

## Curriculum Vitae

### Dan Yamamoto (Daniel Evans-Yamamoto)

Ph.D. Student

Institute for Advanced Biosciences, Keio University

Systems Biology Program, Graduate School of Media and Governance, Keio University

Tel: +81-90-1258-7842 / +1-508-744-3752

E-mail: [daney@sfc.keio.ac.jp](mailto:daney@sfc.keio.ac.jp) / [dan.yamamoto.evans@gmail.com](mailto:dan.yamamoto.evans@gmail.com)

## Education

- March 2020      Master of Media and Governance, *Systems Biology Program, 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, *Keio University, Tokyo, Japan*.  
Thesis title: Development of high-throughput technologies to screen protein interactomes  
Supervisors: Drs. Nozomu Yachie and Masaru Tomita  
Graduation Thesis Award

## Research Experiences

October 2014–March 2020

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

- Projects:    a. Development of a plasmid based DHFR-PCA system  
              b. Implementation of Barcode Fusion Genetics to DHFR-PCA

- 1- Design and construction of a new DHFR-PCA system
- 2- Design and construction of pooled DHFR-PCA screening using DNA barcodes
- 3- Development of a novel DNA barcoding method

November 2020–Today

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

Project: Characterization of function and protein interaction characters of orthologous genes

- 1- Yeast genetic screening
- 2- Interaction screening of protein variants

## Work Experiences

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

- 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- Data analysis of protein-protein interaction data
- 5- Mentoring interns associated in the interactome project

## Awards/Fellowships

August 2021      Best Poster Award, *IBIS student day (internal conference)* 150 CAD

April 2020–Today    Research Fellowship for Young Scientists, *Japan Society for Promotion of Science* 2,400,000 JPY / Year

April 2015–Today    TTCK Research Fellowship, *Keio University*

(April 2021–March 2023)	1,600,000 JPY ( \$20,000 CAD)
(April 2020–March 2021)	1,200,000 JPY ( \$15,000 CAD)
(April 2019–March 2020)	800,000 JPY ( \$10,000 CAD)
(April 2018–March 2019)	291,200 JPY ( \$3,640 CAD)

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(Awards/Fellowships continued)

(April 2017–March 2018) 460,000 JPY ( \$5,750 CAD) )

(April 2016–March 2017) 433,330 JPY ( \$5,416 CAD)

(April 2015–March 2016) 454,900 JPY ( \$5,686 CAD)

June 2021–Today Watanabe Foundation International Scholarship, *The Watanabe Foundation*, 150,000 JPY (\$1,722 CAD)/ month

July 2020 Graduate Fellowship for Young Leaders, *Syllff organization through Keio University* 1,000,000 JPY (\$12,500 CAD)

March 2018 Graduation Thesis Award, SFC, *Keio University*

## Publications

### Peer-reviewed articles

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

## Poster Presentations

9. **Daniel Evans-Yamamoto**, François Rouleau, Piyush Nanda, Koji Makanae, Hitoshi Matsuo, Motoaki Seki, Alexandre K. Dube, Diana Ascencio, Nozomu Yachie and Christian 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. **Daniel Evans-Yamamoto**, François Rouleau, Piyush Nanda, Koji Makanae, Hitoshi Matsuo, Motoaki Seki, Alexandre K. Dube, Diana Ascencio, Cristian R. Landry and Nozomu 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. **Daniel Evans-Yamamoto**, François Rouleau, Piyush Nanda, Koji Makanae, Hitoshi Matsuo, Motoaki Seki, Alexandre K. Dube, Diana Ascencio, Cristian R. Landry and Nozomu 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. **Daniel Evans-Yamamoto**, Piyush Nanda, François Rouleau, Koji Makanae, Hitoshi Matsuo, Motoaki Seki, Alexandre K. Dube, Diana Ascencio, Masaru Tomita, Hiroyuki Aburatani, Cristian R. Landry and Nozomu 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. **Daniel Evans-Yamamoto**, Piyush Nanda, Hitoshi Matsuo, Motoaki Seki, Alexandre K. Dube, Diana Ascencio, Masaru Tomita, Hiroyuki Aburatani, Cristian R. Landry and Nozomu 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. **Daniel Evans-Yamamoto**, Piyush Nanda, Hitoshi Matsuo, Motoaki Seki, Alexandre K. Dube, Diana Ascencio, Masaru Tomita, Hiroyuki Aburatani, Cristian R. Landry and Nozomu Yachie, “Development of Barcode Fusion Genetics-DHFR PCA”, *13<sup>th</sup> LSBM Symposium, Hakone, Japan*. April 3<sup>rd</sup>, 2019.
3. **Daniel Evans-Yamamoto**, Piyush Nanda, Hitoshi Matsuo, Motoaki Seki, Alexandre K. Dube, Masaru Tomita, Hiroyuki Aburatani, Cristian R. Landry and Nozomu Yachie, “Development of Barcode Fusion Genetics-DHFR PCA”, *IBIS research day 2018, Quebec City, Canada*. August 23<sup>rd</sup>, 2018
2. **Daniel Evans-Yamamoto**, Masaru Tomita and Nozomu 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. **Daniel Evans-Yamamoto**, Hitoshi Matsuo, Cristian R Landry, Minoru Yoshida, Masaru Tomita and Nozomu 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.

## 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 (\$31,250 CAD)
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 (\$3,000 CAD)
3. Yamagishi Student Project Support Program. (June 2017-February 2018)  
Evolutionary analysis of protein complexes from an inter-species screening approach  
240,000 JPY (\$3,000 CAD)
4. Yamagishi Student Project Support Program. (June 2016-February 2017)  
Expanding high-throughput protein interaction detection methods towards personal interactome technologies  
270,000 JPY (\$3,375 CAD)

## 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 interactions
- 3- **Mammalian culture cell engineering**
  - a. 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 a high-throughput sequencer (Illumina MiSeq)
  - b. Operation of a Nanopore sequencer (Oxford Nanopore Technologies, MinION)
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