Curriculum Vitae

Hideto Mori, Ph.D.

Premium Research Institute for Human Metaverse Medicine (PRIMe), Osaka University

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Bio

森は、これまでソフトウェアツール開発を中心に、ゲノム編集や DNA 配列合成を支援する革新的技術の開発に携わってきた。現在は、大阪大学 RPIMe 特任教授の谷内江と共に、細胞の過去の分子動態を DNA 配列へと記録する技術「DNA イベントレコーディング」の開発に取り組んでいる。また、2023 年 10 月から、AI を活用した DNA 配列設計・合成の自動化プロジェクトを開始した。本プロジェクトは、AI 技術を活用して、DNA 配列の設計と合成プロセスを効率化し、新しい生物学的アプローチの道を開くことを目指している。

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 (TTCK 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 (TTCK Fellow)
	Institute for Advanced Biosciences, Keio University

Research Experiences

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.
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
(2019-2021) Screening of new genome editing tools
(2019-2021) Development of a novel hierarchical DNA assembly method
(2016-Today) Development of software tools to accelerate the development of genome editing tools and their applications
(2016-2018) A software tool to screen new genome editing-associated gene candidates
https://github.com/yachielab/SPADE
(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
(2020-Today) A framework to efficiently describe and share reproducible DNA construction protocols
https://github.com/yachielab/QUEEN

2013-2016   @Naito laboratory,
                 Institute for Advanced Biosciences, Keio University
                 Development of a web-based biological model simulation environment

Fellowships
2020-2022   JSPS Research Fellowship (DC2) Japan Society for the Promotion of Science

Awards
2024.02   The 40th Inoue Research Award for Young Scientists. (TBA)

Funds
2023.10–2029.03 Japan Science and Technology Agency (JST) CREST (BioDX) (JPY 13,000,000 / 5.5 years)

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

Preprints
1- 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
2- 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
3- Hino T, Omura SN, Nakagawa R, Togashi T, Takeda SN, Hiramoto T, Tasaka S, Hirano H, Tokuyama T, Uosaki H, Ishiguro S, Kagieva M, Yamano H, Ozaki Y, Motooka D, **Mori H**, Kirita Y, Kise Y, Itoh Y, Matoba S, Aburatani H, Yachie N, Karvelis T, Siksnys 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.
4- 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.
5-* **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.

6- 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.

7- 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.

8- 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.

9- 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.

10-* 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.

11- 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.

12-* 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.

13- 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.

14- 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.

15-* **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.

16- 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.

17- 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)

18-* 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)

19-* 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)

20-* 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)

21-* **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)

22-* **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)

23-* **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)

24-* **森 秀人** & 谷内江 望（翻訳）CarvunisA-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)

25- 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).

26- 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)

27- 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

28-* **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

29-* **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

30-* **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 analyzeamplicon sequencing data. *Keystone Symposia Conference on GenomeEngineering: From Mechanisms to Therapies*, Victoria, Canada, February 2019

31-* **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

32-* **Mori H**, Evans-YamamotoD, Ishiguro S, Tomita M & Yachie N. Fast and global detection of periodic sequence repeats in large genomicresources. *RECOMB Comparative Genomics 2018*, Quebec, Canada, October 2018

33-* **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

34-* **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

35-* **Mori H**, Evans-Yamamoto D, Ishiguro S, Tomita M &Yachie N. Exploration of periodically patterned DNA elements in genomic andmetagenomic sequences. *12th International Workshop on Advanced Genomics*, Tokyo Japan, June 2017

36-* **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

37-* **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, オンライン講演, 2023 年 11 月

38-* **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(招待講演), 東京都医学総合研究所, 2020 年 2 月

39-* **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

40-* **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

41-* **森 秀人**, 内藤泰宏, 冨田 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

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