [c]PRO \rightleftharpoons D-PROLINE
[c]ACETYL-P + ADP \rightleftharpoons ACET + ATP + PROTON
[c]GLYCEROL-3P + NAD \rightarrow DIHYDROXY-ACETONE-PHOSPHATE + NADH
L-LACTATE[c] \rightleftharpoons L-LACTATE[e]
PUTRESCINE[e] \rightleftharpoons PUTRESCINE[c]
L-ORNITHINE[e] \rightleftharpoons L-ORNITHINE[c]
GLYCEROL[e] \rightleftharpoons GLYCEROL[c]
L-ARABINOSE[e] \rightleftharpoons L-ARABINOSE[c]
[c]L-ARABINOSE \rightleftharpoons L-RIBULOSE
[c]L-RIBULOSE + ATP \rightarrow RIBULOSE-5P + ADP
[c]RIBULOSE-5P \rightleftharpoons XYLULOSE-5-PHOSPHATE
D-XYLOSE[e] \rightleftharpoons D-XYLOSE[c]
[c]D-XYLOSE \rightleftharpoons XYLULOSE
[c]XYLULOSE + ATP \rightarrow XYLULOSE-5-PHOSPHATE + ADP

¹ Reactions were constrained to zero. Abbreviations: 24DINH2-PENTANOATE: 2,4-diaminopentanoate; ACET: acetate; ACETYL-P: acetylphosphate; [c]: cytoplasmic; CPD-217: D-ornithine; CPD-299: 2-amino-4-oxopentanoate; [e]: extracellular; GLT: L-glutamate; PRO: L-proline.

References

1. Schneider, J.; Eberhardt, D.; Wendisch, V.F. Improving putrescine production by *Corynebacterium glutamicum* by fine-tuning ornithine transcarbamoylase activity using a plasmid addiction system. *Appl. Microbiol. Biotechnol.* **2012**, *95*, 169–178, doi:10.1007/s00253-012-3956-9.
2. Shinfuku, Y.; Sorpitiporn, N.; Sono, M.; Furusawa, C.; Hirasawa, T.; Shimizu, H. Development and experimental verification of a genome-scale metabolic model for *Corynebacterium glutamicum*. *Microb. Cell Fact* **2009**, *8*, 43, doi:10.1186/1475-2859-8-43.

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