

## Curriculum Vitae

### Dan Yamamoto (Daniel Evans-Yamamoto)

Ph.D. Candidate

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## Education

- Present Ph.D. candidate  
Systems Biology Program, Graduate school of Media and Governance, Keio University, Tokyo, Japan  
Thesis title: Deciphering the evolution of protein–protein interactions  
Supervisors: Drs. Christian R. Landry and Yasuhiro Naito
- March 2020 Master of Media and Governance with a certificate in Systems Biology  
Systems Biology Program, Graduate school of Media and Governance, Keio University, Tokyo, Japan  
Thesis title: Pooled matrix screen of protein interactomes using Barcode Fusion Genetics-Protein fragment Complementation Assay (BFG-PCA)  
Supervisors: Drs. Nozomu Yachie and Masaru Tomita
- March 2018 Bachelor of Arts in Environment and Information Studies with honor  
Faculty of Environment and Information Studies, Keio University, Tokyo, Japan.  
Thesis title: Development of high-throughput technologies to screen protein interactomes  
Supervisors: Drs. Nozomu Yachie and Masaru Tomita

## Research Experiences

November 2020–Present

**Research Intern @Landry laboratory, Université Laval, Québec, Canada**

Projects:

- 1- Characterization of function and protein interaction characters of orthologous genes
- 2- Characterization of protein-protein interaction characters of orthologous subunits in a protein complex

October 2014–March 2020

**Visiting student @Yachie laboratory, the University of Tokyo, Tokyo, Japan**

Projects:

- 1- Development of a plasmid based DHFR-PCA system
- 2- Implementation of Barcode Fusion Genetics to DHFR-PCA

## Work Experiences

April 2020 – present

**Part-time visiting researcher @Systems Biology Institute, Tokyo, Japan**

Responsibilities and Achievements:

- 1- Analysis of biomedical data
- 2- Literature search of academic publication and patent applications
- 3- Summarizing data analysis and literature search to reports

April 2018 – May 2020

**Part-time researcher @Yachie laboratory, the University of Tokyo, Tokyo, Japan**

Project: Development of a novel high-throughput binary protein-protein interaction detection method

Responsibilities and Achievements:

- 1- Implementation of plasmid system for the protein-protein interaction detection method DHFR-PCA
- 2- High throughput assay of the developed DHFR-PCA with DNA barcodes (Barcode Fusion Genetics-DHFR PCA)
- 3- Development of computational pipelines to analyze massively parallel sequencing data of DNA barcodes
- 4- Mentoring interns associated in the interactome project

## Publications

Preprints and submitted manuscripts

9. **D. Evans-Yamamoto**, A.K. Dubé, G. Saha, S. Plante, D. Bradley, I. Gagnon-Arsenault, C.R. Landry "Parallel nonfunctionalization of CK1δ/ε kinase ohnologs following a whole-genome duplication event", (2023) *BioRxiv* Available from [doi.org/10.1101/2023.10.02.560513](https://doi.org/10.1101/2023.10.02.560513)

Peer-reviewed articles

8. Y. Kijima, **D. Evans-Yamamoto**, H. Toyoshima, N. Yachie "A universal sequencing read interpreter", (2023) *Science Advances*, 9(1):eadd2793. Doi: 10.1126/sciadv.add2793
7. **D. Evans-Yamamoto**, F.D. Rouleau, P. Nanda, K. Makanae, Y. Liu, P.C. Després, H. Matsuo, M. Seki, A.K. Dube, D. Ascencio, N. Yachie & C.R. Landry "BFG-PCA: tools and resources that expand the potential for binary protein interaction discovery", (2022) *Nucleic Acids Research*, gkac045. Doi: 10.1093/nar/gkac045
6. G. Suzuki, Y. Saito, M. Seki, **D. Evans-Yamamoto**, M. Negishi, K. Kakoi, H. Kawai, C. Landry, N. Yachie & T. Mitsuyama "Machine learning approach for discrimination of genotypes based on bright-field cellular images", (2021) *npj Systems Biology and Applications*, 7:31. Doi: 10.1038/s41540-021-00190-w
5. Y. Murai, T. Masuda, Y. Onuma, **D. Evans-Yamamoto**, N. Takeuchi, H. Mori, N. Masuyama, S. Ishiguro, N. Yachie, K. Arakawa "Complete Genome Sequence of Bacillus sp. Strain KH172YL63, Isolated from Deep-Sea Sediment", (2019) *Microbiology Resource Announcements*, 9:e00291-20. Doi: 10.1128/MRA.00291-20
4. A. Marchant, A. Cisneros, A. Dube, I. Gagnon-Arsenault, D. Ascencio, H. Jain, S. Aube, C. Eberlein, **D. Evans-Yamamoto**, N. Yachie, C. Landry., "The role of structural pleiotropy and regulatory evolution in the retention of heteromers of paralogs", (2019) *eLife*, 8:e46754. Doi: 10.7554/eLife.46754
3. **D. Evans-Yamamoto**¶, N. Takeuchi¶, T. Masuda, Y. Murai, Y. Onuma, H. Mori, N. Masuyama, S. Ishiguro, N. Yachie, K. Arakawa "Complete Genome Sequence of Psychrobacter sp. Strain KH172YL61, Isolated from Deep-Sea Sediments in the Nankai Trough, Japan", (2019) *Microbiology Resource Announcements*, 8:e00326-19. Doi: 10.1128/MRA.00326-19(¶ equal contribution)
2. H. Mori, **D. Evans-Yamamoto**, S. Ishiguro, M. Tomita, and N. Yachie., "Fast and global detection of periodic sequence repeats in large genomic resources", (2018) *Nucleic Acid Research*, 47(2):e8 Doi: 10.1093/nar/gky890
1. N. Yachie, Robotic Biology Consortium (**D. Evans-Yamamoto** was involved in the IT group), and T. Natsume., "Robotic Crowd Biology: LabDroids accelerates life science experiments", (2017) *Nature Biotechnology*, 35(4):310-312. Doi: 10.1038/nbt.3758

## Conference presentations (Poster format presentation)

10. **D. Evans-Yamamoto**, F. Rouleau, P. Nanda, K. Makanae, H. Matsuo, M. Seki, A. K. Dube, D. Ascencio, N. Yachie and C. R. Landry. "Barcode Fusion Genetics-Protein-fragment Complementation Assay (BFG-PCA): tools and resources that expands the potential for binary protein interaction discovery", *2022 Wellcome connecting science, Evolutionary Systems Biology*. February 10<sup>th</sup>, 2022
9. **D. Evans-Yamamoto**, F. Rouleau, P. Nanda, K. Makanae, H. Matsuo, M. Seki, A. K. Dube, D. Ascencio, N. Yachie and C. R. Landry. "Barcode Fusion Genetics-Protein-fragment Complementation

Assay (BFG-PCA): tools and resources that expands the potential for binary protein interaction discovery”, **2021 IBIS student day**. August 25<sup>th</sup>, 2021

8. **D. Evans-Yamamoto**, F. Rouleau, P. Nanda, K. Makanae, H. Matsuo, M. Seki, A. K. Dube, D. Ascencio, C. R. Landry and N. Yachie. “Pooled matrix screen of protein interactomes using Barcode Fusion Genetics-Protein-fragment Complementation Assay (BFG-PCA)”, **2021 PROTEO symposium**. May 18<sup>th</sup>, 2021
7. **D. Evans-Yamamoto**, F. Rouleau, P. Nanda, K. Makanae, H. Matsuo, M. Seki, A. K. Dube, D. Ascencio, C. R. Landry and N. Yachie. “Pooled matrix screen of protein interactomes using Barcode Fusion Genetics-Protein-fragment Complementation Assay (BFG-PCA)”, **2021 Cold Spring Harbor meeting: Network Biology**. (Virtual). March 17<sup>th</sup>, 2021
6. **D. Evans-Yamamoto**, P. Nanda, F. Rouleau, K. Makanae, H. Matsuo, M. Seki, A. K. Dube, D. Ascencio, M. Tomita, H. Aburatani, C. R. Landry and N. Yachie. “Pooled matrix screen of protein interactomes using Barcode Fusion Genetics-Protein-fragment Complementation Assay (BFG-PCA)”, **International Conference on Systems Biology 2019 (ICSB 2019)**. Okinawa, Japan. November 4<sup>th</sup>, 2019.
5. **D. Evans-Yamamoto**, P. Nanda, H. Matsuo, M. Seki, A. K. Dube, D. Ascencio, M. Tomita, H. Aburatani, C. R. Landry and N. Yachie, “Development of Barcode Fusion Genetics-DHFR PCA”, **19th Symposium on Life Sciences of the University of Tokyo**, Tokyo, Japan. April 20<sup>th</sup>, 2019.
4. **D. Evans-Yamamoto**, P. Nanda, H. Matsuo, M. Seki, A. K. Dube, D. Ascencio, M. Tomita, H. Aburatani, C. R. Landry and N. Yachie, “Development of Barcode Fusion Genetics-DHFR PCA”, **13<sup>th</sup> LSBM Symposium**, Hakone, Japan. April 3<sup>rd</sup>, 2019.
3. **D. Evans-Yamamoto**, P. Nanda, H. Matsuo, M. Seki, A. K. Dube, M. Tomita, H. Aburatani, C. R. Landry and N. Yachie, “Development of Barcode Fusion Genetics-DHFR PCA”, **IBIS student day 2018**, Quebec City, Canada. August 23<sup>rd</sup>, 2018
2. **D. Evans-Yamamoto**, M. Tomita and N. Yachie. “Development of high-throughput technologies to screen protein interactomes”, **12<sup>th</sup> LSBM Symposium**, Fuefuku, Japan. March 8<sup>th</sup>, 2018.
1. **D. Evans-Yamamoto**, H. Matsuo, C. R. Landry, M. Yoshida, M. Tomita and N. Yachie. “Screening inter-species protein interactomes using Barcode Fusion Genetics”, **From Genetic Networks to a Cellular Wiring Diagram**, Tokyo, Japan. April 27<sup>th</sup>, 2017.

## Awards/Fellowships

April 2020–September 2023	Research Fellowship for Young Scientists, <i>Japan Society for Promotion of Science</i> 200,000 JPY / Month
April 2015–Today	TTCK Research Fellowship, <i>Keio University</i> (April 2021–March 2023) 1,600,000 JPY (April 2020–March 2021) 1,200,000 JPY (April 2019–March 2020) 800,000 JPY (April 2018–March 2019) 291,200 JPY (April 2017–March 2018) 460,000 JPY (April 2016–March 2017) 433,330 JPY (April 2015–March 2016) 454,900 JPY
June 2021–February 2023	Watanabe Foundation International Scholarship <i>The Watanabe Foundation</i> , 150,000 JPY / month
August 2021	Best Poster Award, <i>IBIS student day</i> , awarded 150 CAD as prize
July 2020	Graduate Fellowship for Young Leaders <i>Sylff organization through Keio University</i> , 1,000,000 JPY
March 2018	Graduation Thesis Award, SFC, <i>Keio University</i>

## Research Funding

1. April 2020–March 2023, Grant-in-Aid for JSPS Fellows, *Japan Society for Promotion of Science*  
Development of a novel analysis pipeline on protein evolution based on biophysical functionality  
2,500,000 JPY
2. April 2019–March 2020, Taikichiro Mori Memorial Research Grant, *Taikichiro Mori Memorial Research Fund*  
Evolution analysis on proteins from biophysical interaction properties  
240,000 JPY
3. Yamagishi Student Project Support Program. (June 2017-February 2018)  
Evolutionary analysis of protein complexes from an inter-species screening approach  
240,000 JPY
4. Yamagishi Student Project Support Program. (June 2016-February 2017)  
Expanding high-throughput protein interaction detection methods towards personal interactome technologies  
270,000 JPY

## Skills

### 1- Genetic engineering

- a. Design and construction of various plasmid DNAs for bacteria, yeast and mammalian cells
- b. Design and construction of various gene induction circuits with DNA recombination
- c. Design and construction of plasmid DNA libraries including ORFeome libraries and DNA barcodes
- d. Design and construction of gRNAs for CRISPR/Cas9 genome editing

### 2- Yeast molecular biology and genetics

- a. Yeast cell culture and transformation
- b. Deletion of genes in Yeast cells
- c. In-yeast DNA assembly
- d. Yeast two-hybrid method and DHFR-PCA to detect protein-protein interactions

### 3- Mammalian culture cell engineering

- a. Basic cell culture and passage of mammalian cells
- b. Plasmid DNA transfection of mammalian cells
- c. CRISPR/Cas9 base editing in mammalian cells

### 4- Computational skills

- a. Python
  - i. Data analysis on public data
  - ii. Analyzing high-throughput DNA sequencing data
  - iii. Parallel computing on Sun Grid Engine servers
- b. R
  - i. Statistical testing
  - ii. Data visualization
- c. Genome editing outcome analyses
- d. Single-cell transcriptome data analysis using Drop-seq tools (Moderate)
- e. Single-cell transcriptome data analysis using R, Seurat package (Moderate)

### 5- Other skills

- a. Operation of high-throughput sequencers (Illumina MiSeq)
- b. Operation of Nanopore sequencers (Oxford Nanopore Technologies, MinION)