

Curriculum Vitae

Hideto Mori, Ph.D.

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Web: <https://sites.google.com/view/hidetomori>

Biosketch

My work involves the development of innovative technologies that support genome editing and DNA synthesis, with a particular emphasis on creating new software tools. In collaboration with Professor Yachie from UBC and Osaka University, we are currently engaged in developing 'DNA Event Recording' technology. This technology is designed to encode the historical molecular dynamics of cells into DNA sequences. Furthermore, as of October 2023, I have started a project that empowers AI to automate the design and synthesis of DNA sequences. The goal of this project is to harness AI technology to enhance the efficiency and innovation of DNA sequence design and synthesis, thereby advancing biological methodologies.

Education

March 2023 Ph.D., Systems Biology Program, Keio University, Tokyo, Japan
March 2018 M.M.G., Systems Biology Program, Keio University, Tokyo, Japan
March 2016 B.A., Faculty of Environmental Information, Keio University, Tokyo, Japan.

Work Experiences

2023-Today Specially Appointed Associate Professor (Full-Time)
Premium Research Institute for Human Metaverse Medicine (PRIME), Osaka University
2021-2023 Research Assistant (ITCK Fellow)
Institute for Advanced Biosciences, Keio University
2016-2021 Research Assistant
Research Center for Advanced Science and Technology, The University of Tokyo
2018-2019 Research Associate (Fixed term/Research incentive)
Graduate School of Media and Governance, Keio University
2014-2018 Research Assistant (ITCK Fellow)
Institute for Advanced Biosciences, Keio University

Research Experiences

2016-Today @Yachie laboratory
Research Center for Advanced Science and Technology
The University of Tokyo
Premium Research Institute for Human Metaverse Medicine (PRIME)
Osaka University
(2023-Today) Automating DNA Design & Synthesis Using Conversational AI
(2016-Today) Development of software tools to accelerate the development of genome editing tools and their applications
(2020-2022) A framework to efficiently describe and share reproducible DNA construction protocols <https://github.com/yachielab/QUEEN>
(2019-2021) Screening of new genome editing tools
(2019-2021) Development of a novel hierarchical DNA assembly method
(2018-Today) A universal platform to analyze genome editing outcomes
(2018-2020) A machine learning model to predict base editing outcomes
<https://github.com/yachielab/base-editing-prediction>

(2016-2018) A software tool to screen new genome editing-associated gene candidates
<https://github.com/yachielab/SPADE>

- 2021-2023 @Ikawa laboratory
The Institute of Medical Science, The University of Tokyo
Exploring the mechanism for species-specific fusion of male and female gametes.
- 2013-2016 @Naito laboratory,
Institute for Advanced Biosciences, Keio University
Development of a web-based biological model simulation environment

Fellowships and Research grants (as PI)

- 2023.10–2029.03 Japan Science and Technology Agency (JST) CREST (BioDX) (JPY 13,000,000 / 5.5 years)
- 2020.04–2022.09 JSPS Research Fellowship (DC2) Japan Society for the Promotion of Science

Awards

- 2024.05 The 23rd Funai Information Technology Award for Young Scientists
- 2024.02 The 40th Inoue Research Award for Young Scientists.

Research Achievements

+Equal contribution. Mori H is **bolded and underlined**. *Mori H is (co-)first author. Selected papers.

Preprints

- 1- Ishikawa Y Y, Emori C, **Mori H**, Endo T, Kobayashi K, Watanabe Y, Sagara H, Nagata T, Motooka D, Ninomiya A, Ozawa M, Ikawa M. Age-associated aberrations of cumulus-oocyte interaction and microfilamentous structure in the zona pellucida decline female fertility.
bioRxiv. 2023 Dec 30, <https://doi.org/10.1101/2023.12.30.573680>
- 2- Ishiguro S+, Ishida K+, Sakata RC+, **Mori H**, Takana M, King S, Bashth O, Ichiraku M, Masuyama N, Takimoto R, Kijima Y, Adel A, Toyoshima H, Seki M, Oh JH, Archambault AS, Nishida K, Kondo A, Kuhara S, Aburatani H, Klein Geltink RI, Takashima Y, Shakiba N & Yachie N. A multi-kingdom genetic barcoding system for precise target clone isolation.
bioRxiv. 2023 Jan 19, <https://www.biorxiv.org/content/10.1101/2023.01.18.524633v2>

Peer-reviewed articles

- 3- Ozawa M, **Mori H**, Endo T, Ishikawa-Yamauchi Y, Motooka D, Emori C, & Ikawa M. Age-related decline in spermatogenic activity accompanied with endothelial cell senescence in male mice. *iScience*. 2023, 108456. <https://doi.org/10.1016/j.isci.2023.108456>
- 4- Hino T, Omura SN, Nakagawa R, Togashi T, Takeda SN, Hiramoto T, Tasaka S, Hirano H, Tokuyama T, Uosaki H, Ishiguro S, Kagineva M, Yamano H, Ozaki Y, Motooka D, **Mori H**, Kirita Y, Kise Y, Itoh Y, Matoba S, Aburatani H, Yachie N, Karvelis T, Siksnyš V, Ohmori T, Hoshino A, Nureki O. An AsCas12f-based compact genome-editing tool derived by deep mutational scanning and structural analysis. *Cell*. 2023 Sep 22:S0092-8674(23)00963-7. doi: 10.1016/j.cell.2023.08.031.
- 5- Oura S, **Mori H** & Ikawa M. Genome editing in mice and its application to the study of spermatogenesis. *Gene and Genome Editing*. 2022 Dec;3-4:100014. doi:10.1016/j.ggedit.2022.100014.
- 6-* **Mori H** & Yachie N. A framework to efficiently describe and share reproducible DNA materials and construction protocols.
Nature Communications. 2022 May 24;13(1):2894. doi: 10.1038/s41467-022-30588-x. PMID: 35610233.
- 7- Nakagawa R, Ishiguro S, Okazaki S, **Mori H**, Tanaka M, Aburatani H, Yachie N, Nishimasu H & Nureki O. Engineered *Campylobacter jejuni* Cas9 variant with enhanced activity and broader targeting range. *Communications Biology*. 2022 Mar 8;5(1):211. doi: 10.1038/s42003-022-03149-7. PMID: 35260779.
- 8- Konno N, Kijima Y+, Watano K+, Ishiguro S+, Ono K, Tanaka M, **Mori H**, Masuyama N, Pratt D, Ideker T, Iwasaki W & Yachie N. Deep distributed computing to reconstruct extremely large lineage trees. *Nature Biotechnology*. 2022 Apr;40(4):566-575. doi: 10.1038/s41587-021-01111-2. PMID: 34992246.

- 9- Fukushima T, Tanaka Y, Adachi K, Masuyama N, Tsuchiya A, Asada S, Ishiguro S, Mori H, Seki M, Yachie N, Goyama S & Kitamura T. CRISPR/Cas9-mediated base-editing enables a chain reaction through sequential repair of sgRNA scaffold mutations.
Scientific Reports. 2021 Dec 13;11(1):23889. doi: 10.1038/s41598-021-02986-6. PMID: 34903756.
- 10- Yamamuro T, Nakamura S, Yamano Y, Endo T, Yanagawa K, Tokumura A, Matsumura T, Kobayashi K, Mori H, Enokidani Y, Yoshida G, Imoto H, Kawabata T, Hamasaki M, Kuma A, Kuribayashi S, Takezawa K, Okada Y, Ozawa M, Fukuhara S, Shinohara T, Ikawa M & Yoshimori T. Rubicon prevents autophagic degradation of GATA4 to promote Sertoli cell function.
PLOS Genetics. 2021 Aug 5;17(8):e1009688. doi: 10.1371/journal.pgen.1009688. PMID: 34351902.
- 11-* Sakata RC+, Ishiguro S+, Mori H+, Tanaka M, Tatsuno K, Ueda H, Yamamoto S, Seki M, Masuyama N, Nishida K, Nishimasu H, Arakawa K, Kondo A, Nureki O, Tomita M, Aburatani H & Yachie N. Base editors for simultaneous introduction of C-to-T and A-to-G mutations.
Nature Biotechnology. 2020 Jul;38(7):865-869. doi: 10.1038/s41587-020-0509-0. PMID: 32483365.
- 12- Murai Y, Masuda T, Onuma Y, Evans-Yamamoto D, Takeuchi N, Mori H, Masuyama N, Ishiguro S, Yachie N & Arakawa K. Complete Genome Sequence of *Bacillus* sp. Strain KH172YL63, Isolated from Deep-Sea Sediment.
Microbiology Resource Announcements. 2020 Apr 16;9(16):e00291-20. doi: 10.1128/MRA.00291-20. PMID: 32299884.
- 13-* Masuyama N+, Mori H+, & Yachie N. DNA barcodes evolve for high-resolution cell lineage tracing.
Current Opinion in Chemical Biology. 2019 Oct;52:63-71. doi: 10.1016/j.cbpa.2019.05.014. PMID: 31212208.
- 14- Ishiguro S, Mori H & Yachie N. DNA event recorders send past information of cells to the time of observation.
Current Opinion in Chemical Biology. 2019 Oct;52:54-62. doi:10.1016/j.cbpa.2019.05.009. PMID: 31200335.
- 15- Evans-Yamamoto D, Takeuchi N, Masuda T, Murai Y, Onuma Y, Mori H, Masuyama N, Ishiguro S, Yachie N & Arakawa K. Complete Genome Sequence of *Psychrobacter* sp. Strain KH172YL61, Isolated from Deep-Sea Sediments in the Nankai Trough, Japan.
Microbiology Resource Announcements. 2019 Apr 18;8(16):e00326-19. doi: 10.1128/MRA.00326-19. PMID: 31000557.
- 16-* Mori H, Evans-Yamamoto D, Ishiguro S, Tomita M & Yachie N. Fast and global detection of periodic sequence repeats in large genomic resources.
Nucleic Acids Research. 2019 Jan 25;47(2):e8. doi: 10.1093/nar/gky890. PMID: 30304510.
- 17- Nishimasu H, Shi X, Ishiguro S, Gao L, Hirano S, Okazaki S, Noda T, Abudayyeh OO, Gootenberg JS, Mori H, Oura S, Holmes B, Tanaka M, Seki M, Hirano H, Aburatani H, Ishitani R, Ikawa M, Yachie N, Zhang F & Nureki O. Engineered CRISPR-Cas9 nuclease with expanded targeting space.
Science. 2018 Sep 21;361(6408):1259-1262. doi: 10.1126/science.aas9129. PMID: 30166441.
- 18- Yachie, N., Robotic Biology Consortium (Mori H was involved in the IT group) & Natsume, T. Robotic Biology Consortium, Natsume T. Robotic crowd biology with Maholo LabDroids.
Nature Biotechnology. 2017 Apr 11;35(4):310-312. doi: 10.1038/nbt.3758. PMID: 28398329.

Review articles (in Japanese)

- 19-* 坂田 莉奈+ & 森 秀人+ 細胞プログラミング技法と治療応用③. *実験医学* 37, 13, 2197-2202 (2019)
- 20-* 坂田 莉奈+ & 森 秀人+ 細胞プログラミング技法と治療応用②. *実験医学* 37, 10, 1838-1846 (2019)
- 21-* 坂田 莉奈+ & 森 秀人+ 細胞プログラミング技法と治療応用①. *実験医学* 37, 8, 1324-1333 (2019)
- 22-* 森 秀人 & 谷内江 望 新規ゲノム編集ツールを探索する. *月刊細胞* 51, 3, 114-118 (2019)
- 23-* 森 秀人 DNA イベントレコーダーによって細胞の過去の状態を知る. *実験医学* 37, 3, 440-448 (2019)
- 24-* 森 秀人 & 石黒 宗 ウェットなデータストレージメディアとしての DNA. *実験医学* 37, 1, 106-112 (2019)
- 25-* 森 秀人 & 谷内江 望 (翻訳) Carvunis A-R & Ideker T. Siri of the cell. ～生物学は iPhone から何を学べるだろうか～. *実験医学別冊* (2017)
- 26- 石黒宗, 森 秀人 & 谷内江望 DNA バーコードおよびゲノム編集を用いた細胞系譜の一斉追跡技術. *生体の科学* 68, 3, 273-281 (2017).
- 27- 石黒宗, 森 秀人 & 谷内江望 DNA バーコードによる生命科学実験の限界突破. *実験医学増刊号* 35 (2017)

Books (in Japanese)

- 28- 谷内江 望, 増山 七海, 関 元昭, 山本-エヴァンス 楠, 石黒 宗, 森 秀人, 坂田 莉奈, 今野 直輝, 松尾 仁嗣 & 木島 佑輔. 超生物学—次の X〜私たちがいま手にしている細胞工学.
編集/谷内江 望, 羊土社, ISBN 978-4-7581-2252-8, 2021

Poster presentations

- 29-* Mori H, Evans-Yamamoto D, Ishiguro S, Tomita M & Yachie N. SPADE for exploring periodic sequence repeats as potential genome editing modules, *The 20th International Conference on Systems Biology*, Okinawa, Japan, November 2019
- 30-* Mori H, Evans-YamamotoD, Ishiguro S, Tomita M & Yachie N. SPADE for exploring and analyzing genome editing systems. *第19回 東京大学 生命科学シンポジウム*, 東京, 2019年 4月
- 31-* Mori H, Masuyama N, Evans-Yamamoto D, Ishiguro S, Sakata R, Nishimatsu H, Tomita M, Miyaoka Y, Nureki O, Hiroyuki A and Yachie N. DIAMOND: fully automated software to analyze amplicon sequencing data. *Keystone Symposia Conference on Genome Engineering: From Mechanisms to Therapies*, Victoria, Canada, February 2019
- 32-* Mori H, Evans-YamamotoD, Ishiguro S, Tomita M & Yachie N. Global detection of periodic sequence repeats in large genomic resources. *第2回 慶應ライフサイエンスシンポジウム*, 日吉, 2018年 9月
- 33-* Mori H, Evans-YamamotoD, Ishiguro S, Tomita M & Yachie N. Fast and global detection of periodic sequence repeats in large genomic resources. *RECOMB Comparative Genomics 2018*, Quebec, Canada, October 2018
- 34-* Mori H, Evans-YamamotoD, Ishiguro S, Tomita M & Yachie N. Global landscape of periodically repeating DNA elements in prokaryotic genomes. *第18回 東京大学 生命科学シンポジウム*, 東京, 2018年 4月
- 35-* Mori H, Evans-Yamamoto D, Ishiguro S, Tomita M & Yachie N. Global landscape of periodically patterned DNA elements in prokaryotic genomes. *第 40 回日本分子生物学会*, 神戸, 2017年 12 月
- 36-* Mori H, Evans-Yamamoto D, Ishiguro S, Tomita M & Yachie N. Exploration of periodically patterned DNA elements in genomic and metagenomic sequences. *12th International Workshop on Advanced Genomics*, Tokyo Japan, June 2017
- 37-* Mori H, Evans-Yamamoto D, Ishiguro S, Tomita M & Yachie N. Exploration of periodically patterned DNA elements in genomic and metagenomic sequences. *From Genetic Networks to a Cellular Wiring Diagram*, Tokyo Japan, April 2017

Talks

- 38-* Hideto Mori. DNA event recording system through advanced DNA engineering technologies. *Frontiers of bioinformatics and its clinical application*, Osaka, Japan, February 2024
- 39-* Hideto Mori. DNA event recording system through advanced DNA engineering technologies. *Seminar in Nara Institute of Science and Technology (Invited talk)*, Nara, Japan, December 2023
- 40-* 森 秀人. DNA 配列の設計・合成の自動化に向けたソフトウェアツールの開発.
京都大学 物質・細胞統合システム拠点 (iCeMS) 藤田研究室 (招待講演), 2023 年 12 月
- 41-* 森 秀人. DNA 配列設計を支援するソフトウェアツールの開発.
生命情報科学若手の会 第 9 回セミナー (招待講演), オンライン講演, 2023 年 11 月
- 42-* 森 秀人. 新規ゲノム編集システムの開発にむけた汎用的ソフトウェア群の開発.
2019 年度 医学研セミナー 東京都医学総合研究所 (招待講演), 2020 年 2 月
- 43-* Mori H, Evans-Yamamoto D, Ishiguro S, Tomita M & Yachie N. Global landscape of periodically patterned DNA elements in prokaryotic genomes. *E. coli Systems Biology Workshop*, Awaji, Japan, March 2018
- 44-* Mori H, Evans-Yamamoto D, Ishiguro S, Tomita M & Yachie N. Exploration of periodically patterned DNA elements as potential genome editing modules. *E. coli Systems Biology Workshop*, Awaji, Japan, March 2017
- 45-* 森 秀人, 内藤泰宏, 富田 勝. Web ブラウザを用いた汎用的細胞シミュレーション環境の構築. *SFC Open Research Forum 2015*, 東京, 2015 年 11 月

Patents submitted

- 46- Mori H, Yamaguchi N & Yachie N. FRACTAL Assembly (Japan)
Application number: JP2021151200A