

Louise Hillier Moncla

Curriculum vitae

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I. Education and employment

- 2022-** **Assistant Professor (tenure-track)**
Department of Pathobiology, School of Veterinary Medicine
University of Pennsylvania, Philadelphia, PA
- 2017-2022** **Post-doctoral Research Fellow**
Mentor: Dr. Trevor Bedford
Fred Hutchinson Cancer Research Center, Seattle, WA
- 2012-2017** **Ph.D. in Microbiology**
Mentor: Dr. Thomas Friedrich
Thesis title: “Disentangling the relative contributions of selection and stochastic processes in RNA virus evolution”
University of Wisconsin-Madison, Madison, WI
- 2008-2012** **Bachelor of Science in Biology**, Genetics and Development (Distinction and Honors)
Bachelor of Musical Arts (High Distinction)
Mentor: Dr. Beth Shapiro (2010-2012)
Honors thesis title: “An Examination of Polar Bear and Brown Bear Phylogeny Using Nuclear Genes as Molecular Markers”
The Pennsylvania State University, University Park, PA

II. Research

Research grants

- 2022-2025** **CDC Broad Agency Announcement: “Applied Research to Address Emerging Public Health Priorities”**
“Impact of local differences in vaccine uptake on SARS-CoV-2 evolution and spread across three Upper Midwestern states”
Direct costs to lab: \$195,277, **Role: Co-Investigator**
- 2020-2024** **K99/R00 Pathway to Independence Award, NIAID/NIH**, impact score: 10
“Quantifying the genetic and environmental factors driving avian influenza spillover”
Direct costs: \$555,962, **Role: Principal Investigator**

Peer-reviewed publications

‡ denotes corresponding author, * denotes equal contribution, [Google Scholar link](#)

1. Katarina Braun*, Gage Moreno*, Cassia Wagner, Molly A. Accola, William M. Rehauer, David Baker, Katia Koelle, David H. O'Connor, Trevor Bedford, Thomas C. Friedrich‡, **Louise H. Moncla‡**. “Acute SARS-CoV-2 infections harbor limited within-host diversity and transmit via tight

transmission bottlenecks.” **PLOS Pathogens**, August 23, 2021, DOI: 10.1371/journal.ppat.1009849. ‡ **Corresponding author**

2. **Louise H. Moncla***‡, Allison Black*, Chas DeBolt, Misty Lang, Nicholas R. Graff, Ailyn C. Pérez-Osorio, Nicola F. Müller, Dirk Haselow, Scott Lindquist, Trevor Bedford‡. “Repeated introductions and intensive community transmission fueled a mumps virus outbreak in Washington State.” **eLife**, April 19, 2021, DOI: 10.7554/eLife.66448. *‡ **Co-first and co-corresponding author**
3. Nicola F. Müller‡, Cassia Wagner*, Chris D. Frazar*, Pavitra Roychoudhury*, Jover Lee, **Louise H. Moncla**, Benjamin Pelle, Matthew Richardson, Erica Ryke, Hong Xie, Lasata Shrestha, Amin Addetia, Victoria M. Rachleff, Nicole A. P. Lieberman, Meei-Li Huang, Romesh Gautom, Geoff Melly, Brian Hiatt, Philip Dykema, Amanda Adler, Elisabeth Brandstetter, Peter D. Han, Kairsten Fay, Misja Ilcisin, Kirsten Lacombe, Thomas R. Sibley, Melissa Truong, Caitlin R. Wolf, Michael Boeckh, Janet A. Englund, Michael Famulare, Barry R. Lutz, Mark J. Rieder, Matthew Thompson, Jeffrey S. Duchin, Lea M. Starita, Helen Y. Chu, Jay Shendure, Keith R. Jerome, Scott Lindquist, Alexander L. Greninger‡, Deborah A. Nickerson‡, Trevor Bedford‡. “Viral genomes reveal patterns of the SARS-CoV-2 outbreak in Washington State”. **Science Translational Medicine**, May 3, 2021, DOI: 10.1126/scitranslmed.abf0202.
4. Bedford T, Greninger AL, Roychoudhury P, Starita LM, Famulare M, Huang ML, Nalla A, Pepper G, Reinhardt A, Xie H, Shrestha L, Nguyen TN, Adler A, Brandstetter E, Cho S, Giroux D, Han PD, Fay K, Frazar CD, Ilcisin M, Lacombe K, Lee J, Kiavand A, Richardson M, Sibley TR, Truong M, Wolf CR, Nickerson DA, Rieder MJ, Englund JA, Hadfield J, Hodcroft EB, Huddleston J, **Moncla LH**, Müller NF, Neher RA, Deng X, Gu W, Federman S, Chiu C, Duchin J, Gautom R, Melly G, Hiatt B, Dykema P, Lindquist S, Queen K, Tao Y, Uehara A, Tong S, MacCannell D, Armstrong GL, Baird GS, Chu HY, Shendure J, Jerome KR. “Cryptic Transmission of SARS-CoV2 in Washington State.” **Science**, October 30, 2020, DOI: 10.1126/science.abc0523
5. **Louise H. Moncla**‡, Trevor Bedford, Philippe Dussart, Srey Viseth Horm, Sareth Rith, Philippe Buchy, Erik A. Karlsson, Lifeng Li, Yongmei Liu, Huachen Zhu, Yi Guan, Thomas C. Friedrich, Paul F. Horwood‡. “Quantifying within-host diversity of H5N1 influenza viruses in humans and poultry in Cambodia.” **PLOS Pathogens**, January 17, 2020, DOI: 10.1371/journal.ppat.1008191. ‡ **Co-corresponding author**
6. Allison Black*, **Louise H. Moncla***, Katherine Laiton-Donato, Barney Potter, Lissethe Pardo, Angelica Rico, Catalina Tovar, Diana P. Rojas, Ira M. Longini, M. Elizabeth Halloran, Dioselina Peláez-Varvajal, Juan D. Ramírez, Marcela Mercado-Reyes, Trevor Bedford‡. “Genomic Epidemiology supports multiple introductions and cryptic transmission of Zika virus in Colombia.” **BMC Infectious Diseases**, November 12, 2019. * **Co-first author**
7. YQ Shirleen Soh, **Louise H. Moncla**, Rachel Eguia, Trevor Bedford, Jesse D. Bloom. “Comprehensive mapping of the avian influenza polymerase protein PB2 to humans.” **eLife**, April 30, 2019.
8. Mauricio A. Salvo, Mathew T. Aliota, **Louise H. Moncla**, ID Velez, AL Trujillo, Thomas C. Friedrich, Jorge E. Osorio‡. “Tracking dengue virus type 1 genetic diversity during lineage replacement in an hyperendemic area in Colombia.” **PLOS One**, March 7, 2019.
9. Hirotaka Imai, Jorge M. Dinish, Gongxun Zhong, **Louise H. Moncla**, Tiago J.S. Lopexs, Ryan McBride, Andrew J. Thompson, Wenjie Peng, Mai thi Q. Le, Anthony Hanson, Michael Lauck,

Yuko Sakai-Tagawa, Shinya Yamada, Julie Eggenberger, David H. O'Connor, Yasuo Suzuki, Masato Hatta, James C. Paulson, Gabriele Neumann, Yoshihiro Kawaoka[‡]. "Diversity of influenza A(H5N1) viruses in infected humans, northern Vietnam, 2004-2010." **Emerging Infectious Diseases** 24, 7, July 2018.

10. Katherine S. Xue, **Louise H. Moncla**, Trevor Bedford, Jesse D. Bloom[‡]. "Within-host evolution of human influenza virus." **Trends in Microbiology**, March 10, 2018.
11. Maki Kiso, Kiyoko Iwatsuki-Horimoto, Seiya Yamayoshi, Ryuta Uraki, Mutsumi Ito, Eiryo Kawakami, Yuriko Tomita, Satoshi Fukuyama, Tiago J.S. Lopes, Tokiko Watanabe, **Louise H. Moncla**, Thomas C. Friedrich, Gabriele Neumann, Yoshihiro Kawaoka[‡]. "Emergence of oseltamivir-resistant H7N9 influenza viruses in immunosuppressed cynomolgus macaques." **Journal of Infectious Diseases**, Volume 216, issue 5, September 1, 2017.
12. **Louise H. Moncla**, Nicholas W. Florek, Thomas C. Friedrich[‡]. "Influenza evolution: new insights into an old foe." **Trends in Microbiology**, June 25, 2017. PMID: 28478941.
13. **Louise H. Moncla**, Andrea M. Weiler, Gabrielle Barry, Jason Weinfurter, Jorge M. Dinis, Olivia Charlier, Michael Lauck, Adam Bailey, Jens Kuhn, Victoria Wahl-Jensen, Joshua C. Johnson, Peter B. Jahrling, Tony L. Goldberg, David H. O'Connor, Thomas C. Friedrich[‡]. "Within-host evolution of simian arteriviruses in crab-eating macaques." **Journal of Virology**, August 12, 2016.
14. Elizabeth A. Caine, **Louise H. Moncla**, Monica Ronderos, Thomas C. Friedrich, Jorge E. Osorio[‡]. "A Single Mutation in the VP1 of Enterovirus 71 is Responsible for Increased Virulence and Neurotropism in Adult Interferon Deficient Mice." **Journal of Virology**. July 20, 2016. PMID: 27440896.
15. Dudley DM, Aliota MT*, Mohr EL*, Weiler AM, Lehrer-Brey G, Weisgrau KL, Mohns MS, Breitbach ME, Rasheed MN, Newman CM, Gellerup DD, **Moncla LH**, Post J, Schultz-Darken N, Schotzko ML, Hayes JM, Eudailey JA, Moody MA, Permar SR, O'Connor SL, Rakasz EG, Simmons HA, Capuano S, Golos TG, Osorio JE, Friedrich TC, O'Connor DH[‡]. "A rhesus macaque model of Asian-lineage Zika virus infection." **Nature Communications**; 7:12204. Jun 28, 2016.
16. **Louise H. Moncla**, Gongxun Zhong, Chase W. Nelson, Austin L. Hughes, James Mutschler, Tokiko Watanabe, Yoshihiro Kawaoka, Thomas C. Friedrich[‡]. "Selective bottlenecks shape evolutionary pathways taken during mammalian adaptation of a 1918-like avian influenza virus." **Cell Host and Microbe** 19, 169-190, February 10, 2016. **(Featured Article)**
17. Victoria Wahl-Jensen, Joshua Johnson*, Michael Lauck, Jason Weinfurter, **Louise Moncla**, Andrea Weiler, Olivia Charlier, Oscar Rojas, Russell Byrum, Dan Ragland, Louis Huzella, Erika Zommer, Melanie Cohen, John Bernbaum, Yíngyún Cai, Hannah Sanford, Steven Mazur, Reed Johnson, Gustavo Palacios, Adam Bailey, Peter Jahrling, Tony Goldberg, David O'Connor, Thomas Friedrich, and Jens Kuhn[‡]. "Divergent simian arteriviruses cause simian hemorrhagic fever of different severity in macaques." **MBio**. 2016 February 23; 7(1).
18. Jorge M. Dinis, Nicholas W. Florek*, Omolayo O. Fatola, **Louise H. Moncla**, James P. Mutschler, Jennifer K. Meece, Edward A. Belongia, Thomas C. Friedrich[‡]. "Deep sequencing reveals potential antigenic drift variants at low frequency in influenza A-infected humans." **Journal of Virology**. 2016 January 6.

19. Nelson CW, **Moncla LH**, Hughes AL[‡]. “SNPGenie: estimating evolutionary parameters to detect natural selection using pooled next-generation sequencing data.” **Bioinformatics**. 2015 July 29.
20. **Louise H. Moncla**, Ted M. Ross*, Jorge M. Dinis, Jason T. Weinfurter, Tatum D. Mortimer, Nancy Schultz-Darken, Kevin Brunner, Saverio V. Capuano III, Carissa Boettcher, Jennifer Post, Michael Johnson, Chalise E. Bloom, Andrea M. Weiler, Thomas C. Friedrich[‡]. “A novel nonhuman primate model for influenza transmission.” **PLOS One** 8, e78750. November 14, 2013.

Non-published research

Developer for nextstrain.org

Nextstrain.org is a website that provides real-time phylogenetic inference for currently circulating viruses. During the emergence of the SARS-CoV-2 pandemic in spring of 2020, I maintained and updated the SARS-CoV-2 builds daily. These updates involved curating and cleaning new full-genome sequence data deposited in public databases, running the phylogenetics pipeline, error-checking results, and using the resulting phylogeny to infer new introduction and community transmission patterns. To ensure that data submitters were credited for their contributions and to alert them to noteworthy patterns in the data, I finished each update by tweeting relevant observations from the Nextstrain twitter account (@nextstrain) with data submitters tagged.

From 2017 to present, I have provided development effort and actively maintain the Nextstrain builds for mumps viruses and avian influenza viruses hosted at nextstrain.org/mumps/na and nextstrain.org/flu/avian. These builds track transmission of mumps virus in North America, and global avian influenza transmission and evolution patterns of H5N1, H5Nx, H7N9, and H9N2 subtypes. These builds are updated monthly.

Fellowships, Honors, and Awards

- 2019 **Life Sciences Research Foundation Post-doctoral Fellowship**, *The Life Sciences Research Foundation* (2019-2020, left early upon receipt of K99/R00)
- 2019 **Best Poster Award**, *Human Biology Division Annual Retreat*, Fred Hutchinson Cancer Research Center
- 2016 **Macrae Foundation Young Investigator Award**, *XVIII International Symposium on Respiratory Viral Infections, Lisbon, Portugal*
- 2016 **Wisconsin Distinguished Graduate Fellowship**, *University of Wisconsin-Madison*
- 2016 **Student Research Travel Grant**, *University of Wisconsin-Madison*
- 2015 **Pasteur Institute Young Investigator Award**, *1st International Meeting on Respiratory Pathogens, Singapore*
- 2012 **NIH T32 Molecular Biosciences Training Grant**, *University of Wisconsin-Madison* (2012-2016)
- 2011 **Phi Beta Kappa Honors Society**
- 2008 **Schreyer Honors College Academic Scholarship**, *The Pennsylvania State University* (2008-2012)

Invited research talks

- 2022 “Using multi-scale genomics to disentangle H5N1 emergence and transmission” American Society for Virology Annual meeting, Satellite Symposium: “Shaking the Trees: Sequence-Based Inference in Virus Ecology and Evolution”, *Madison, WI, USA* (July 16, 2022)

- 2021 "Nextstrain as a tool kit for tracking avian influenza virus evolution and transmission"
Toward Mitigating Pandemic Influenza Risk: A regional consultation on avian influenza surveillance in Asia, virtual (December 2, 2021)
- 2020 "Repeated introductions and intensive community transmission fueled a mumps virus outbreak in Washington State"
UC Berkeley Evolution Seminar Series, virtual (December 2, 2020)
- 2020 "Harnessing viral genomics to interrogate SARS-CoV2 transmission at the community to individual scale"
Chilean Genetics Society annual meeting, Roche invited speaker, virtual (November 25, 2020)
- 2020 "Repeated introductions and intensive community transmission fueled a mumps virus outbreak in Washington State"
Virus Evolution Seminar Series, virtual series joint-hosted by University of Wisconsin-Madison and UC Davis (November 23, 2020)
- 2020 "Repeated introductions and intensive community transmission fueled a mumps virus outbreak in Washington State"
Vaccine and Infectious Disease Departmental Scientific Seminar Series, Fred Hutchinson Cancer Research Center, Seattle, WA, virtual (May 5, 2020)
- 2018 "Genomic characterization of H5N1 spillover infection in humans and poultry in Cambodia"
Institut Pasteur du Cambodge, Phnom Penh, Cambodia (September 5, 2018)

Oral research presentations (submitted abstracts)

- 2018 "Genomic characterization of H5N1 spillover infection in humans and poultry in Cambodia"
Orthomyxovirus 2018 Conference, Hanoi, Vietnam (September 12-14, 2018)
- 2018 "Genomic reconstruction of a mumps virus outbreak in Washington state"
Models of Infectious Disease Agent Study network meeting, Washington D.C, USA (April 3-5, 2018)
- 2016 "Selective bottlenecks shape evolutionary pathways taken during mammalian adaptation of a 1918-like avian influenza virus"
The Macrae Foundation's XVIII International Symposium on Respiratory Viral Infections, Lisbon, Portugal (March 31-April 2, 2016)
- 2015 "Selective bottlenecks shape evolutionary pathways taken during mammalian adaptation of a 1918-like avian influenza virus"
1st International Meeting on Respiratory Pathogens, Furama Riverfront, Singapore (September 2-4, 2015)
- 2013 "A novel nonhuman primate model for influenza transmission."
Joint University of Minnesota-University of Wisconsin Virology Training Grant Symposium, University of Wisconsin-La Crosse, La-Crosse, WI, USA

Poster presentations (submitted abstracts)

- 2019 "Quantifying within-host evolution of H5N1 viruses in humans and poultry in Cambodia"
Options X for the Control of Influenza, Singapore
- 2016 "Quantifying the limits of accurate and reproducible influenza sequencing"
Options IX for the Control of Influenza, Chicago, Illinois, USA

- 2015 “Selective bottlenecks shape evolutionary pathways during mammalian adaptation of a 1918 like avian virus”
ISIRV workshop on the next-generation sequencing of viruses, Pasteur Institute, Paris, France

III. Professional Service

Ad-hoc peer review service

Cell Host and Microbe, Nature Communications, Nature Ecology and Evolution, eLife, PLOS Pathogens, Virus Evolution, MBio, Journal of Virology, Epidemics, Scientific Reports, Cell Reports, Cell Reports Medicine, Infection Genetics and Evolution, PLOS One, Evolution Medicine and Public Health, Communications Medicine, Ecology and Evolution, Virulence, BMC Bioinformatics, Open Forum ID

Science communication during SARS-CoV2 pandemic

Commentary for **Science News**, May 26, 2020: <https://www.sciencenews.org/article/coronavirus-covid19-mutations-strains-variants>

Commentary for **KNKX radio**, May 28, 2020: <https://www.knkx.org/post/new-research-suggests-nations-first-covid-19-case-was-not-source-washingtons-outbreak>

Commentary for **Wall Street Journal**, May 4, 2020:
https://www.wsj.com/articles/the-search-is-on-for-americas-earliest-coronavirus-deaths-11588597831?shareToken=st53246b5625b043cb89ec5493cb64017a&reflink=article_email_share

Commentary for **Kiro7 news**, April 22, 2020: <https://www.kiro7.com/news/local/cdc-first-us-coronavirus-deaths-happened-weeks-before-first-death-kirkland/HCTCEX45XFCRVE5742JWR7ZP44/?website=cmg-tv-10090>

IV. Teaching, Mentorship and Outreach

Classroom

Teaching Assistant, Biochemistry 575: Biology of Viruses (2014)

Biochemistry 575 is a course designed for undergraduate students to teach the fundamentals of virology. As a teaching assistant for this course, I provided weekly tutoring sessions, lectured, wrote exam questions, and administered and graded exams.

Mentorship

Cassia Wagner, graduate student (2020-2021)

Between spring of 2020 and 20221, I mentored Cassia Wagner, a new MD-PhD student in the Bedford lab. Cassia and I worked together on a project testing whether within-host variation can be used to infer transmission linkage between SARS-CoV2 positive individuals. Cassia and I met regularly to discuss progress, to develop next steps, and to interpret new data.

Gage Moreno, graduate student (2020-2021); now post-doctoral researcher at the Broad Institute in the laboratory of Pardis Sabeti

Gage Moreno was a PhD student in Dave O'Connor's laboratory at the University of Wisconsin in Madison. I provided mentorship to Gage during the end of his PhD, providing guidance on post-doc

searching, project management, and formulating next steps. In the spring of 2020, we began collaborating on a project aimed at investigating patterns of SARS-CoV-2 within-host diversity within acutely-infected individuals in Wisconsin. I directly oversaw this project, providing mentorship on project conceptualization, hypothesis generation, formulating analytic approaches, experimental and bioinformatic controls, narrative framing, and manuscript writing. This project resulted in a last-author manuscript (Katarina and Gage as co-first authors) which was published in PLOS Pathogens in 2021 (Braun et al, PLOS Pathogens, 2021).

Katarina Braun, MD/PhD student (2015-2021); *now finishing medical training at University of Wisconsin*

Kat Braun was an MD-PhD student who rotated and subsequently joined the Friedrich lab. I planned and oversaw both of her rotation projects: the first was aimed at assessing variant reproducibility in duplicate nasal swab sequences, and the second focused on developing protocols for PacBio sequencing. Following my departure, we have remained in contact, and I continue to mentor Kat virtually. In the spring of 2020, we began collaborating on a project aimed at investigating patterns of SARS-CoV-2 within-host diversity within acutely-infected individuals in Wisconsin. I directly oversaw this project, providing mentorship on project conceptualization, hypothesis generation, formulating analytic approaches, experimental and bioinformatic controls, narrative framing, and manuscript writing. This project resulted in a last-author manuscript (Katarina and Gage as co-first authors) which was published in PLOS Pathogens in 2021 (Braun et al, PLOS Pathogens, 2021).

Macy Pell, undergraduate research assistant (2015-2017); *now PhD student at Michigan State University in laboratory of Shannon Manning*

I mentored Macy for two years as an undergraduate research assistant in the Friedrich laboratory. I trained Macy in laboratory techniques for sequencing viral isolates, providing mentorship, and directed her project aimed at quantifying the reproducibility of influenza within-host variant detection. Macy is now a graduate student at Michigan State University where she is performing research in microbiology.

Mauricio Salvo, graduate student (2014-2017); *now research scientist at Roche*

Mauricio Salvo was a Masters student with dual mentorship between the Friedrich lab and the laboratory of Dr. Jorge Osorio. I was responsible for mentoring him, guiding him through his projects and overseeing his progress in the lab. Our work together resulted in a publication in 2019 (Salvo et al, PLoS One, 2019).

Olivia Charlier, undergraduate research assistant (2012-2014); *now a physician's assistant*

Olivia Charlier was an undergraduate research assistant from 2012-2014. During this time I trained and oversaw her completion of an undergraduate research project aimed at sequencing simian hemorrhagic fever viruses and seasonal influenza viruses.

Kelsey Florek, Microbiology Doctoral Training Program rotation student (2013); *now lead bioinformatician at the Wisconsin State Lab of Hygiene*

Kelsey Florek was a microbiology graduate student who rotated in the Friedrich laboratory and subsequently joined in 2013. I developed and oversaw her rotation project and trained her when she joined the lab. Kelsey is now a bioinformatician at the Wisconsin State Lab of Hygiene.

Outreach

Facilitator for Girls Who Code (2017-present)

Girls who code is an outreach program targeting high-school aged girls who are interested in learning to code. During my post-doc, I have served each year as a course facilitator. As a facilitator, I volunteer with coding sessions during which participants learn fundamentals of coding in python or R, and work towards completing a coding-based project that is showcased for parents and researchers at the end of the semester. During each session, I assist in trouble shooting, answer questions, and provide general support while participants develop coding skills.

Expanding Your Horizons Outreach program (2015-2016)

Expanding Your Horizons is an outreach program intended to promote interest and confidence in middle school girls to pursue STEM fields. During my PhD, I participated as a student volunteer, where I led an activity introducing the participants to programming in python and shared my path to becoming a scientist.

Madison Science Museum Women in STEM Symposium (2016)

The Madison Science Museum Women in STEM Symposium is an event targeted to high school girls who are interested in STEM fields. The event brings in successful women working in STEM fields to speak about their career paths, the challenges they have faced and why it is important to build a diverse work environment. As a volunteer I helped register and direct participants to the talks and activities and discussed my own aspirations as a scientist with the participating young women.