



Simulation of Sustainable Amino Acid Recycling Using a Cooperative Microbial Biosynthesis Pathway

Salman Kamali, Ashraf Gholizadeh*

Division of Biochemistry, Faculty of Natural Sciences and Research Center for Biosciences and Biotechnology (RCBB), University of Tabriz, Tabriz, Iran.

Article Info	Abstract
Document Type: Research Paper Received 12/05/2026 Received in revised form 01/07/2026 Accepted 11/07/2026 Published 01/10/2026 Keywords: <i>Chlamydomonas reinhardtii</i>, Metabolic engineering, Microbial consortium, <i>Neurospora crassa</i>, Nitrogen recycling, <i>Katushka</i>	The global protein dearth represents a major nutritional challenge, with profound consequences for physical health and neurodevelopment. Current protein supplements are costly and expensive, energy-intensive, and inaccessible to the populations most in need. In the present work, we propose a synthetic microbial consortium designed to recycle amino acids from cheap and abundant waste resources, including urea and plant-derived lipids. Our system integrates the photosynthetic algae <i>Chlamydomonas reinhardtii</i> and the filamentous fungus <i>Neurospora crassa</i>, each genetically engineered for complementary metabolic functions. Using COBRApy and MICOM simulations, we modelled amino acid biosynthesis, nitrogen fluxes, and growth stability within the consortium. The obtained data indicate that (i) <i>N. crassa</i> can efficiently convert excess urea into nitrate for transfer to algal cells, (ii) lipid-derived acetate serves as a robust carbon backbone for <i>C. reinhardtii</i>, and (iii) pathway engineering enables overproduction and secretion of the nine essential amino acids. Additionally, the incorporation of the red fluorescent protein Katushka in one algal strain allows optical monitoring of consortium balance and provides a regulatory mechanism via light modulation. We hope that a co-culture of <i>C. reinhardtii</i> and <i>N. crassa</i> can be engineered into a system for amino acid biosynthesis. This engineered metabolic cooperation can achieve stable flux partitioning while maintaining overall productivity.

1. Introduction

Protein malnutrition remains one of the hardest and most persistent global health challenges, disproportionately affecting populations in low- and middle-income countries where access to high-quality dietary protein is limited. An intense deficiency in essential amino acids not only impairs muscle development and immune function but also disrupts neurological growth and cognitive performance, resulting in long-term intergenerational consequences for human health and productivity (Yeh *et al.*, 1988). According to recent estimates by FAO (Food and Agriculture Organization of the United Nations) and WHO (World Health Organization), nearly 10% of the global population suffers from protein-energy malnutrition, a burden intensified by rapid population growth and climate change (Boliko, 2019). Solutions, including protein supplementation, fortified foods, and industrial production of synthetic amino acids, have demonstrated some effectiveness but remain constrained by high costs (Dong & Chen, 2025; Hao *et al.*, 2024), dependence on petrochemical feedstocks, and limited scalability (Möckel & Eggeling, 1994). One strategy for providing nitrogen lies in leveraging waste-derived nitrogen and industrial byproducts as inputs for microbial biosynthesis (Pajares & Bohannan, 2016; Kuypers *et al.*,

2018). Urea, the primary nitrogenous compound (Davis, 1970), and palm oil, a cheap yet underutilized byproduct of global agriculture (Pascoal *et al.*, 2021), represent two inexpensive and renewable precursors for amino acid production. Harnessing these substrates for biosynthetic purposes not only addresses malnutrition but also promotes circular bioeconomy principles by recycling waste streams into high-value nutritional products. In this study, we propose the development of a synthetic microbial consortium for amino acid production, integrating complementary metabolic capacities across distinct microbial partners, including *C. reinhardtii*, a model photosynthetic alga with a well-characterized genome and high carbon fixation capacity, and *N. crassa*, a robust filamentous fungus widely used in genetic and metabolic studies, as key organisms. Through targeted genetic modifications and division-of-labor design (Garrett & Roell *et al.*, 2019), we aimed to engineer a co-culture capable of: (i) assimilating urea as a nitrogen source, (ii) converting lipid-derived carbon skeletons into metabolic precursors, and (iii) efficiently channelling flux toward essential amino acid biosynthesis. By combining computational metabolic modelling with synthetic biology, this platform has the potential to overcome current limitations in amino acid supply, providing a scalable and cost-effective solution for addressing future

*Corresponding author E-mail: aghz_bioch@yahoo.co.in

DOI: 10.22104/mmb.2026.8244.1204

https://mmb.irost.ir/article_1746.html



global protein malnutrition.

2. Materials and Methods

2.1. Consortium design

C. reinhardtii serves as the primary chassis for amino acid biosynthesis, exploiting both photosynthesis (light/CO₂ fixation) and acetate metabolism. To balance the metabolic load, engineering efforts were split into two strains: Chlamy1: acetate-dependent, secreting lysine, histidine, and glucose for *N. crassa*; and Chlamy2: photosynthetic, secreting the other seven essential amino acids, including isoleucine, leucine, methionine, phenylalanine, threonine, tryptophan, and valine.

To prevent competitive dominance, Chlamy2 was engineered to express the Katushka red fluorescent protein. Katushka fluorescence not only serves as an optical marker but also provides a regulatory mechanism: if red fluorescence intensity increases (indicating Chlamy2 overgrowth), light input is adjusted to favor Chlamy1, restoring consortium balance (Shcherbo *et al.*, 2007).

N. crassa was included as a nitrogen-processing partner, with the ability to tolerate high urea concentrations and convert them into nitrate for algae uptake. Lipase secretion from *N. crassa* further enables hydrolysis of palm oil into acetate for algal utilization.

2.2. Genetic modifications

In *C. reinhardtii*: Flagellar genes (*fla10*, *xap5*) deleted to reduce energy burden (Cole *et al.*, 1998); Acetate transporter genes detected in Chlamy2 (*acp1*, *NcMCT1*, *NcSatP*) to minimize competition (Durante *et al.*, 2019); Pathway engineering for essential amino acid overproduction: mutated aspartate kinase, *dap-DC*, *hisG*, *aro7*, α -IPMS, threonine dehydratase (Schmidheini *et al.*, 1989); Secretion enhanced via amino acid transporters (CAT2, AAP); and for glucose secretion in Chlamy1: knockout of AGPase to block amylose synthesis and promoter weakening of glucokinase (Chang *et al.*, 2020).

In *N. crassa*: Hyphal-specific promoter (*gpdA*) driving nitrate transporter expression (*nit3*, *nit6*, *nit10*) (Rubinelli and Marzluf 2004); Overexpressed nitrate/nitrite reductases for reverse flux (urea $\rightarrow$ nitrate export); Lipase secretion under control of *alcA/alcR* promoters (Thomas and Baxter 1987); Inducible arginine secretion system via *Aox1/Mit1* promoter (Lin *et al.*, 2008).

2.3. Growth regulation via light

Hyphal growth of *N. crassa* controlled with blue light (~450 nm) (Madi *et al.*, 1997); Cyclic light-dark regimes reduced metabolic stress.

2.4. In silico simulations

Models constructed in COBRApy and MICOM included: C1: acetate-dependent *C. reinhardtii*; C2: photosynthetic *C. reinhardtii*.

In *N. crassa*: Flux balance analyses evaluated growth rates, amino acid secretion fluxes, and nitrogen redistribution under varied urea/glucose ratios.

3. Results and Discussion

3.1. Growth performance

A co-culture of *C. reinhardtii* and *N. crassa* was engineered into a division-of-labor system for amino acid biosynthesis (Figure 1).

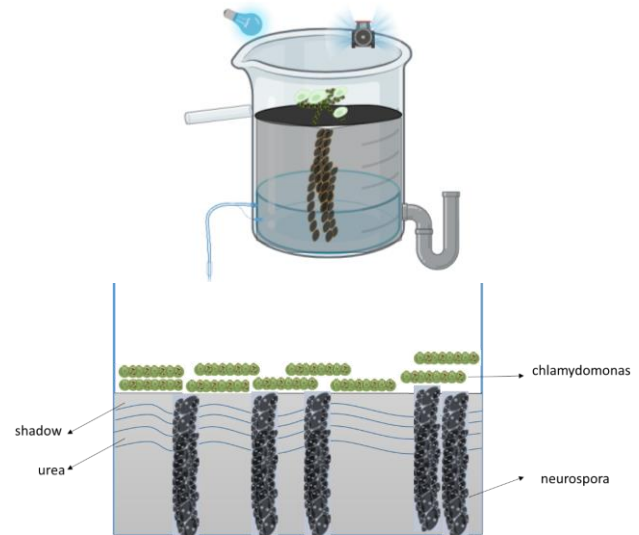


Figure 1. Conceptual model of the proposed microbial consortium. (Note: Schematic overview of the co-culture design between *C. reinhardtii* and *N. crassa*. The alga contributes carbon fixation via photosynthesis, while the fungus assimilates urea-derived nitrogen. Together, the engineered consortium is hypothesized to channel flux toward essential amino acid biosynthesis.)

The wild-type *Chlamydomonas* strain (C1) exhibited a baseline growth rate of 0.18 h⁻¹, which was reduced to 0.09 h⁻¹ after rerouting cytosolic amino acid flux toward secretion. The engineered *Chlamydomonas* strain (C2) maintained a lower baseline growth rate of 1.0 h⁻¹, but secretion of essential amino acids decreased this to 0.05 h⁻¹. The fungal partner (*N. crassa*) displayed a moderate increase in growth rate, from 0.44 h⁻¹ to 1.2 h⁻¹, following nitrate secretion engineering (Figure 2).

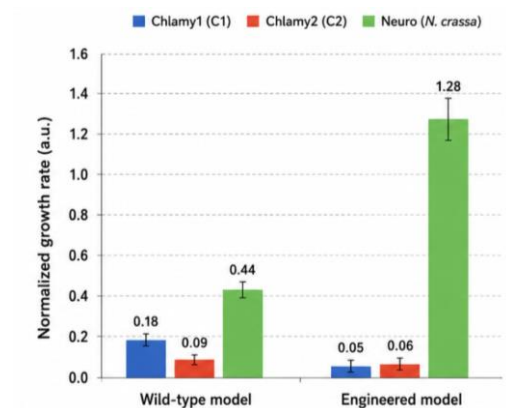


Figure 2. Comparison of growth rate between the wild-type and engineered model. (Note: Growth of *N. crassa* controlled with blue light and Cyclic light-dark regimes. For *in silico* simulations, models constructed in COBRApy and MICOM included: C1: acetate-dependent *C. reinhardtii*; C2: photosynthetic *C. reinhardtii*.)

3.2. Nitrogen fluxes

At urea:glucose ratios $\geq 3:1$, engineered *N. crassa* secreted nitrate, which was taken up by the algal partner. Under balanced nutrient input, fungal cells showed a preference for glucose uptake while retaining intracellular nitrogen. This metabolic division reflects a regulatory bias toward carbon assimilation in the fungal partner.

Urea-synthesizing enzymes were evaluated under defined concentration regimes in which these enzymes exhibit a reverse catalytic activity, converting urea into nitrate. To maintain intracellular homeostasis, nitrate transporters were computationally assessed for their role in exporting the newly generated nitrate across the cell membrane. Metabolic analysis was performed using the COBRApy framework to quantify the bidirectional interplay between glucose uptake, urea availability, and nitrate secretion. Flux balance simulations indicated that variations in glucose and urea influx exerted a direct influence on nitrate export fluxes, confirming a tightly coupled regulatory interaction between carbon and nitrogen metabolic pathways (Figure 3).

Taken together, comparison of the wild-type and engineered model outputs showed that the engineered strains achieved the intended redistribution of amino acid and nitrogen fluxes toward secretion and cross-feeding, despite the associated reduction in growth capacity.

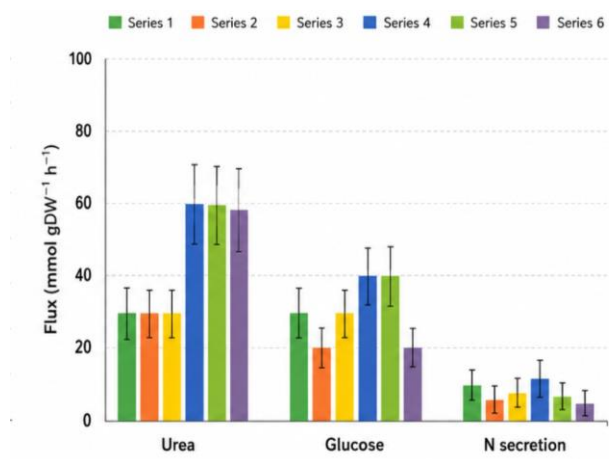


Figure 3. Flux variations in response to glucose and urea availability. (Note: Fluxes are expressed as mmol gDW⁻¹ h⁻¹. The bar plot summarizes the modelled metabolic fluxes associated with urea utilization, glucose uptake, and nitrogen secretion under six distinct nutrient-input scenarios. Series 1–6 represent independent COBRApy-based flux balance simulations performed under different combinations of urea and glucose availability, with each series corresponding to a predefined nutrient-constraint scenario. Thus, differences among the series reflect changes in the imposed nutrient-input constraints rather than differences in the metabolic pathways themselves. For each scenario, fluxes are shown for urea utilization, glucose uptake, and nitrogen secretion, allowing comparison of the predicted carbon–nitrogen metabolic response across nutrient conditions. Values are presented as mean $\pm$ SD where replicate simulations were available.)

3.3. Amino acid production

Engineered *C. reinhardtii* was capable of secreting all nine essential amino acids. Pathway-specific mutations relieved feedback inhibition (Kulis-Horn 2014), while

transporter overexpression reduced intracellular accumulation.

The claim that the engineered *C. reinhardtii* strains are capable of secreting all nine essential amino acids is based on the introduction of suitable transporters that can be engineered in this species. These transporters naturally function as exporters (e.g., transferring metabolites from the plastid to the cytosol). Their localization in the plasma membrane is therefore expected to result in amino acid secretion. Although the exact secretion levels are not quantified in this study and the secretion burden is distributed between the two strains, the mechanistic basis for secretion is the exporter activity of these transporters. To our knowledge, simultaneous secretion of all nine essential amino acids has not been previously reported in *C. reinhardtii*. This study aimed to demonstrate the feasibility of essential amino acid production through *in silico* metabolic engineering in the constructed models.

Since the exact titers, productivity, and optimization of secretion were not the focus of the current computational work, these aspects were not quantified in the main text. Such parameters (e.g., yield consistency, scalability, and optimization under different culture conditions) would require experimental validation in wet-lab cultures, which is planned for future studies.

3.4. Metabolic interdependence and stability

Despite individual reductions in growth rate under engineered secretion pathways, the co-culture exhibited complementary metabolic exchange. *N. crassa* secreted nitrate to support algal nitrogen assimilation, while *C. reinhardtii* (strain C2) exported glucose to be utilized by the fungus. Importantly, amino acid exchange was constrained by transporter regulation, preventing uncontrolled cross-feeding and preserving metabolic autonomy. In this arrangement, C1 specialized in secreting lysine and histidine, while C2 provided the remaining seven essential amino acids. This partitioned production allowed the strains to coexist in a stable division-of-labor consortium, highlighting the potential of rationally designed microbial partnerships for cost-efficient amino acid biosynthesis (Figures 1 and 2).

Our simulations demonstrate the feasibility of a synthetic algal-fungal consortium for amino acid recycling. The fungal nitrogen conversion and algal amino acid biosynthesis offer:

1. Use of inexpensive substrates (urea, palm oil, CO₂).
2. Robust growth control via light-based regulation.
3. Secretion of bioavailable amino acids.
4. Built-in feedback stabilization via Katushka fluorescence.
5. Resilience: even if algal-fungal interactions destabilise, direct urea feeding to *Chlamydomonas* can sustain amino acid output (albeit with less efficiency).

Compared to previous microbial consortia for biofuels (Doebbe et al., 2007; Trost et al., 1997), this system specifically targets nutritional challenges, representing a unique application in food security.

Our simulation results align with earlier findings that demonstrate how microbial consortia can distribute metabolic load for improved biosynthetic yields (Elisáková et al., 2005; Oba et al., 2005). The concept of

“division of labor” in amino acid production is supported by work in *Corynebacterium glutamicum* and yeast, where feedback-resistant enzymes (e.g., acetohydroxy acid synthase, Leu4p) enhanced valine and leucine output, respectively (Elisáková *et al.*, 2005; Oba *et al.*, 2005).

Similarly, our use of *C. reinhardtii* as a carbon-fixing chassis builds on prior reports identifying acetate and sugar transport systems critical for photoheterotrophic balance (Durante *et al.*, 2019; Fleet *et al.*, 2022). The inclusion of the red fluorescent protein Katushka as a dynamic regulatory element introduces an optical feedback control not explored in earlier algal-fungal co-culture systems (Shcherbo *et al.*, 2007; Rasheed *et al.*, 2023). The inclusion of the protein Katushka was proposed as a conceptual strategy, based on previous studies demonstrating its utility as a visible, non-invasive reporter in microbial systems. However, no experimental data regarding its implementation or performance in our co-culture system is presented, as this was not performed in the current study.

We clarify that this remains a suggested approach for future experimental work to enable real-time visual monitoring of culture conditions.

In the fungal partner, *N. crassa*, nitrate secretion and conidiation-linked gene expression were exploited for nitrogen flux control (Rerngsamran *et al.*, 2005; Llamas *et al.*, 2023). The light-sensitive growth inhibition observed here is consistent with known photoregulation in *N. crassa* (Madi *et al.*, 1997). Additionally, our model draws on classical insights into fungal acetate metabolism and

amino acid transport regulation (DeBusk & DeBusk, 1980; DeBusk & DeBusk, 1977; Thomas & Baxter, 1987). The biosynthetic pathway is briefly shown in the following diagram (Figure 4).

From a structural perspective, the presence of hydrophobins may contribute to stable fungal morphology and interfacial assembly within the consortium (Kwan *et al.*, 2006), further enhancing cell-cell compatibility. Previous studies of *Chlamydomonas* mutants resistant to tryptophan analogs (Dutcher *et al.*, 1992) support the feasibility of metabolic pathway modifications conferring feedback resistance.

In comparison with existing consortia for biofuel or nutrient production (Doebbe *et al.*, 2007; Trost *et al.*, 1997), the present system targets a nutritional goal—amino acid recycling—bridging environmental sustainability and food security. Our findings suggest that engineered metabolic cooperation can achieve stable flux partitioning while maintaining overall productivity.

4. Conclusion

This work outlines a framework for sustainable amino acid recycling by integrating photosynthetic algae and filamentous fungi into a synthetic consortium. By converting nitrogenous and lipid-rich waste into essential amino acids, this system has the potential to provide low-cost nutritional supplementation at scale. Future research will focus on laboratory validation, optimization of promoter systems, and pilot-scale bioreactor testing.

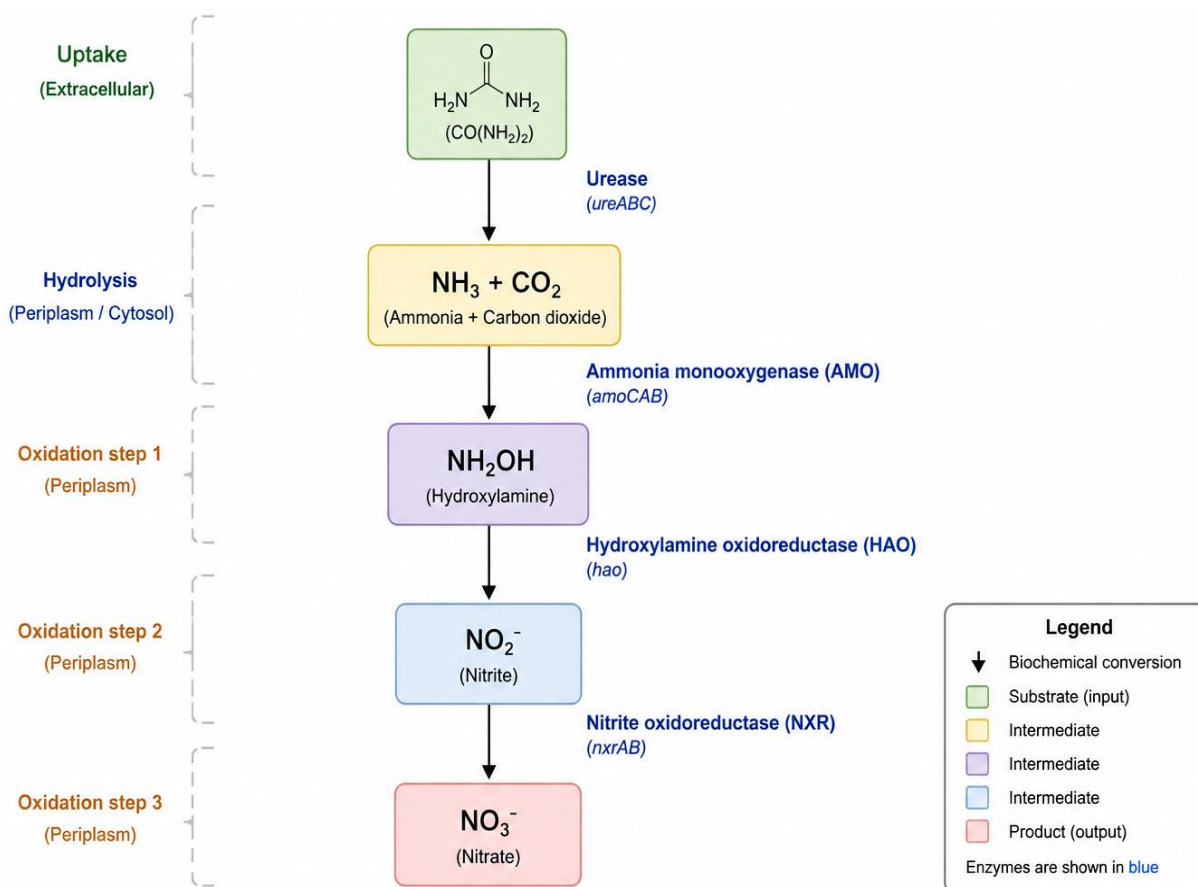


Figure 4. The biosynthetic pathway for nitrate production from urea

Conflict of interest

The authors declare no conflict of interest.

Acknowledgment

The authors thank for the Division of Biochemistry, Faculty of Natural Sciences & Research Center for Biosciences and Biotechnology (RCBB) at the University of Tabriz, Iran, for their assistance and supporting the present research work.

Ethical approval

This article does not contain any studies with human participants or animals performed by any of the authors.

Open access

This article is distributed under the terms of the Creative Commons Attribution License which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

Funding

None declared.

Data availability

Data will be made available on request: Engineered metabolic json models are public in zenodo; Doi chlamy: 10.5281/zenodo.17650156; Doi neuro: 10.5281/zenodo.17650228. Wild model addresses: *Chlamydomonas reinhardtii*: https://github.com/baliga-lab/chlamy_model_iCre1355/blob/master/Neurospora_crassa: <https://github.com/Fxe/biomodels/commit/937e2428935d5d57ff0092231ed5a31c6ab66c0d>

Authors' Contributions

Salman Kamali contributed the conceptualization, methodology, computational analysis, data analysis, visualization, writing and original drafting. Ashraf Gholizadeh did supervision, manuscript review and editing, and manuscript submission. All authors have read and approved the final version of the manuscript.

References

- Boliko, M.C. (2019). FAO and the situation of food security and nutrition in the world. *Journal of Nutritional Science and Vitaminology*, S4-S8. <http://doi.org/10.3177/jnsv.65.S4>
- Chang, K.S., Kim, J., Park, H., Joo Hong, S., Lee, C.G., Jin, E. (2020). Enhanced lipid productivity in AGP knockout marine microalga *Tetraselmis* sp. using a DNA-free CRISPR-Cas9 RNP method. *Bioresource Technology*, 303, 122932. <http://doi.org/10.1016/j.biortech>
- Cole, D.G., Diener, D.R., Himelblau, A.L., Beech, P.L., Fuster, J.C., Rosenbaum, J.L. (1998). *Chlamydomonas kinesin-II-dependent intraflagellar transport (IFT): IFT particles contain proteins required for ciliary assembly in Caenorhabditis elegans sensory neurons. Journal of Cell Biology*, 141(4), 993–1008. <http://doi.org/10.1083/jcb.141.4.993>
- Davis, R.H. (1970). Sources of urea in *Neurospora*. *Biochimica et Biophysica Acta*, 215(2), 412-414. [http://doi.org/10.1016/0304-4165\(70\)90042-5](http://doi.org/10.1016/0304-4165(70)90042-5)
- DeBusk, R.M., DeBusk, A.G. (1977). An inducible acetate transport system in *Neurospora crassa conidia*. *Biochimica et Biophysica Acta*, 470(3), 475–483. [http://doi.org/10.1016/0005-2736\(77\)90138-9](http://doi.org/10.1016/0005-2736(77)90138-9)
- DeBusk, R.M., DeBusk, A.G. (1980). Physiological and regulatory properties of the general amino acid transport system of *Neurospora crassa*. *Journal of Bacteriology*, 143(1), 188–197. <http://doi.org/10.1128/jb>
- Doebbe, A., Rupprecht, J., Beckmann, J., Mussnug, J.H., Hallmann, A., Hankamer, B., Kruse, O. (2007). Functional integration of the HUP1 hexose symporter gene into the genome of *C. reinhardtii*: Impacts on biological H₂ production. *Journal of Biotechnology*, 131(1), 27–33. <http://doi.org/10.1016/j.jbiotech>
- Dong, Y., Chen, Z. (2025). Systems metabolic engineering of *Corynebacterium glutamicum* for efficient L-tryptophan production. *Synthetic and Systems Biotechnology*, 10(2), 511–522. <https://doi.org/10.1016/j.synbio>
- Durante, L., Hübner, W., Lauersen, K.J., Remacle, C. (2019). Characterization of the GPR1/FUN34/YaaH Protein Family in the Green Microalga *Chlamydomonas* Suggests Their Role as Intracellular Membrane Acetate Channels. *Plant Physiology*, 3(6), e00148. <http://doi.org/10.1002/pld3>
- Dutcher, S.K., Galloway, R.E., Poortinga, G. (1992). Tryptophan analog resistance mutations in *Chlamydomonas reinhardtii*. *Genetics*, 131(3), 593–607. <http://doi.org/10.1093/genetics>
- Elisáková, V., Pátek, M., Holátko, J., Nesvera, J., Leyval, D., Goergen, J.L., Delaunay, S. (2005). Feedback-resistant acetoxy acid synthase increases valine production in *Corynebacterium glutamicum*. *Applied Environmental Microbiology*, 71(1), 207–213. <http://doi.org/10.1128/AEM>
- Fleet, J., Ansari, M., Pittman, J.K. (2022). Phylogenetic analysis and structural prediction reveal the potential functional diversity between green algae SWEET transporters. *Frontiers in Plant Science*, 13, 960133. <http://doi.org/10.3389/fpls>
- Hao, Y., Pan, X., You, J., Li, G., Xu, M., Rao, Z. (2024). Microbial production of branched chain amino acids: Advances and perspectives. *Bioresource Technology*, 397, 130502. <https://doi.org/10.1016/j.biortech>
- Kulis-Horn, R.K. (2014). Histidine biosynthesis, its regulation and biotechnological application in *Corynebacterium glutamicum*. *Microbial Biotechnology*, 7(1), 5–25. <http://doi.org/10.1111/1751-7915.12055>
- Kuypers, M.M.M., Marchant, H.K., Kartal, B. (2018). The microbial nitrogen-cycling network. *Nature*

- Reviews of Microbiology*, 16(5), 263–276. <http://doi.org/10.1038/nrmicro.2018.9>
- Kwan, A.H., Winefield, R.D., Sunde, M., Matthews, J.M., Haverkamp, R.G., Templeton, M.D., Mackay, J.P. (2006). Structural basis for rodlet assembly in fungal hydrophobins. *Proceedings of the National Academy of Sciences USA*, 103(10), 3621–3626. <http://doi.org/10.1073/pnas.0505704103>
- Llamas, A., Loen-Miranda, E., Tejada-Jimenez, M. (2023). Microbial and nitrogen fixing bacterial consortia: from interaction to biotechnological potential. *Plants*, 12(13), 2476. <http://doi.org/10.3390/plants12132476>
- Lin, S.H., Kuo, H.F., Canivenc, G., Lin, C.S., Lepetit, M., Hsu, P.K., Tillard, p., Lin, H.L., Wang, Y.Y., Tsai, C.B., Gojon, A., Tsay, Y.F. (2008). Mutation of the Arabidopsis NRT1.5 nitrate transporter causes defective root-to-shoot nitrate transport. *The Plant Cell*, 20(9), 2514–2528. <http://doi.org/10.1105/tpc.108.060244>
- Madi, L., McBride, S.A., Bailey, L.A., Ebbole, D.J. (1997). Rco-3, a gene involved in glucose transport and conidiation in *Neurospora crassa*. *Genetics*, 146(2), 499–508. <http://doi.org/10.1093/genetics>
- Möckel, B., Eggeling, L. (1994). Threonine dehydratases of *Corynebacterium glutamicum* with altered allosteric control: their generation and biochemical and structural analysis. *Molecular Microbiology*, 13(5), 833–842. <http://doi.org/10.1111/j.1365-2958>
- Oba, T., Nomiya, S., Hirakawa, H., Tashiro, K., Kuhara, S. (2005). Asp578 in LEU4p is one of the key residues for leucine feedback inhibition release in sake yeast. *Bioscience, Biotechnology and Biochemistry*, 69(7), 1270–1273. <http://doi.org/10.1271/bbb>
- Pajares, S., Bohannan, B.J. (2016). Ecology of nitrogen fixing, nitrifying, and denitrifying microorganisms in tropical forest soils. *Frontiers in Microbiology*, 7, 1045. <http://doi.org/10.3389/fmicb.2016.01045>
- Pascoal, P.V., Ribeiro, D.M., Cereijo, C.R., Santana, H., Nascimento, R.C., Steindorf, A.S., Calsing, L.C.G., Formighieri, E.F., Brasil, B.S.A.F. (2021). Biochemical and phylogenetic characterization of the wastewater tolerant *Chlamydomonas biconvexa* Embrapa/LBA40 strain cultivated in palm oil mill effluent. *PLOS One*, 16(4), e0249089. <http://doi.org/10.1371/journal.pone.0249089>
- Rasheed, N.R., Pourbakhtiar, A., Mehdizadeh, A.M., Baharlooiean, M., Rafiei, N., Alishah, A.H., Morones-Ramirez, J.R., Winck, F.V. (2023). Microbial co-cultivation recent methods, trends in omic studies, applications and future challenges. *Frontiers in Bioengineering and Biotechnology*, 11, 1193424. <http://doi.org/10.3389/fbioe>
- Rerngsamran, P., Murphy, M.B., Doyle, S.A., Fluffy, D.J.A. (2005). The major regulator of conidiation in *Neurospora crassa*, directly activates a developmentally regulated hydrophobin gene. *Molecular Microbiology*, 56(1), 282–297. <http://doi.org/10.1111/j.1365-2958>
- Roell, G.M., Zha, J., Carr, R.R., Koffas, M.A., Fonf, S.S., Tang, Y.J. (2019). Engineering microbial consortia by division of labor. *Microbial Cell Factories*, 18(1), 35. <http://doi.org/10.1186/s12934-019-1083-3>
- Rubinelli, F.G., Marzluf, G.A. (2004). Identification and characterization of a nitrate transporter gene in *Neurospora crassa*. *Biochemistry and Genetics*, 42(1-2), 21–34. <http://doi.org/10.1023/b:bigi.0000012141.51114.23>
- Schmidheini, T., Sperisen, P., Paravicini, G., Hütter, R., Braus, G. (1989). A single point mutation results in a constitutively activated and feedback-resistant chorismate mutase of *Saccharomyces cerevisiae*. *Journal of Bacteriology*, 171(3), 1245–1253. <http://doi.org/10.1128/jb>
- Shcherbo, D., Merzlyak, E.M., Chepurnykh, T.V., Fradkov, A.F., Ermakova, G.V., Solovieva, E.A., Lukyanov, K.A., Bogdanova, E.A., Zaisky, A.G., Lukyanov, S., Chudakov, D.M. (2007). Bright far-red fluorescent protein Katushka for *in vivo* imaging. *Nature Methods*, 4(9), 741–446. <http://doi.org/10.1038/nmeth1083>
- Thomas, C.M., Baxter, R.L. (1987). Analysis of mutational lesions of acetate metabolism in *Neurospora crassa* by ¹³C nuclear magnetic resonance. *Journal of Bacteriology*, 169(1), 359–366. <http://doi.org/10.1128/jb>
- Trost, J.T., Chisholm, D.A., Jordan, D.B., Diner, B.A. (1997). The D1 C-terminal processing protease of photosystem II from *Scenedesmus obliquus*. Protein purification and gene characterization in wild type and processing mutants. *Journal of Biological Chemistry*, 272(33), 20348–20356. <http://doi.org/10.1074/jbc>
- Yeh, P., Sicard, A.M., Sinskey, A.J. (1988). General organization of the genes specifically involved in the diaminopimelate-lysine biosynthetic pathway of *Corynebacterium glutamicum*. *Molecular and General Genetics*, 212(1), 105–111. <http://doi.org/10.1007/BF00322451>

How to cite this paper:

Kamali, S., & Gholizadeh, A. (2026). Simulation of Sustainable Amino Acid Recycling by Using a Cooperative Microbial Biosynthesis Pathway. (e1746). *Microbiology, Metabolites and Biotechnology*, 9(1), e1746 <https://doi.org/10.22104/mmb.2026.8244.1204>