My V.T. Phan

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EDUCATION

2010 – 2013	The University of Oxford, United Kingdom Doctor of Philosophy in Medical Sciences (Clinical Medicine) Thesis title: "Diarrhoeal disease in children under the age of five in Ho Chi Minh City, Vietnam". Completion date: June 2013. Kellogg College, Nuffield Department of Clinical Medicine, The University of Oxford, United Kingdom. Supervisor: Stephen Baker
2004 – 2006	Flinders University of South Australia, Adelaide, Australia. Bachelor of Medical Science, Major in Biochemistry and Molecular Biology.

PROFESSIONAL EXPERIENCE

2024 – present	Assistant Professor at Biomedical Informatics program, College of Health Solutions, Arizona State University, Arizona, USA.
2021 –2023	Assistant Professor at London School of Hygiene and Tropical Medicine, MRC Uganda Research Unit, Entebbe, Uganda.
2019 –2021	Assistant Professor at Department of Viroscience, Erasmus Medical Center, Rotterdam, The Netherlands.
2019 –2021	Marie Sklodowska-Curie Individual Fellow, Department of Viroscience, Erasmus Medical Center, Rotterdam, The Netherlands.
2016 –2018	Postdoctoral research fellow, Department of Viroscience, Erasmus Medical Center, Rotterdam, The Netherlands.
Aug –Sep 2015	Local Sequencing Facility in Makeni, Sierra Leone, performing real-time sequencing of Ebola virus from clinical samples in Sierra in responding to the Ebola outbreak in West Africa.
2014 –2016	Postdoctoral research fellow, Virus Genomics group, Wellcome Trust Sanger Institute, Hinxton, United Kingdom.
2013 –2014	Postdoctoral research scientist, Oxford University Clinical Research Unit, Ho Chi Minh City, Vietnam.

FELLOWSHIPS AND GRANTS

2024 – submitted	Center for Disease Control (CDC) - Broad Agency Announcement call 75D301-24-R-72894. Topic 7. Project title: "Improved agnostic (arbo)virus surveillance (IMAGNOVIR)". Role: Co-PI. Requested amount of funding: $1.5 million USD (CDC cancelled the funding call after collecting submissions). US Agency for International Development (USAID) – Ethiopia Health Security Activity, Strategic Funding call. Role: Co-I. Requested amount of funding: $26,999,990 USD (not funded).
2023 – submitted	National Institutes of Health (NIH) R01. Project title: "Development of a risk assessment tool for human transmissible avian influenza using phylodynamic and geospatial

	modeling in Vietnam”. Role: Co-I. Requested amount of funding: $3,070,844.00 USD (not funded).
2021 - 2023	Projects “African COVID-19 Preparedness” (AFRICO19, ca £2.5 million, funder: Wellcome Trust, UK) and “Enhancing the Unit Support of Uganda's Efforts to Contain COVID-19” (DIASEQCO, £1.5 million, funder: MRC/UKRI, UK). **Total**: **£4 million Sterling pounds** in funding. Role: project leader.
2019 - 2021	Bacteriophage research on immune response, clinical use and knowledge of virome changes (BRICK). **Award: €250,000 Euros**. Funder: Netherlands Centre of One Health. Role: Co-PI.
2019 - 2021	Project title: “Novel PHAge Methods for improved virus inactivation (NoPHAME)”. **Award:** individual fellowship of **€165,598.80 Euros**. Funder: European Union’s Horizon 2020 research and innovation under scheme Marie Sklodowska-Curie Individual Fellowship (MSCA-IF-EF-ST). Role: PI.
2014	British Council Researchers Link award to work on Rotavirus genomics at the Wellcome Trust Sanger Institute. **Award: £7,190 Sterling pounds**. Role: PI.
2012	Australian Agency for International Development (AusAID, Australia) for the investigation of rotavirus infections in children living in Ho Chi Minh City, Vietnam. **Award: $5,000 USD**. Role: PI.
2012	The University of Oxford Vice Chancellors’ Fund (Oxford, UK) grant support for rotavirus genomics work. **Award: £1,000 Sterling pounds**. Role: PI.
2011	The International Society for Infectious Diseases (USA), project title: “The prevalence and phylodynamics of norovirus, an agent of diarrhea in symptomatic and asymptomatic in children in Ho Chi Minh City, Vietnam”. **Award: $6,000 USD.** Role: PI.
2009 – 2013	PhD Fellowship from the Wellcome Trust Major Overseas Programme (OUCRU-VN), supported by the Wellcome Trust (United Kingdom).
2004 – 2006	Full scholarship from Australian Development Scholarship programme (ADS) for undergraduate degree training in Australia.

TRAVEL AWARDS

2016	Travel award to present at the 6th International Calicivirus Conference, Savannah, GA, USA.
2015	Travel fellowship to present at the 12th International Double-Stranded RNA virus symposium, Goa, India.
2013	Travel fellowship from the Wellcome Trust to present at the Oxford Tropical Network Meeting, Kilifi, Kenya.
	Travel fellowship from European Society of Virology to present at the 5th European Congress of Virology, Lyon, France.
2012	Travel fellowship for young investigators awarded by Wellcome Trust to present at the 15th International Congress on Infectious Diseases, Bangkok, Thailand.
2011	Travel fellowship to present and Best abstract award at the 7th Annual Meeting of the World Society for Pediatric Infectious Diseases, Melbourne, Australia.
2010	Travel fellowship supported by Bill & Melinda Gates Foundation to present at the 59th Annual Meeting of the American Society for Tropical Medicine and Hygiene, Atlanta, Georgia, USA.
	Student fellowship awarded by HKU-Pasteur Insititute to attend the 7th HKU-Pasteur Virology Course, Hong Kong.

TEACHING

2025 Spring	BMD 514 Molecular Diagnostics (Instructor), Graduate online course, Arizona State University.
2024 Fall	BMI 465 Comparative Genomics (Course designer and instructor), Undergraduate in-person course, Arizona State University.
Before ASU	Master of Infection and Immunity, Erasmus University/Erasmus MC; Biomedical Research in Practice (BRiP), Erasmus University/Erasmus MC.

STUDENT MENTORING

2024 – present	PhD Committee Co-Chair at ASU: Ainsley Atherton, GSA PhD student, College of Health Solutions – BMI. Mentor for Barrett Honors Contract at ASU: Sanyam Paresh Shah, Undergraduate student, College of Health Solutions – BMI. Mentor for Barrett Honors Project at ASU: Jingyeong (Dana) Lee, Undergraduate student, School of Molecular Sciences. Mentor for master's student at ASU: Unnati Agarwal, Graduate student, College of Health solutions – Master of BMI and data science.

Prior to joining Arizona State University:

- 2021 – 2022: GeMVi fellow student Phionah Tushabe, EPI-Uganda Virus Research Institute, Uganda. **Project**: "Whole genome sequencing of enteroviruses from Acute Flaccid Paralysis patients in Uganda".
- 2021 – 2022: GeMVi fellow, PhD student Prossy Namuwulya, EPI-Uganda Virus Research Institute, Uganda. **Project**: "Genetic characterization of the measles viral genomes obtained from vaccinated individuals in Uganda".
- 2022: Master student Lucile Prevost Sansac De Traversay, London school of hygiene and tropical medicine. **Project:** "Evaluation of SARS-CoV-2 sentinel surveillance system in Abidjan, Côte d'Ivoire".
- 2019 – 2021: PhD student Michèle Molendijk, the Erasmus MC, Erasmus University, the Netherlands. **Project**: "Bacteriophage research on immune response, clinical use and knowledge on virome changes".
- 2028 – 2021: PhD student Kirsty Kwok, the Erasmus MC, Erasmus University, the Netherlands. **Project**: "Metagenomic analysis of animal, environmental and human microbiomes in the context of excess pneumonia risk around livestock production farms in the Netherlands: flow of microorganisms".
- 2019 – 2020: Master student Ms. Felisita Fideline Sinartio, the Erasmus MC, Erasmus University, the Netherlands. **Project**: "Bacteriophages as surrogates for human viruses in water quality assessment".
- 2012: Master student Mr. Yoshihara Keisuke, London School Hygiene and Tropical Medicine, UK. **Project**: "Pathogenic *E.coli* infections in diarrhoeal children in Ho Chi Minh City, Vietnam", at Oxford University Clinical Research Unit, Ho Chi Minh City, Vietnam..
- 2013: Mentored a pilot study, as part of PhD work, of Ms Jacqueline Leung, PhD student at the Princeton University, New Jersey, USA, at Oxford University Clinical Research Unit, Ho Chi Minh City, Vietnam.
- 2016 – 2017: Training and mentoring on deep sequencing and bioinformatics analyses for virome sequencing of sewage and oysters for Julien Schaeffer and other lab members, through strategic collaboration with IFREMER, Laboratoire de Microbiologie-LNR, Departement RBE, Nantes, France.
- 2017: Training on deep sequencing and bioinformatics analyses for norovirus next-generation sequencing for Dr Janet Mans, Senior Lecturer, Department of Medical Virology, University of Pretoria, Pretoria, South Africa, at Erasmus MC.
- 2016 – 2019: Mentored Mr Mike Mwanga, Bioinformatician, Epidemiology and Demography Department, Kenya Medical Research Institute (KEMRI), Wellcome Trust Research Collaborative Programme, Kilifi,

Kenya. **Project**: Rotavirus whole genome sequencing and phylogenetic analyses to understand dynamics and evolution at the genome scale.

PRESENTATIONS AT CONFERENCES

2018	**Invited talk** at the 11th Global Microbial Identifier (GMI) program, Geneva, Switzerland.
2017	**Invited talk** at the Molecular Diagnostics of Infectious Diseases meeting, Utrecht, The Netherlands.
	Invited talk at the 3th annual Molecular Diagnostics Europe, Lisbon, Portugal.
	Module: Advanced Diagnostics for Infectious Disease
	Co-chair for the session: Applying new technologies to clinical care: What is needed to make them useful tools for the virologist**.**
2015	The 12th International Double-Stranded RNA virus symposium, Goa, India.
	The 3rd International One Health Congress, Amsterdam, the Netherlands.
	Theme: Emerging diseases in a changing world: pathogens and interface.
	Co-chair for the session: Novel technologies: from molecular to modelling.
2013	The 5th European Congress of Virology, Lyon, France.
2012	The 15th International Congress on Infectious Diseases, Bangkok, Thailand.
2011	The 7th Annual Meeting of World Society for Pediatric Infectious Diseases, Melbourne, Australia.
2010	The 59th Annual Meeting of American Society for Tropical Medicine and Hygiene, Atlanta, USA.

UNIVERSITY/COLLEGE SERVICE

2024 – present	Member of Biomedical Informatics (BMI) Graduate Student Admission Committee, College of Health Solutions (CHS), Arizona State University (ASU).
	Co-Chair of the CHS BMI/BMD Affinity Network.
2024	Member of BMI PhD Comprehensive Oral Examination Committee, CHS, ASU.
	Member of BMI PhD Candidate Interview Committee.
	BMI PhD student credit transfer assessor.

PROFESSIONAL SERVICE

Editorial Board member:	Microbiology Spectrum (ASM, 2025 - ongoing); Infection, Genetics and Evolution (Elsevier, 2024 - ongoing).
Ad-hoc reviewer:	Nature Microbiology, Scientific Reports, BMC Infectious Diseases, Journal of General Virology.
Grant reviewer:	KU Leuven C2 grant for senior/established researchers.

PUBLICATIONS

Summary:	68 peer-reviewed papers, with 8 papers as last author (name bold and underline), 18 as first or co-first author (name bold with an asterisk) and 9 as second-author; 1 Science book chapter; and 2 manuscripts under review. **H-index 32, and i10-index 52. Number of citations 3,229.**
My Bibliography:	https://www.ncbi.nlm.nih.gov/myncbi/my%20vt.phan.1/bibliography/public/

1. Kieran D Lamb, Martha M Luka, Megan Saathoff, Richard Orton, **My Phan**, Matthew Cotten, Ke Yuan, David L Robertson. *Mutational signature dynamics indicate SARS-CoV-2's evolutionary capacity is driven by host antiviral molecules*. PLoS Comput Biol. 2024 Jan 25;20(1):e1011795. doi: 10.1371/journal.pcbi.1011795.
2. Matthew Cotten, **My V.T. Phan.** *Evolution to increased positive charge on the viral spike protein may be part of the adaptation of SARS-CoV-2 to human transmission*. iScience. 2023 March; 26(3): 106230. doi: 10.1016/j.isci.2023.106230.
3. Miguel Julián Martínez, Matthew Cotten, **My VT Phan**, Karsten Becker, Mateu Espasa, Truls M Leegard, Gorm Lisby, Uffe Vest Schneider, Climent Casals-Pascual. *Viral epidemic preparedness: a perspective from five clinical microbiology laboratories in Europe*. Clinical Microbiology and Infection. 2023 May; 30(5): 582-585. doi: 10.1016/j.cmi.2023.04.024.
4. Timothy Makori, Joel Bargul, Arnold Lambisia, Mike Mwanga, Nickson Murunga, Zaydah de Laurent, Clement Lewa, Martin Mutunga, Paul Kellam, Matthew COtten, D. James Nokes, **My VT Phan**, Charles Agoti, *Genomic epidemiology of the rotavirus G2P[4] strains in coastal Kenya pre- and post-rotavirus vaccine introduction, 2012 – 2018*. Virus Evolution. 2023; 9(1): vead025. doi: 10.1093/ve/vead025.
5. Joseph Mugisha, Bernard Mpairwe, Robert Newton, Matthew Cotten and **My V.T. Phan**. *SARS-CoV-2 Omicron (BA.5) infections in vaccinated individuals in rural Uganda*. Emerging Infectious Diseases. 2022 Dec 18; 29(1):224-226. doi: 10.3201/eid2901.220981.
6. Michèle M. Molendijk, **My V.T. Phan**, Lonneke G. M. Bode, Nikolas Strepis, Divyae K. Prasad, Nathalie Worp, David Nieuwenhuijse, Claudia M.E. Schapendonk, Bouke Boekema, Annelies Verbon, Marion P.G. Koopmans, Willem J. B. Van Wamel, Miranda de Graaf. *Bacteriophage susceptibility of clinical Staphylococcus aureus isolates in human serum*. Viruses. 2022; 15(1): 14. doi: 10.3390/v15010014.
7. Kirsty T. T. Kwok, Myrna M. T. de Rooij, Aniek B. Messink, Inge M. Wouters, Lidwien A. M. Smit, Matthew Cotten, Dick J.J. Heederik, Marion P.G. Koopmans, **My V.T. Phan**. *Establishing farm dust as a useful viral metagenomic surveillance matrix*. Sci Rep. 2022 Sep 29;12(1):16308. doi: 10.1038/s41598-022-20701-x
8. Houriiyah Tegally on behalf of the consortium. *The evolving SARS-CoV-2 epidemic in Africa: Insights from rapidly expanding genomic surveillance*. Science. 2022 Oct 7;378(6615):eabq5358. doi: 10.1126/science.abq5358.
9. Bailey Lubinski, Laura E. Frazier, **My V.T. Phan,** Daniel L. Bugembe, Jessie L Cunningham, Tiffany Tang, Susan Daniel, Matthew Cotten, Javier A. Jaimes, Gary R. Whittaker. *Spike Protein Cleavage-Activation in the Context of the SARS-CoV-2 P681R Mutation: an Analysis from Its First Appearance in Lineage A.23.1 Identified in Uganda*. Microbiol Spectr. 2022 Aug 31;10(4):e0151422. doi: 10.1128/spectrum.01514-22.
10. Prossy Namuwulya, Henry Bukenya, Phionah Tushabe, Robert Tweyongyere, Josephine Bwogi, Matthew Cotten, **My V.T. Phan**. Near-Complete Genome Sequences of Measles Virus Strains from 10 Years of Uganda Country-wide Surveillance. Microbiol Resour Announc. 2022 Aug 18;11(8):e0060622. doi: 10.1128/mra.00606-22
11. Charles N Agoti, Lynette Isabella Ochola-Oyier, Khadija Said Mohammed, Arnold W Lambisia, Zaydah R de Laurent, John M Morobe, Maureen W Mburu, Donwilliams O Omuoyo, Edidah M Ongera, Leoard Ndwiga, Eric Maitha, Benson Kitole, Thani Suleiman, Mohamed Mwakinangu, John Nyambu, John Otieno, Barke Salim, Jennifer Musyoki, Nickson Murunga, Edward Otieno, John Kiiru, Kadondi Kasera, Patrick Amoth, Mercy Mwangangi, Rashid Aman, Samson Kinyanjui, George Warimwe, **My Phan**, Ambrose Agweyu, Matthew Cotten, Edwine Barasa, Benjamin Tsofa, D James Nokes, Philip Bejon, George Githinji. *Transmission networks of SARS-CoV-2 in Coastal Kenya during the first two waves: A retrospective genomic study*. Elife**.** 2022 Jun 14;11:e71703. doi: 10.7554/eLife.71703
12. **My VT Phan**, Charles Agoti, Patrick Munywoki, Grieven Otieno, Mwanajuma Ngama, Paul Kellam, Matthew Cotten and D. James Nokes. *Identification of missed respiratory viruses by metagenomic sequencing of clinical respiratory samples from Kenya* 2021. Scientific Reports. 2022, 12:202-213.
13. Eduan Wilkinson on behalf of the consortium. *A year of genomic surveillance reveals how the SARS-CoV-2 pandemic unfolded in Africa.* Science. 2021, 374(6566): 423-431. doi: 10.1126/science.abj4336

14. Daniel Lule Bugembe*, **My V.T. Phan***, Abe G Abias, James Ayei, Lul Lojok Deng, Richard Lino Loro Lako, John Rumunu, Pontiano Kaleebu, Joseph Francis Wamala, Juma John HM, Dennis Kenyi Lodiongo, Sudhir Bunga, Matthew Cotten. Recent SARS-CoV-2 variants in South Sudan, Jan-Mar 2021. Emerging Infectious Diseases. 2021, 27(12): 3133-3136. *These first authors contributed equally to the article.

15. Matthew Cotten, David L. Robertson, **My V.T. Phan**. *Unique protein features of SARS-CoV-2 relative to other Sarbecoviruses*. Virus Evolution. 2021, 7(2), veab06

16. Daniel Lule Bugembe*, **My V.T. Phan***, Isaac Ssewanyana, Patrick Semanda, Hellen Nansumba, Beatrice Dhaala, Susan Nabadda, Áine Niamh O'Toole, Andrew Rambaut, Pontiano Kaleebu, Matthew Cotten. *Emergence and spread of a SARS-CoV-2 lineage A variant (A.23.1) with altered spike protein in Uganda.* Nature Microbiology. 2021, 6: 1094-1101. *These first authors contributed equally to the article.

17. Michael Roach, Adrian Cantu, Melissa Krizia Vieri, Matthew Cotten, Paul Kellam, **My Phan**, Lia van der Hoek, Michel Mandro, Floribert Tepage, Germain Mambandu, Gisele Musinya, Anne Laudisoit, Robert Colebunders, Robert Edwards, John L Mokili. *No Evidence Known Viruses Play a Role in the Pathogenesis of Onchocerciasis-Associated Epilepsy. An Explorative Metagenomic Case-Control Study.* Pathogens. 2021, 10(7):787.

18. Kirsty TT Kwok, Myrna MT de Rooij, Felisita F Sinartio, Lidwien AM Smit, Marion PG Koopmans, **My V.T. Phan**. *Genome Sequence of a* Minacovirus *Strain from a Farmed Mink in The Netherlands.* Microbial Resource Announcements. 2021, 10(8): e01451-20.

19. Matthew Cotten, Daniel Lule Bugembe, Pontiano Kaleebu, **My VT Phan**. *Alternate primers for whole-genome SARS-CoV-2 sequencing.* Virus Evolution. 2021, 7(1): veab006.

20. Arnold W. Lambisia, **My V.T. Phan**, Zaydah R. de Laurent, Matthew Cotten, D. James Nokes, Charles N. Agoti. *Near-complete Genome Sequences of Eight Human Astroviruses Recovered from Diarrheal Stool Samples of Hospitalized Children in Coastal Kenya in 2019.* Microbial Resource Announcements. 2021, 10(15): e00162-21

21. Kirsty Kwok, Myrna de Rooij, Aniek Messink, Inge Wouters, Marion Koopmans, **My VT Phan**. *Genome Sequences of* Seven Megrivirus *Strains from Chickens in the Netherlands.* Microbial Resource Announcements. 2020, 9(47).

22. Rosa L. Allesøe and Camilla K. Lemvigh, **My V.T. Phan**, Philip T. L. C. Clausen, Alfred Ferrer Florensa, Marion P.G. Koopmans, Ole Lund, Matthew Cotten. *Automated download and clean-up of family specific databases for kmer-based virus identification*. Bioinformatics. 2021, 37(5): 705-710.

23. Daniel Lule Bugembe*, John Kayiwa*, **My V.T. Phan***, Phionah Tushabe, Stephen Balinandi, Beatrice Dhaala, Jonas Lexow, Henry Mwebesa, Jane Aceng, Henry Kyobe, Deogratius Ssemwanga, Julius Lutwama, Pontiano Kaleebu, Matthew Cotten. *Main Routes of Entry and Genomic Diversity of SARS-CoV-2, Uganda*. Emerging Infectious Diseases. 2020, 26(10): 2411. *These first authors contributed equally to the article.

24. David Nieuwenhuijse*, **My VT Phan***, Bas Oude Munnink*, Patrick Munk, Shweta Venkatakrishnan, Frank Aarestrup, Matthew Cotten, Marion Koopmans. *Setting a baseline for global urban virome surveillance in sewage*. Scientific Reports. 2020, 10(1): 1-13. *These first authors contributed equally to the article.

25. Mazin Barry, **My VT Phan**, Layan Akkielah, Fahad Al-Majed, Abdulkarim Alhetheel, Ali Somily, Sarah Suliman Alsubaie, Scott JN McNabb, Matthew Cotten, Alimuddin Zumla, Ziad A Memish. *Nosocomial outbreak of the Middle East Respiratory Syndrome coronavirus: A phylogenetic, epidemiological, clinical and infection control analysis*. Travel Med Infect Dis. 2020, 37: 101807.

    *All authors contributed equally to the article.

26. Gregorius J Sips, Mariëlle JG Dirven, Joke T Donkervoort, Francien M van Kolfschoten, Claudia ME Schapendonk, **My VT Phan**, Annemieke Bloem, Anna F van Leeuwen, Mariechristine E Trompenaars, Marion PG Koopmans, Annemiek A van der Eijk, Miranda de Graaf, Ewout B Fanoy. *Norovirus outbreak in a natural playground: A One Health approach*. Zoonoses and Public Health. 2020, 67(4):453-459.

27. Charles Masembe, **My VT Phan**, David L Robertson, Matthew Cotten. *Increased resolution of African Swine Fever Virus genome patterns based on profile HMMs of protein domains*. Virus Evolution. 2020, Jun 19: veaa044. https://doi.org/10.1093/ve/veaa044.
28. **My VT Phan**, Mariana Mendonca Melo, Els van Nood, Georgina Aron, Jolanda JC Kreeft-Voermans, Marion PG Koopmans, Chantal Reusken, Corine H GeurtsvanKessel, Matthew Cotten. *Shedding of Yellow Fever Virus From an Imported Case in the Netherlands After Travel to Brazil*. Open Forum Infectious Diseases. 2020, 7(2): ofaa020.
29. Everlyn Kamau, John W Oketch, Zaydah R de Laurent, **My VT Phan**, Charles N Agoti, D James Nokes, Matthew Cotten. *Whole genome sequencing and phylogenetic analysis of human metapneumovirus strains from Kenya and Zambia*. BMC Genomics. 2020, 21(1):1-10.
30. Kirsty TT Kwok, David F Nieuwenhuijse, **My VT Phan**, Marion PG Koopmans. *Virus Metagenomics in Farm Animals: A Systematic Review*. Viruses. 2020, 12(1):107.
31. Sofia Strubbia, Julien Schaeffer, Oude Munnink, B Bass, Alban Besnard, **My VT Phan**, David Nieuwenhuijse, Miranda de Graaf, Claudia Schapendon, Candice Wacrenier, Matthew Cotten, Marion PG Koopmans, Francoise S Le Guyader. *Metavirome sequencing to evaluate norovirus diversity in sewage and related bioaccumulated oysters.* Frontiers in Microbiology. 2019, 10: 2394.
32. Sofia Strubbia, **My VT Phan**, Julien Schaeffer, Marion Koopmans, Matthew Cotten, Françoise S Le Guyader. *Characterization of Norovirus and Other Human Enteric Viruses in Sewage and Stool Samples Through Next-Generation Sequencing*. Food and Environmental Virology. 2019, 11(4):400-409.
33. **My VT Phan**, Sarwa Darwish Murad, Annemiek A van der Eijk, Herold J Metselaar, Hermien Hartog, Femme Harinck, Corine H GeurtsvanKessel, Richard Molenkamp, Matthew Cotten, Marion PG Koopmans. *Genomic sequence of yellow fever virus from a Dutch traveller returning from the Gambia-Senegal region, the Netherlands, November 2018*. Eurosurveillance. 2019, 24(4).
34. **My VT Phan**, Georgina Arron, Corine H GeurtsvanKessel, Robin C Huisman, Richard Molenkamp, Marion PG Koopmans, Matthew Cotten. *Complete Genome Characterization of Eight Human Parainfluenza Viruses from the Netherlands*. Microbiol Resour Announc. 2019, 8(15):e00125-19.
35. Charles N Agoti, **My VT Phan**, Patrick K Munywoki, George Githinji, Graham F Medley, Patricia A Cane, Paul Kellam, Matthew Cotten, D James Nokes. *Genomic analysis of respiratory syncytial virus infections in households and utility in inferring who infects the infant.* Scientific Reports**.** 2019, 9(1):10076.
36. Avraam Tapinos, Bede Constantinides, **My VT Phan**, Samaneh Kouchaki, Matthew Cotten, David L Robertson. *The Utility of Data Transformation for Alignment, De Novo Assembly and Classification of Short Read Virus Sequences*. Viruses. 2019, 11(5):394.
37. Everlyn Kamau, Charles N Agoti, Joyce M Ngoi, Zaydah R de Laurent, John Gitonga, Matthew Cotten, **My VT Phan**, D James Nokes, Eric Delwart, Eduard Sanders, George M Warimwe. *Complete Genome Sequences of Dengue Virus Type 2 Strains from Kilifi, Kenya*. Microbiol Resour Announc. 2019, 8(4):e01566-18.
38. **My VT Phan**, Tue Ngo Tri, Pham Hong Anh, Stephen Baker, Paul Kellam, Matthew Cotten. *Identification and characterization of Coronaviridae genomes from Vietnamese bats and rats based on conserved protein domains*. Virus Evol. 2018, 4(2):vey035.
39. **My VT Phan**, Claudia ME Schapendonk, Bas B Oude Munnink, Marion PG Koopmans, Rik L de Swart, Matthew Cotten. *Complete genome of six measles virus strains***.** Genome Announc. 2018, 6(13):e00184-18.
40. A Berto on behalf of the VIZIONS Consortium. *Hepatitis E in southern Vietnam: Seroepidemiology in humans and molecular epidemiology in pigs*. Zoonoses and public health. 2018, 65(1):43-50.
41. A Berto on behalf of the VIZIONS Consortium. *Detection of potentially novel paramyxovirus and coronavirus viral RNA in bats and rats in the Mekong Delta region of southern Viet Nam*. Zoonoses and public health. 2018, 65(1):30-42.
42. Janko van Beek, Miranda de Graaf, Saskia L. Smits, Claudia M.E. Schapendonk, George M. Verjans, Harry Vennema, Annemiek A. van der Eijk, **My V.T. Phan**, Matthew L. Cotten, Marion P.G. Koopmans. *Whole*

genome next generation sequencing to study within-host evolution of chronic norovirus infection among immunocompromised patients. J Infect Dis. 2017, 216(12):1513-1524.

43. Bas Oude Munnink, **My V.T Phan**, The VIZIONS Consortium, Peter Simmonds, Marion P.G. Koopmans, Paul Kellam, Lia van der Hoek, Matthew Cotten. *Characterization of Posa and Posa-like virus genomes in fecal samples from humans, pigs, rats, and bats collected from a single location in Vietnam.* Virus Evol. 2017, 3(2):vex022.

44. Gytis Dudas, Luiz Max Carvalho, Trevor Bedford, Andrew J. Tatem, Guy Baele, Nuno R. Faria, Daniel J. Park, Jason T. Ladner, Armando Arias, Danny Asogun, Filip Bielejec, Sarah L. Caddy, Matthew Cotten, Jonathan D'Ambrozio, Simon Dellicour, Antonino Di Caro, Joseph W. Diclaro II, Sophie Duraffour, Michael J. Elmore, Lawrence S. Fakoli III, Ousmane Faye, Merle L. Gilbert, Sahr M. Gevao, Stephen Gire, Adrianne Gladden-Young, Andreas Gnirke, Augustine Goba, Donald S. Grant, Bart L. Haagmans, Julian A. Hiscox, Umaru Jah, Brima Kargbo, Jeffrey R. Kugelman, Di Liu, Jia Lu, Christine M. Malboeuf, Suzanne Mate, David A. Matthews, Christian B. Matranga, Luke W. Meredith, James Qu, Joshua Quick, Suzan D. Pas, **My VT Phan**, Georgios Pollakis, Chantal B. Reusken, Mariano Sanchez-Lockhart, Stephen F. Schaffner, John S. Schieffelin, Rachel S. Sealfon, Etienne Simon-Loriere, Saskia L. Smits, Kilian Stoecker, Lucy Thorne, Ekaete Alice Tobin, Mohamed A. Vandi, Simon J. Watson, Kendra West, Shannon Whitmer, Michael R. Wiley, Sarah M. Winnicki, Shirlee Wohl, Roman Wölfel, Nathan L. Yozwiak, Kristian G. Andersen, Sylvia O. Blyden, Fatorma Bolay, Miles W. Carroll, Bernice Dahn, Boubacar Diallo, Pierre Formenty, Christophe Fraser, George F. Gao, Robert F. Garry, Ian Goodfellow, Stephan Günther, Christian T. Happi, Edward C. Holmes, Brima Kargbo, Sakoba Keita, Paul Kellam, Marion P.G. Koopmans, Jens H. Kuhn, Nicholas J. Loman, N'Faly Magassouba, Dhamari Naidoo, Stuart T. Nichol, Tolbert Nyenswah, Gustavo Palacios, Oliver G. Pybus, Pardis C. Sabeti, Amadou Sall, Ute Ströher, Isatta Wurie, Marc A. Suchard, Philippe Lemey & Andrew Rambaut. *Virus genomes reveal the factors that spread and sustained the West African Ebola epidemic*. Nature**.** 2017, 544(7650):309-315.

45. Charles N. Agoti, Patrick K. Munywoki, **My VT Phan,** James R. Otieno, Everlyn Kamau, Anne Bett, Ivy Kombe, George Githinji, Graham F. Medley, Patricia A. Cane, Paul Kellam, Matthew Cotten and D. James Nokes. *Transmission patterns and evolution of respiratory syncytial virus in a community outbreak identified by genomic analysis.* Virus Evol. 2017, 3(1):1–12.

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SCIENCE BOOK CHAPTER:

My V.T Phan, Matthew Cotten, and Marion Koopmans, in chapter: "Ebola" in the Popular science book on Microbes: "Might Microbes – The amazing world of microorganisms", edited by Joop van Doorn, Joen Luirink, John van der Oost, Bauke Oudega, Lesley Robertson, Henk Smit, Peter Willemsen, Claud Biemans. Available online at http://www.microcanon.nl/

Under review:

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