BIOGRAPHICAL SKETCH

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NAME: Hernandez, Matthew M.

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POSITION TITLE: Assistant Professor

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
Brown University, Providence, RI, USA	BS	06/2011	Biochemistry and Molecular Biology
Icahn School of Medicine at Mount Sinai (ISMMS), New York, NY, USA	MD/PhD	06/2020	Medicine, Microbiology (PhD)
ISMMS, New York, NY, USA	Residency	06/2023	Clinical Pathology
Beth Israel Deaconess Medical Center (BIDMC), Boston, MA, USA	Fellowship	06/2024	Medical and Public Health Microbiology

A. Personal Statement

I am a physician-scientist whose interests bridge clinical diagnostics, microbial genomics, and systems-level approaches to understanding disease pathogenesis and prognosis. My work follows a central conviction: that integrating high-resolution microbial characterization with clinical phenotyping can unlock diagnostic and therapeutic opportunities that are, otherwise, hidden within complex microbial disease states. My career trajectory reflects a deliberate accumulation of complementary skills from basic virology to genomic epidemiology to laboratory medicine. These uniquely position me to investigate how pathogen diversity drive disease severity, predict clinical outcomes, and inform impactful diagnostic strategies.

Growing up along the South Texas-Mexico border, I experienced, first-hand how infectious diseases disproportionately affect marginalized communities with limited access to timely diagnostics and care. These experiences instilled in me a commitment to build diagnostic and research frameworks that serve broad populations and generate fundamental insights into disease pathogenesis. Specifically, my research foundation is based on three pillars: 1) the mechanistic understanding of pathogen-host interactions and virulence, 2) the systematic characterization of microbial diversity in disease states, and 3) the linking emerging microbial systems to innovative clinical testing approaches.

During the PhD phase of my physician-scientist training, I used sophisticated genomic approaches to investigate how host immune pressure shapes HIV evolution and drug-resistance development. This work showed how host mechanisms designed to restrict pathogens can paradoxically directly drive viral evolution and accelerate disease pathogenesis. Understanding this dynamic is foundational to comprehend how microbial diversity translates to heterogeneous phenotypes. I continue to apply these insights to other pathogens to elucidate how genomic diversity correlates with clinical disease severity.

At ISMMS (2018-2023), I established pathogen surveillance and genomic epidemiology systems spanning multiple centers in NYC to track thousands of infection events. I led real-time tracking of circulating pathogens and, through phylogenomics, revealed cryptic transmission chains exposed gaps in detecting underrecognized microbes. Furthermore, I established various molecular diagnostic approaches to address gaps in clinical testing. Critically, I developed an expertise in integrating diagnostic and genomic data which proves valuable for understanding microbial dynamics and their impact on spread of disease.

After completing my clinical training and obtaining my board certification in clinical pathology and medical microbiology, I currently serve as an Associate Director of Stanford's Clinical Microbiology and Virology Laboratories. There, I oversee infectious disease diagnostics for >1 million patient encounters annually which

informs a robust translational research program integrating clinical data and pathogen diversity. Together with my expertise in microbial genomics and diagnostics, I am poised to uncover distinct relationships between microbial diversity and clinical phenotypes in order to develop novel diagnostic and prognostic approaches to optimize patient care.

Ongoing projects that I would like to highlight include:

Investigator Sponsored Study, Gilead Sciences
Hernandez (PI)
03/2026-03/2028
Closing the Delta Gap: Universal HDV Screening and Epidemiology in a US Medical Center
Specific Aims: 1) Characterize the demographic, systemic, and clinical factors associated with HDV testing among HBV-infected patients; 2) Determine the seroprevalence of HDV across all stages of HBV infection in US patients.

Stanford University Pathology Trainee Mentored Award
Hernandez (PI)
09/2025-06/2026
Unveiling the phenotypic and genotypic diversity of clinical Aeromonas isolates
Specific Aims: 1) Elucidate the epidemiology of diverse *Aeromonas* infections in Stanford patients; 2) Dissect the patho-genomic diversity of clinical *Aeromonas* isolates.

B. Positions, Scientific Appointments, and Honors

Positions and Scientific Appointments

2024-Present	Assistant Professor, Stanford University, Palo Alto, CA, USA
2024-Present	Associate Director, Clinical Microbiology and Virology Laboratories, Stanford Health Care, Palo Alto, CA, USA
2024	Instructor, Stanford University, Palo Alto, CA, USA
2023-2024	ACGME Medical Microbiology Fellow, BIDMC, Boston, MA, USA
2022-2023	Chief Pathology Resident, ISMMS, New York, NY, USA
2020-2023	Clinical Pathology Resident, Physician-Scientist Training in Experimental Pathology (PSTEP) Track, ISMMS, New York, NY, USA

Other Experience and Professional Memberships

2024-Present	State of California Medical License, No: A196381
2024-Present	The American Board of Medical Microbiology, Medical and Public Health Microbiology, Certificate No: 1469
2023-Present	Massachusetts State Medical License, No: 1013887
2023-Present	The American Board of Pathology, Clinical Pathology, Certificate No: 23-501
2022-Present	New York State Medical License, No: 315161
2022-2023	Distinction in Medical Education (DIME) Selection Committee Member, ISMMS, New York, NY, USA
2021	Guest Lecturer (“Emerging pathogens in transfusion medicine: lessons from the past and present”), New York Blood Center Fellows’ Webinar Series, New York, NY, USA
2019-2020	Guest Lecturer, Structures course, ISMMS, New York, NY, USA. Supervisor: Daniella Curcio, PhD and Jeffrey Laitman, PhD.

Honors and Awards

2024	Peggy Cotter Award for Early Career Branch Members, American Society for Microbiology (ASM)
2024	Clinical Pathology Fellow Teaching Award, Department of Pathology, BIDMC
2023	Top 5 – 40 Under Forty, American Society for Clinical Pathology (ASCP)
2023	Alpha Omega Alpha (AOA), ISMMS, AOA Lambda Chapter
2021	Paul E. Strandjord Young Investigator Award, Association for Clinical Laboratory Physicians and Scientists (ACLPS)
2020	Graduate with Distinction in Medical Education, ISMMS
2020	Graduate with Distinction in Research, ISMMS
2017	NYC Department of Education Recognition of Mentorship, Center for Excellence in Youth Education, ISMMS
2017	Medical Student Excellence in Teaching Award, Institute of Medical Education, ISMMS
2016	Best Talk Award, Twenty-Ninth NYC Virus-Host Interactions Symposium
2016	Young Investigator Scholarship Award, Conference on Retroviruses and Opportunistic Infections (CROI)
2012	Science and Leadership Merit Award, ISMMS
2011	Intramural NIAID Research Training Opportunities Training Award, NIH/NIAID
2011	Scientific Research Society Membership Award, Sigma Xi, Brown University
2010	Travel Award, Annual Biomedical Research Conference for Minority Students (ABRCMS)
2009	Undergraduate Teaching and Research Award (UTRA), Brown University

C. Contributions to Science

(, indicates equal contribution; ‡, corresponding author)*

1. Mechanisms Shaping Pathogen Evolution and Drivers of Disease: My PhD research established how host immune factors (e.g., APOBEC3, SAMHD1) bidirectionally interact with pathogens, driving both viral restriction and evolution. Using humanized mouse models and custom genomic pipelines, I demonstrated that suboptimal activity of APOBEC3G can paradoxically increase HIV diversity and drug resistance development. We also expanded this work to cellular-level mechanisms using primary cells and novel *in vitro* systems. Specifically, we showed IL-15 signaling makes CD4+ T-cells susceptible to HIV through phosphorylation of the SAMHD1 with stem cell memory T-cells becoming a self-renewing viral reservoir. Together, these findings show how host immunity simultaneously constrains and drives pathogen evolution which are principles that guide my translational work.
    a. (**Hernandez MM,** Fahrny A)*, Jayaprakash A, Gers-Huber G, Dillon-White M, Audigé A, Mulder LCF, Sachidanandam R, Speck RF, Simon V. *Impact of Suboptimal APOBEC3G Neutralization on the Emergence of HIV Drug Resistance in Humanized Mice.* J Virol. 2020 Feb 14;94(5). PubMed PMID: 31801862; PubMed Central PMCID: PMC7022346.
    b. Manganaro L, Hong P, **Hernandez MM,** Argyle D, Mulder LCF, Potla U, Diaz-Griffero F, Lee B, Fernandez-Sesma A, Simon V. *IL-15 regulates susceptibility of CD4+ T cells to HIV infection.* Proc Natl Acad Sci USA. 2018 Oct 9;115(41):E9659-E9667. PubMed PMID: 30257946; PubMed Central PMCID: PMC6187195.

2. Genomic Epidemiology to Dissect Pathogen Spread and Evolution: I established large-scale banking and surveillance infrastructure across >4,000 clinical specimens to enable real-time pathogen tracking and outbreak detection. During the COVID-19 pandemic, I led groundbreaking genomic epidemiology efforts that revealed multiple independent European introductions which explained its explosive trajectory. Moreover, our systematic analysis identified SARS-CoV-2 in NYC as early as January 2020, weeks before clinical recognition. I extended this approach to the characterization of a large nosocomial

H1N1 outbreak driven by a single viral clone across two hospitals which enabled precise outbreak source identification and targeted infection control. With my expertise, I have contributed globally by characterizing SARS-CoV-2 spread in South America and demonstrated how systematic surveillance informs public health interventions in resource-limited settings.

a. (Gonzalez-Reiche AS, **Hernandez MM**)*, Sullivan MJ, Ciferri B, Alshammary H, Obla A, Fabre S, Kleiner G, Polanco J, Khan Z, Alburquerque B, van de Guchte A, Dutta J, Francoeur N, Melo BS, Oussenko I, Deikus G, Soto J, Sridhar SH, Wang YC, Twyman K, Kasarskis A, Altman DR, Smith M, Sebra R, Aberg J, Krammer F, García-Sastre A, Luksza M, Patel G, Paniz-Mondolfi A, Gitman M, Sordillo EM, Simon V, van Bakel H. *Introductions and early spread of SARS-CoV-2 in the New York City area.* Science. 2020 Jul 17;369(6501):297-301. PubMed PMID: 32471856; PubMed Central PMCID: PMC7259823.

b. (**Hernandez MM**, Gonzalez-Reiche AS)*, Alshammary H, Fabre S, Khan Z, van De Guchte A, Obla A, Ellis E, Sullivan MJ, Tan J, Alburquerque B, Soto J, Wang CY, Sridhar SH, Wang YC, Smith M, Sebra R, Paniz-Mondolfi AE, Gitman MR, Nowak MD, Cordon-Cardo C, Luksza M, Krammer F, van Bakel H, Simon V, Sordillo EM. *Molecular evidence of SARS-CoV-2 in New York before the first pandemic wave.* Nat Commun. 2021 Jun 8;12(1):3463. PubMed PMID: 34103497; PubMed Central PMCID: PMC8187428.

c. Javaid W, Ehni J, Gonzalez-Reiche AS, Carreño JM, Hirsch E, Tan J, Khan Z, Kriti D, Ly T, Kranitzky B, Barnett B, Cera F, Prespa L, Moss M, Albrecht RA, Mustafa A, Herbison I, **Hernandez MM,** Pak TR, Alshammary HA, Sebra R, Smith ML, Krammer F, Gitman MR, Sordillo EM, Simon V, van Bakel H. *Real-Time Investigation of a Large Nosocomial Influenza A Outbreak Informed by Genomic Epidemiology.* Clin Infect Dis. 2021 Dec 6;73(11):e4375-e4383. PubMed PMID: 33252647; PubMed Central PMCID: PMC8653627.

d. Ballesteros N, Muñoz M, Patiño LH, Hernández C, González-Casabianca F, Carroll I, Santos-Vega M, Cascante J, Angel A, Feged-Rivadeneira A, Palma-Cuero M, Flórez C, Gomez S, van de Guchte A, Khan Z, Dutta J, Obla A, Alshammary HA, Gonzalez-Reiche AS, **Hernandez MM,** Sordillo EM, Simon V, van Bakel H, Paniz-Mondolfi AE, Ramírez JD. *Deciphering the introduction and transmission of SARS-CoV-2 in the Colombian Amazon Basin.* PLoS Negl Trop Dis. 2021 Apr;15(4):e0009327. PubMed PMID: 33857136; PubMed Central PMCID: PMC8078805.

3. Linking Diagnostic Performance to Circulating Microbial Diversity: My work is also based on the critical principle that diagnostic performance reflects circulating microbial diversity and can illuminate real-time variant dynamics. By analyzing RT-PCR/MALDI-TOF target detection patterns across thousands of SARS-CoV-2-positive specimens paired with whole-genome sequencing, I demonstrated that target dropout patterns directly correlate with variant-specific mutations arising among emergent Alpha and Delta variants in NYC. Building on these findings, we also developed and validated the highly multiplexed mass spectrometry assay to capture ≥11 known variants of concern and determined diagnostic patterns could be used to anticipate emerging strains at the time (e.g., Lambda, Mu, Omicron (BA.2.12.1, BA.2-5). This approach highlights the benefit of redundancy in diagnostic design and reveals how systematic analysis of diagnostic performance can serve as a vital tool to capture pathogen evolution.

a. **Hernandez MM‡,** Banu R, Gonzalez-Reiche AS, van de Guchte A, Khan Z, Shrestha P, Cao L, Chen F, Shi H, Hanna A, Alshammary H, Fabre S, Amoako A, Obla A, Alburquerque B, Patiño LH, Ramírez JD, Sebra R, Gitman MR, Nowak MD, Cordon-Cardo C, Schutzbank TE, Simon V, van Bakel H, Sordillo EM, Paniz-Mondolfi AE‡. *Robust clinical detection of SARS-CoV-2 variants by RT-PCR/MALDI-TOF multitarget approach.* J Med Virol. 2022 Apr;94(4):1606-1616. PubMed PMID: 34877674; PubMed Central PMCID: PMC8854350.

b. **Hernandez MM‡,** Banu R, Gonzalez-Reiche AS, Gray B, Shrestha P, Cao L, Chen F, Shi H, Hanna A, Ramírez JD, van de Guchte A, Sebra R, Gitman MR, Nowak MD, Cordon-Cardo C, Schutzbank TE, Simon V, van Bakel H, Sordillo EM, Paniz-Mondolfi AE‡. *RT-PCR/MALDI-TOF Diagnostic Target Performance Reflects Circulating SARS-CoV-2 Variant Diversity in New York City.* J Mol Diagn. 2022 Jul;24(7):738-749. PubMed PMID: 35525388; PubMed Central PMCID: PMC9067105.

c. **Hernandez MM‡,** Banu R, Shrestha P, Gonzalez-Reiche AS, van de Guchte A, Farrugia K, Sebra R, Gitman MR, Nowak MD, Cordon-Cardo C, Simon V, van Bakel H, Sordillo EM, Luna N, Ramirez A, Castañeda SA, Patiño LH, Ballesteros N, Muñoz M, Ramírez JD, Paniz-Mondolfi AE‡. *A Robust, Highly Multiplexed Mass Spectrometry Assay to Identify SARS-CoV-2 Variants.* Microbiol Spectr. 2022 Oct 26;10(5):e0173622. PubMed PMID: 36069609; PubMed Central PMCID: PMC9604185.

4. Optimizing Diagnostic Performance and Utilization Through Evidence-Based Strategies: Diagnostic stewardship is critical for capturing emergent pathogens while maintaining accurate testing and surveillance programs. I have developed systematic approaches to optimize specimen collection, validate alternative specimen types, and implement proactive surveillance protocols that enable early detection of emerging threats. For example, to enable scalable, noninvasive testing, I optimized saliva as a specimen type for SARS-CoV-2 detection. We demonstrated saliva exhibits diagnostic sensitivity comparable to nasopharyngeal specimens. Critically, we also determined that pre-collection meal consumption causes transient interference resolving within 20 minutes which informed evidence-based collection guidelines. Additionally, I recently contributed to the expansion of subtyping protocols to address gaps in detection of the recent H5N1 avian influenza outbreak. Through these strategies, we identified California's first pediatric case during the 2024-2025 outbreak. This work showcased how proactive subtyping of influenza-A-positive specimens enables early detection of emerging zoonotic threats that prompt immediate public health responses.

   a. **Hernandez MM‡,** Banu R, Shrestha P, Patel A, Chen F, Cao L, Fabre S, Tan J, Lopez H, Chiu N, Shifrin B, Zapolskaya I, Flores V, Lee PY, Castañeda S, Ramírez JD, Jhang J, Osorio G, Gitman MR, Nowak MD, Reich DL, Cordon-Cardo C, Sordillo EM, Paniz-Mondolfi AE‡. *RT-PCR/MALDI-TOF mass spectrometry-based detection of SARS-CoV-2 in saliva specimens.* J Med Virol. 2021 Sep;93(9):5481-5486. PubMed PMID: 33963565; PubMed Central PMCID: PMC8242556.

   b. **Hernandez MM‡,** Riollano-Cruz M, Boyle MC, Banu R, Shrestha P, Gray B, Cao L, Chen F, Shi H, Paniz-Perez DE, Paniz-Perez PA, Rishi AL, Dubinsky J, Dubinsky D, Dubinsky O, Baine S, Baine L, Arinsburg S, Baine I, Ramirez JD, Cordon-Cardo C, Sordillo EM, Paniz-Mondolfi AE‡. *Food for thought: Eating before saliva collection and interference with SARS-CoV-2 detection.* J Med Virol. 2022 Jun;94(6):2471-2478. PubMed PMID: 35171508; PubMed Central PMCID: PMC9088375. **BACK COVER**.

   c. Karan A, Higerd-Rusli G, **Hernandez MM**, Dhillon R, Pinsky B. *Expanding testing early in the H5N1 outbreak.* Lancet. 2025. Mar 8;405(10481):779-780. PubMed PMID: 40057336; PubMed Central PMCID: PMC11987165.

   d. Higerd-Rusli GP, Karan A, Hoffman SA, Morante IEA, Huang C, Sahoo MK, **Hernandez MM**, Pinsky BA. *One confirmed and one potential human case of influenza A(H5N1) detected through an expanded subtyping protocol.* ASM Case Rep. 2026 Jan;1(2). doi: 10.1128/asmcr.00165-25. eCollection 2026 Jan. PubMed PMID: 41503532; PubMed Central PMCID: PMC12772291.

Complete List of Published Work in MyBibliography:

https://www.ncbi.nlm.nih.gov/myncbi/1XGAe5NLTIdQh/bibliography/public/