

# Andrew S. Beck

VIROLOGY · PUBLIC HEALTH GENOMICS · BIOINFORMATICS

Atlanta GA USA

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## Professional Experience

### US Centers for Disease Control and Prevention - Viral Vaccine Preventable Diseases Branch

Atlanta, USA

VIROLOGIST - BIOINFORMATICIAN

2015 - Present

- Led a laboratory genomics unit, analyzing time-critical outbreak investigation data.
- Consulted on molecular surveillance of vaccine-preventable childhood diseases, including measles, mumps, rubella, and others.
- Led development of multiple whole-genome sequencing assays for measles and mumps clinical specimens.
- Led genetic studies of measles virus transmission.
- Led studies contributing to revision of measles virus molecular nomenclature.
- Consulted extensively on the use of Bayesian phylogenetic methods.
- Established partnerships and delivered genomics data to domestic and international stakeholders.
- Published findings in peer-reviewed articles.

### US Centers for Disease Control and Prevention - COVID-19 Pandemic Response

Atlanta, USA

VIROLOGIST - BIOINFORMATICIAN

2020 - 2022

- Developed backend applications to scale ETLs of SARS-CoV-2 sequence data from multiple offsite sources. Current daily refresh volume is > 16 million sequences plus metadata.
- Performed unit and regression testing to ensure quality and error-tolerance of viral sequence processing applications.
- Monitored and optimized performance of distributed databases.
- Consulted on implementation of phylogenetic modeling for molecular studies of SARS-CoV-2 surveillance datasets.
- Analyzed SARS-CoV-2 sequence repositories with machine learning models (Collaboration: MIT) to predict immunologically significant sequence divergence.
- Contributed findings to peer-reviewed articles.
- Languages: Scala, Python, R, SQL
- Frameworks: Apache Spark, Hadoop, HDFS, YARN, Apache Hive/Impala, Nextstrain

## Education

### University of Texas Medical Branch School of Biomedical Sciences

Galveston, TX USA

PH.D. IN EXPERIMENTAL PATHOLOGY

2009 - 2015

- Mentor: Alan Barrett, PhD
- Dissertation: Population Structure of Yellow Fever Virus: Influence of Viral Diversity on Vaccine Attenuation
- Themes: Virology, Genomics, Bioinformatics, Biosecurity

## Peer-Reviewed Publications

- Bankamp, B., G. Kim, D. Hart, A. Beck, M. Ben Mamou, A. Penedos, Y. Zhang, R. Evans, and P. A. Rota (2024). "Global Update on Measles Molecular Epidemiology". In: *Vaccines* 12.7. ISSN: 2076-393X. doi: 10.3390/vaccines12070810.
- Beck, A. S., E. N. Lopareva, H. Hwang, D. Hart, M. de Almeida, R. Anderson, P. A. Rota, and B. Bankamp (July 2024). "Evaluation of the sensitivity of a measles diagnostic real-time RT-PCR assay incorporating recently observed priming mismatch variants, 2024." In: *Euro Surveill* 29.28. ISSN: 1560-7917 (Electronic); 1025-496X (Print); 1025-496X (Linking). doi: 10.2807/1560-7917.ES.2024.29.28.2400410.
- Masters, N. B., A. S. Beck, A. D. Mathis, J. Leung, K. Raines, P. Paul, S. E. Stanley, A. L. Weg, E. G. Pieracci, S. Gearhart, M. Jumabaeva, B. Bankamp, P. A. Rota, D. E. Sugerman, and P. A. Gastañaduy (Aug. 2023). "Measles virus transmission patterns and public health responses during Operation Allies Welcome: a descriptive epidemiological study". In: *The Lancet Public Health* 8.8, e618–e628. doi: 10.1016/S2468-2667(23)00130-5.
- Williams, D., A. Penedos, B. Bankamp, R. Anderson, J. Hubschen, M. Ben Mamou, A. Beck, D. Brown, G. Rey-Benito, R. Evans, A. Ghoniem, L. Sangal, C. Byabamazima, A. Dosseh, A. Kfutwah, M. Mulders, K. Brown, and P. Rota (Sept. 2022). "Update: circulation of active genotypes of measles virus and recommendations for use of sequence analysis to monitor viral transmission". In: *Weekly Epidemiological Record* 39.
- Lambrou, A. S. et al. (Feb. 2022). "Genomic Surveillance for SARS-CoV-2 Variants: Predominance of the Delta (B.1.617.2) and Omicron (B.1.1.529) Variants - United States, June 2021-January 2022." In: *MMWR Morb Mortal Wkly Rep* 71.6, pp. 206–211. doi: 10.15585/mmwr.mm7106a4.

- Link-Gelles, R., E. Lutterloh, P. S. Ruppert, P. B. Backenson, K. St. George, E. S. Rosenberg, B. J. Anderson, M. Fuschino, M. Popowich, C. Punjabi, M. Souto, K. McKay, S. Rulli, T. Insaf, D. Hill, J. Kumar, I. Gelman, J. Jorba, T. F. F. Ng, N. Gerloff, N. B. Masters, A. Lopez, K. Dooling, S. Stokley, S. Kidd, M. S. Oberste, and J. Routh (Jan. 2022). “Public health response to a case of paralytic poliomyelitis in an unvaccinated person and detection of poliovirus in wastewater; New York, June-August 2022”. In: *American Journal of Transplantation* 22.10, pp. 2470–2474. doi: 10.1111/ajt.16677.
- Wang, L. et al. (July 2022). “Differential neutralization and inhibition of SARS-CoV-2 variants by antibodies elicited by COVID-19 mRNA vaccines”. In: *Nature Communications* 13.1, p. 4350. doi: 10.1038/s41467-022-31929-6.
- Stinnett, R. C., A. S. Beck, E. N. Lopareva, R. J. McNall, D. R. Latner, C. J. Hickman, P. A. Rota, and B. Bankamp (Nov. 2020). “Functional Characterization of Circulating Mumps Viruses with Stop Codon Mutations in the Small Hydrophobic Protein.” In: *mSphere* 5.6. ISSN: 2379-5042 (Electronic); 2379-5042 (Linking). doi: 10.1128/mSphere.00840-20.
- Davis, E. H., A. S. Beck, A. E. Strother, J. K. Thompson, S. G. Widen, S. Higgs, T. G. Wood, and A. D. T. Barrett (Oct. 2019). “Attenuation of Live-Attenuated Yellow Fever 17D Vaccine Virus Is Localized to a High-Fidelity Replication Complex.” In: *mBio* 10.5. ISSN: 2150-7511 (Electronic). doi: 10.1128/mBio.02294-19.
- Collins, N. D., A. S. Beck, S. G. Widen, T. G. Wood, S. Higgs, and A. D. T. Barrett (Oct. 2018). “Structural and Nonstructural Genes Contribute to the Genetic Diversity of RNA Viruses”. In: *MBio* 9.5. doi: 10.1128/mBio.01871-18.
- Beck, A. S., T. G. Wood, S. G. Widen, J. K. Thompson, and A. D. T. Barrett (Sept. 2018). “Analysis By Deep Sequencing of Discontinued Neurotropic Yellow Fever Vaccine Strains”. In: *Scientific Reports* 8.1. ISSN: 2045-2322. doi: 10.1038/s41598-018-31085-2.
- Coughlin, M. M., A. S. Beck, B. Bankamp, and P. A. Rota (Jan. 2017). “Perspective on Global Measles Epidemiology and Control and the Role of Novel Vaccination Strategies.” In: *Viruses* 9.1, p. 11. doi: 10.3390/v9010011.
- Xia, H., A. S. Beck, A. Gargili, N. Forrester, A. D. T. Barrett, and D. A. Bente (Oct. 2016). “Transstadial Transmission and Long-term Association of Crimean-Congo Hemorrhagic Fever Virus in Ticks Shapes Genome Plasticity.” In: *Scientific Reports* 6.1, p. 35819. doi: 10.1038/srep35819.
- Beck, A. S. and A. D. Barrett (Sept. 2015). “Current Status and Future Prospects of Yellow Fever Vaccines.” In: *Expert Review of Vaccines*, pp. 1–14. doi: 10.1586/14760584.2015.1083430.
- Beck, A., R. B. Tesh, T. G. Wood, S. G. Widen, K. D. Ryman, and A. D. T. Barrett (Feb. 2014). “Comparison of the Live Attenuated Yellow Fever Vaccine 17D-204 to its Virulent Parental Strain Asibi by Deep Sequencing”. In: *Journal of Infectious Diseases* 209.3, pp. 334–344. doi: 10.1093/infdis/jit546.
- Beck, A., H. Guzman, L. Li, B. Ellis, R. B. Tesh, and A. D. T. Barrett (Mar. 2013). “Phylogeographic Reconstruction of African Yellow Fever Virus Isolates Indicates Recent Simultaneous Dispersal into East and West Africa”. In: *PLoS Neglected Tropical Diseases* 7.3, e1910. doi: 10.1371/journal.pntd.0001910.
- Amant, D. S., M. Campbell, A. Beck, L. Williams, J. Minter, P. Collett, C. Zhu, and A. Samuels (2008). “Detection and Differentiation of Spore and Vegetative Forms of *Bacillus* spp. Using Infrared Spectroscopic Methods”. In: *International Journal of High Speed Electronics and Systems* 18.02, pp. 417–427. doi: 10.1142/S012915640800545X.

## Selected Abstracts and Presentations

- Beck, A., E. Lopareva, D. Lamson, P. Bryant, S. Griesemer, K. St. George, A. D. Mathis, R. Arciolo, W. Probert, J. Hacker, and B. Bankamp (2022). “Molecular Epidemiology of a Complex, Post-Elimination Measles Outbreak Incorporating Validation of Whole-Genome Phylogenetics with Case Linkage”. In: *Annual Meeting of the American Society for Virology*. Madison.
- Beck, A. S., M. M. Coughlin, B. Bankamp, and P. A. Rota (July 2018a). “Characterization of Defective Interfering Genomes of Measles Virus by RT-qPCR and Deep Sequencing”. In: *Annual Meeting of the American Society for Virology*. American Society for Virology. College Park.
- Beck, A. S., M. M. Coughlin, B. Bankamp, and P. A. Rota (Sept. 2018b). “Deep Sequencing of a Measles Vaccine Strain Reveals Complexity of Defective Interfering Genomes”. In: *ASM Conference on Rapid Applied Microbial Next-Generation Sequencing And Bioinformatic Pipelines*. American Society for Microbiology. Tysons.
- Beck, A. S., M. M. Coughlin, P. A. Rota, and B. Bankamp (June 2017). “Measurement and Molecular Detection of Measles Virus Defective Interfering Particles”. In: *Helen Levitt Measles Virus Mini-Symposium*. Mayo Clinic. Rochester.
- Beck, A. S., T. G. Wood, S. G. Widen, J. Thompson, G. Thaxton, M. C. Whiteman, and A. D. T. Barrett (June 2016). “Comparison of the Live-Attenuated Japanese Encephalitis Vaccine Strain SA14-14-2 to Its Wild-Type Parental Strain SA14 by Deep Sequencing”. In: *Annual Meeting of the American Society for Virology*. American Society for Virology. Blacksburg.
- Beck, A., S. G. Widen, J. Thompson, and A. D. Barrett (Apr. 2015). “Massively Parallel Sequencing of 17D Strain Yellow Fever Vaccines Identifies Stable Population Structure and Limited Genetic Divergence Along the Vaccine Seed Lineage”. In: *The Annual Conference on Vaccine Research*. National Foundation for Infectious Diseases. Bethesda.
- Beck, A., R. B. Tesh, S. G. Widen, T. G. Wood, J. Thompson, and A. D. T. Barrett (Oct. 2014). “Deep Sequencing Along the Lineage of the Yellow Fever Vaccine Strain 17D Reveals Low Diversity and Population Stability for Primary and Secondary Seed Lots”. In: *Annual Meeting of the International Society of Vaccines*. International Society of Vaccines. Philadelphia.

Beck, A., R. B. Tesh, S. G. Widen, T. G. Wood, J. Thompson, and A. D. Barrett (July 2014). “Deep Sequencing Along the Lineage of the Yellow Fever Vaccine Strain 17D Reveals Low Diversity and Population Stability For Primary and Secondary Seed Lots”. In: *Annual Meeting of the American Society for Virology*. American Society for Virology. Fort Collins.

Beck, A., R. B. Tesh, T. G. Wood, S. G. Widen, and A. D. Barrett (Apr. 2014). “Population Structure and *In Vitro* Genomic Stability of the Live Attenuated Yellow Fever Vaccine 17D-204 by Deep Sequencing”. In: *The Annual Conference on Vaccine Research*. National Foundation for Infectious Diseases. Bethesda.

Beck, A., H. Guzman, L. Li, B. R. Ellis, R. B. Tesh, and A. D. Barrett (Apr. 2013). “Comparison of the Live Attenuated Yellow Fever Vaccine 17D-204 to its Virulent Parental Strain Asibi by Deep Sequencing”. In: *The Annual Conference on Vaccine Research*. National Foundation for Infectious Diseases. Baltimore.

Beck, A., H. Guzman, L. Li, B. R. Ellis, R. B. Tesh, and A. D. Barrett (Nov. 2012a). “Bayesian Phylogeographic Reconstruction Using African Yellow Fever Virus Isolates Indicates Recent Simultaneous Dispersal of East and West Lineages”. In: *Annual Meeting of the American Society of Tropical Medicine and Hygiene*. American Society of Tropical Medicine and Hygiene. Atlanta.

Beck, A., H. Guzman, L. Li, B. R. Ellis, R. B. Tesh, and A. D. Barrett (June 2012b). “Bayesian Phylogeographic Reconstruction Using African Yellow Fever Virus Isolates Indicates Recent Simultaneous Dispersal of East and West Lineages”. In: *Annual Meeting of the American Society for Virology*. American Society for Virology. Madison.

Book Chapters

MacCannell, D. R., T. F. F. Ng, N. Chow, J. Jorba, A. Beck, and H. Carleton (2023). “Molecular Epidemiology”. In: *Manual of Clinical Microbiology*. Ed. by K. Carroll and M. Pfaller. Vol. 1. ASM Press.

Selected Honors & Awards

INSTITUTIONAL AWARDS

2024	<b>CDC/NCIRD Honor Award (As Group Member)</b> , For contributions to measles response activities during the 2024 Chicago outbreak.	Atlanta, USA
2024	<b>CDC On-the-Spot Cash Award</b> , For leading urgent investigations of measles sequence variants influencing diagnostic assay sensitivity.	Atlanta, USA
2024	<b>Nominee, CDC Shepard Award (As contributing author)</b> , For key contributions to a manuscript describing measles cases imported during Operation Allies Welcome.	Atlanta, USA
2024	<b>Mentor Appreciation Award, CDC Division of Viral Diseases</b> , For activities related to mentorship of students and junior staff.	Atlanta, USA
2023	<b>NCIRD Honor Award (As Group Member)</b> , For activities related to large-scale viral genomics studies supporting national COVID-19 surveillance.	Atlanta, USA
2023	<b>CDC Honor Award (As Group Member)</b> , For activities related to large-scale viral genomics studies supporting national COVID-19 surveillance.	Atlanta, USA
2023	<b>Mentor Appreciation Award, CDC Division of Viral Diseases</b> , For activities related to mentorship of students and junior staff.	Atlanta, USA
2024	<b>CDC Excellence in Property Management Award</b> , For activities related to stewardship of agency capital assets.	Atlanta, USA
2023	<b>CDC Excellence in Property Management Award</b> , For activities related to stewardship of agency capital assets.	Atlanta, USA

EXTRAMURAL AWARDS

2014	<b>Finalist</b> , National Foundation for Infectious Diseases, Maurice Hilleman Early Career Investigator Award	Bethesda, USA
2014	<b>Awardee</b> , American Society for Virology, Annual Conference Travel Grant	Fort Collins, USA
2011	<b>Awardee</b> , American Society for Virology, Annual Conference Travel Grant	Madison, USA

DURING GRADUATE STUDY

2015	<b>Pathology Day Poster Award</b>
2015	<b>James W. McLaughlin Colloquium Travel Award</b>
2015	<b>Sealy Center for Vaccine Development Travel Grant</b>
2014	<b>Sealy Center for Vaccine Development Travel Grant</b>
2014	<b>Pathology Day Poster Award</b>
2013	<b>Center for Tropical Diseases Graduate Student Award</b>
2013	<b>Robert Bennett Tuition Scholarship</b>
2012	<b>Sealy Center for Vaccine Development Travel Grant</b>
2012	<b>James W. McLaughlin Colloquium Travel Award</b>
2012	<b>Pathology Day Poster Award</b>
2011	<b>James W. McLaughlin Colloquium Travel Award</b>

## Professional Memberships

- American Society for Virology
- American Society for Microbiology
- American Society for Tropical Medicine and Hygiene

## Service and Committees

<b>WHO Global Measles and Rubella Laboratory Network (GMRLN)</b>	<i>Geneva, Switzerland</i>
VOTING MEMBER - MEASLES NUCLEOTIDE SURVEILLANCE (MEANS) STEERING COMMITTEE	<i>2024 - Present</i>
<ul style="list-style-type: none"> <li>Deliberated on the use of database resources used for molecular surveillance of measles and rubella.</li> <li>Periodically reviewed feature updates and quality of data outputs.</li> </ul>	
<b>WHO Global Measles and Rubella Laboratory Network (GMRLN)</b>	<i>Geneva, Switzerland</i>
ORGANIZER - NEXT-GENERATION AND EXTENDED WINDOW SEQUENCING WORKING GROUP	<i>2024 - Present</i>
<ul style="list-style-type: none"> <li>Promoted next-generation genomics methods to international surveillance network of &gt; 200 laboratories.</li> <li>Organized research presentations to network leadership.</li> </ul>	
<b>University of Texas Medical Branch - Institutional Animal Care and Use Committee (IACUC)</b>	<i>Galveston, USA</i>
STUDENT MEMBER	<i>2011 - 2012</i>
<ul style="list-style-type: none"> <li>Reviewed animal use protocols for use in research studies.</li> <li>Contributed to protocol reviews with high institutional visibility, including those at BSL3 and BSL4 containment levels.</li> </ul>	

## Grants and Support

<b>CDC Office of Advanced Molecular Detection (OAMD)</b>	<i>Atlanta, USA</i>
DEVELOPMENT OF MEASLES VIRUS WHOLE GENOME SEQUENCING ASSAYS USING MULTIPLEX AMPLICON STRATEGIES	<i>2023 - 2024</i>
<b>US Centers for Disease Control and Prevention - Viral Vaccine Preventable Diseases Branch</b>	<i>Atlanta, USA</i>
POSTDOCTORAL FELLOWSHIP - ASM PUBLIC HEALTH MICROBIOLOGY	<i>2015 - 2017</i>
<b>University of Texas Medical Branch - Biodefense Training Program</b>	<i>Galveston, USA</i>
NIH TRAINING GRANT T32 AI060945	<i>2013 - 2015</i>

## Teaching

<b>US Centers for Disease Control and Prevention</b>	<i>Atlanta, USA</i>
RESEARCH FELLOWSHIP MENTOR - OAK RIDGE INSTITUTE FOR SCIENCE AND EDUCATION	<i>2023 - 2025</i>
<b>US Centers for Disease Control and Prevention</b>	<i>Atlanta, USA</i>
RESEARCH FELLOWSHIP MENTOR - OAK RIDGE INSTITUTE FOR SCIENCE AND EDUCATION	<i>2020 - 2022</i>
<b>University of Texas Medical Branch School of Medicine</b>	<i>Galveston, USA</i>
TEACHING ASSISTANT - SON 1011 PATHOBIOLOGY AND HOST DEFENSES	<i>Spring 2011</i>

## Skills

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<b>Soft</b>	Communication of Scientific Findings, Cross-Functional Leadership, Strategic Research Studies, Technical Communication
<b>Virology</b>	Mammalian Cell Culture, Cell-based Assays (Plaque, TCID50, Immunoassay), Microneutralization Assays, Flavivirus Cultivation, Paramyxovirus Cultivation, Molecular Cloning, Infectious Clone Systems
<b>Molecular</b>	RT-qPCR Assay Development, Detection of Viral Quasispecies, Detection of Viral Single-Nucleotide Variants, Detection of Low-Abundance Templates in Clinical Specimens, Safety of Vaccine Strains, Viral Vaccinology, Cloning and Analysis of Synthetic Viruses
<b>Bioinformatics</b>	High-Performance Computing, Workflow Languages, Cluster Computing, Python, R, LaTeX, Scala, Hadoop, Jupyter, Pandas, Apache Spark, SQL, Git, Snakemake, Nextflow, Next-Generation Sequencing Analyses, Analysis Pipeline Development
<b>Genomics</b>	Next Generation Sequencing, Illumina, Oxford Nanopore, Nextflow, Snakemake, BEAST, Bayesian Phylogenetics, Phylodynamics, Whole-Genome Sequencing, Maximum Likelihood Phylogenetics
<b>Epidemiology</b>	Measles Surveillance, Mumps Surveillance, Outbreak Response, Integration of Epidemiological Linkage with Genomic Models
<b>Containment</b>	BSL-3/ABSL-3 Operations (>1000 Hours), General Biosafety, Aerobiology and Aerosol Exposure Methods
<b>Operations</b>	Familiarity with Laboratory Quality Control Systems, Writing and Use of Quality System Documentation