Gyumin Lee

Systems biology researcher dissecting microbial adaptation mechanisms through integrated multi-omics analysis

Affiliation | Postdoctoral Researcher, Center for Synthetic Biology, Korea Research Institute of Bioscience and Biotechnology (KRIBB), C1 team led by Hyewon Lee, Ph.D. **Email** | sysbiogyumin@kribb.re.kr | sysbio.gyumin@gmail.com **Date** | May 2026

Education

Period	Degree	Institution
2019.03 – 2026.02	Ph.D. (Integrated M.S./Ph.D.), Chemical Engineering	Ulsan National Institute of Science and Technology (UNIST), advisor: Donghyuk Kim, Ph.D.
2011.03 – 2017.02	B.S., Genetic Engineering	Kyung Hee University

Dissertation: Systems-Level Dissection of Methanol Adaptation in *Methylorubrum extorquens*

Research Experience

Period	Position	Institution
2026.03 – present	Postdoctoral Researcher	Korea Research Institute of Bioscience and Biotechnology (KRIBB), Center for Synthetic Biology, C1 team led by Hyewon Lee, Ph.D.
2019.03 – 2026.02	Graduate Researcher (Integrated M.S./Ph.D.)	Department of Chemical Engineering, Systems Biology and Machine Learning Lab, UNIST (Donghyuk Kim, Ph.D.)

Research Interests

- AI-augmented synthetic biology workflows
- Systems metabolic engineering
- Strain improvement via adaptive laboratory evolution (ALE)
- C1 (methane, methanol) carbon metabolism and utilization
- Multi-omics integration (genomics, transcriptomics)
- Protein function analysis with AI-driven structure prediction

Doctoral Research

Three-axis dissection of methanol adaptation mechanisms across *Methylorubrum extorquens* species. An 8-strain pan-genome comparison defined the evolutionary divergence between the complex, plasmid-rich AM1 and the streamlined PA1; AM1 wild-type ~800-generation ALE identified *metY* (F36L, S383L) and *kefB* adaptive variants; ALE of engineered PA1 Δ*fdh234* converged on the *metY-1* Y57D substitution. Together these findings propose OAHS substrate-specificity rewiring as a primary adaptive lever that takes precedence over catabolic flux optimization.

Selected Research Projects

1. Methanol adaptation mechanisms via ALE of *M. extorquens* AM1

- Methods: ALE (~800 generations) of AM1 wild-type, integrated WGS + RNA-seq analysis, AlphaFold3-based structural interpretation of mutations
- Outcomes: Identification of *metY* F36L/S383L and *kefB* variants; mechanism proposing substrate-specificity rewiring as primary adaptive lever over catabolic flux optimization
- Contribution: First author (experimental design, analysis, writing)
- Publication: Published in *J Biol Eng* 2025. https://doi.org/10.1186/s13036-025-00557-1

2. Convergent adaptation in engineered *M. extorquens* PA1 (Δ*fdh234*)

- Methods: ALE (~800 generations) of PA1 Δ*fdh234*, integrated WGS + RNA-seq analysis, AlphaFold3-based structural interpretation of mutations
- Outcomes: Convergent *metY-1* Y57D substitution recapitulating substrate-specificity rewiring mechanism observed in AM1; "Anabolic accuracy over catabolic engineering" framing
- Contribution: First author (experimental design, analysis, writing)
- Publication: Manuscript under revision at *BITE*. Title: "Anabolic accuracy over catabolic engineering in adaptive laboratory evolution of methanol tolerance"

3. Pan-genome comparison of C1 metabolic pathways across 8 *M. extorquens* strains

- Methods: Pan-genome-based comparison of central metabolic networks, quantification of intra-species metabolic diversity
- Outcomes: Genomic differences and accessible metabolic pathways across strains
- Contribution: First author (analysis design, data processing, writing)
- Publication: *Biotechnol. Bioprocess Eng.* 2022 (IF 3.0 / Q2)

4. Characterization of bacteriophages as antibiotic alternatives

- Methods: Genomic analysis and host-range characterization of three novel phages targeting *Staphylococcus aureus*
- Outcomes: Confirmed therapeutic applicability
- Contribution: Co-first author (data analysis and writing)
- Publication: *J. Virol.* 2025 (IF 3.8 / Q2)

5. Comparative genomics of a plant pathogen

- Methods: Comparative genome analysis of *Erwinia pyrifoliae* strains
- Outcomes: Characterization of conservation and natural variation of pathogenicity-related genes
- Contribution: First author (analysis and writing)
- Publication: *Plant Pathol. J.* 2020 (IF 2.5 / Q2)

6. Autotrophic growth pathways in *Clostridium drakei* (collaborative project)

- Contribution: Data analysis collaborator
- Publication: *PNAS* 2020 (IF 9.1 / Q1), co-author

AI-Augmented Research Workflow

Building and operating a Claude Code–based automation environment for synthetic biology data workflows.

- **Claude Code environment design**: Personal dotfiles repository hosting multiple skills/agents/hooks covering data analysis, literature review, and visualization automation
- **Multi-agent workflow**: Domain-specific agents for data processing (@data), visualization (@viz), literature synthesis (@lit), manuscript editing (@editor)
- **Synthetic biology pipeline integration**: Ongoing effort to integrate code agents (e.g., Claude Code) into ALE, RNA-seq, and WGS analyses; plan to extend across synbio pipelines to shorten the data→hypothesis→experiment iteration cycle
- **GitHub**: `https://github.com/gyuminlee-repo`

Internal Seminars

- 2026-05-22, "A practical seminar on Claude Code", Korea Research Institute of Bioscience and Biotechnology (KRIBB)

Selected Publications

9 SCI journal articles total, 5 as first author. Own name in bold.

1. Cho J-h*, **Lee GM***, Ko S, Kim Y, Kim D. "Characterization and therapeutic potential of newly isolated bacteriophages against *Staphylococcus* species in bovine mastitis". *J Virol*. 2025;99(3). doi:10.1128/jvi.01901-24 *Co-first author. IF 3.8 (Q2).
2. **Lee GM**, Pham KN, Bang I, Ko S, Kim D. "Integrated genomic and transcriptomic insights into methanol tolerance mechanisms in *Methylobacterium extorquens* AM1, identifying key targets for strain engineering". *J Biol Eng*. 2025. doi:10.1186/s13036-025-00557-1 First author.
3. **Lee GM**, Scott-Nevros ZK, Lee S-M, Kim D. "Pan-genome Analysis Reveals Comparative Genomic Features of Central Metabolic Pathways in *Methylorubrum extorquens*". *Biotechnol Bioprocess Eng*. 2023;28(6):990-1004. doi:10.1007/s12257-022-0154-1 First author. IF 3.0 (Q2).
4. **Lee GM**, Ko S, Oh E-J, Song Y-R, Kim D, Oh C-S. "Comparative Genome Analysis Reveals Natural Variations in the Genomes of *Erwinia pyrifoliae*, a Black Shoot Blight Pathogen in Apple and Pear". *Plant Pathol J*. 2020;36(5):428-439. doi:10.5423/PPJ.OA.06.2020.0097 First author. IF 2.5 (Q2).
5. Song Y, Lee JS, Shin J, **Lee GM**, Jin S, Kang S, et al. "Functional cooperation of the glycine synthase-reductase and Wood–Ljungdahl pathways for autotrophic growth of *Clostridium drakei*". *PNAS*. 2020;117(13):7516-7523. doi:10.1073/pnas.1912289117 Co-author (4th of 13). IF 9.1 (Q1).
6. **Lee GM**, et al. "Anabolic accuracy over catabolic engineering in adaptive laboratory evolution of methanol tolerance". Manuscript under revision (*BITE*). First author.

Technical Skills

Wet lab Adaptive laboratory evolution (ALE), growth phenotyping, gene editing and mutation reconstruction (allelic exchange), RNA-seq library preparation, bacterial cultivation

Omics analysis WGS, pan-genome analysis, RNA-seq, differential expression (DEG) analysis, functional gene-set analysis, AlphaFold3-based protein structure prediction, COBRApy-based genome-scale metabolic modeling (GEM)

Programming & AI Tooling Python and R pipelines for large-scale omics analysis and visualization automation Claude Code–based agentic workflows (multi-agent orchestration, custom skills/hooks/agents) Synthetic biology data workflow automation (a working case of integrating AI coding agents into systems biology research)

Differentiating Strengths

- **AI-integrated workflow**: Coupling synthetic biology research with AI coding agents to gain analysis speed and reproducibility together
- **Integration of experiment and analysis**: End-to-end execution from ALE experimental design to multi-omics interpretation
- **Systems-level interpretation**: Mechanistic insight from integration of genome, transcriptome, and protein-structure data rather than a single omics layer