

# Gytis Dudas

## Curriculum Vitae

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### Postgraduate career

- 2018– Remote consultant, *CZ Biohub*, San Francisco, CA, USA.  
Based at the Gothenburg Global Biodiversity Center in Sweden
- 2018– Remote consultant, *The Scripps Research Institute*, San Diego, CA, USA.  
Based at the Gothenburg Global Biodiversity Center in Sweden
- 2016–2018 Mahan Postdoctoral Fellowship, *Fred Hutchinson Cancer Research Center*, Seattle, WA, USA, Mentor: Trevor Bedford.

### Education

- 2011–2016 Doctor of Philosophy, “Inference of Evolutionary and Ecological Processes from Reticulate Evolution in RNA Viruses”, *University of Edinburgh*, Edinburgh, UK.  
Supervisor: Prof. Andrew Rambaut, secondary supervisor: Prof. Andrew Leigh-Brown;  
Thesis examiners: Prof. Oliver G Pybus, Prof. Paul Sharp.
- 2007–2011 BSc in Biological Sciences with Honours in Evolutionary Biology, *University of Edinburgh*, Edinburgh, UK.  
First Class, Ashworth Prize and Class Medal

### Publications

- 2019 Müller NF, **Dudas G**, Stadler T., *Inferring time-dependent migration and coalescence patterns from genetic sequence and predictor data in structured populations*, *Virus Evolution* 5(2): vez030.
- 2019 Müller NF, Stolz U, **Dudas G**, Stadler T, Vaughan TG., *Bayesian inference of reassortment networks reveals fitness benefits of reassortment in human influenza viruses*, bioRxiv: 726042.
- 2019 Karcher MD, Suchard MA, **Dudas G**, Minin VN., *Estimating effective population size changes from preferentially sampled genetic sequences*, arXiv: 1903.11797.
- 2019 **Dudas G**, Bedford T., *The ability of single genes vs full genomes to resolve time and space in outbreak analysis*, bioRxiv: 582957.
- 2019 Tang M, **Dudas G**, Bedford T, Minin VN., *Fitting stochastic epidemic models to gene genealogies using linear noise approximation*, arXiv: 1902.08877.
- 2018 Dellicour S, Baele G, **Dudas G**, Faria NR, Pybus OG, Suchard MA, Rambaut A, Lemey P., *Phylogenetic assessment of intervention strategies for the West African Ebola virus outbreak*, *Nature Communications* 9: 2222.

<sup>1</sup>[ ] denotes joint first authorship

- 2018 Chu DKW, Hui Kenrie PY, ..., **Dudas G**, ..., Drosten C, Chevalier V, Peiris M, *MERS coronaviruses from camels in Africa exhibit region-dependent genetic diversity*, PNAS 115(12): 3144-3149.
- 2018 Whitmer SLM, Ladner JT, ..., **Dudas G**, ..., Palacios G, Ströher U, *Active Ebola Virus Replication and Heterogeneous Evolutionary Rates in EVD Survivors*, Cell Reports 22(5): 1159-1168.
- 2018 **Dudas G**, Carvalho LM, Rambaut A, Bedford T, *MERS-CoV spillover at the camel-human interface*, eLife 7: e31257.
- 2017 Langat P, Raghwan J, **Dudas G**, ..., Russell C, Pybus O, Kellam P, McCauley J, Watson S, *Genome-wide evolutionary dynamics of influenza B viruses on a global scale*, PLOS Pathogens 13(12): e1006749.
- 2017 [<sup>1</sup>Grubaugh ND, Ladner JT, Moritz KUG, **Dudas G**, Tan AL, Gangavarapu K, Wiley MR, White S, Thézé J], ..., Sabeti PC, Gillis LD, Michael SF, Bedford T, Pybus OG, Isern S, Palacios G, Andersen KG, *Multiple introductions of Zika virus into the United States revealed through genomic epidemiology*, Nature 546(7656): 401-405.
- 2017 **Dudas G**, Carvalho LM, Bedford T, Tatem AJ, Baele G, Faria N, Park D, Ladner J, Arias A, ..., Suchard M, Lemey P, Rambaut A, *Virus genomes reveal the factors that spread and sustained the West African Ebola epidemic*, Nature 544(7650): 309-315.
- 2016 Holmes EC, **Dudas G**, Rambaut A, Andersen KG, *The Evolution of Ebola virus: Insights from the 2013-2016 Epidemic*, Nature 538(7624): 193-200.
- 2016 Whitmer SLM, Albariño C, Shepard SS, **Dudas G**, ..., Nichol ST, Ströher U, *Preliminary Evaluation of the Effect of Investigational Ebola Virus Disease Treatments on Viral Genome Sequences*, Journal of Infectious Diseases: jiw177.
- 2016 Rambaut A, **Dudas G**, Carvalho LM, Park DJ, Yozwiak NL, Holmes EC, Andersen KG, *Comment on "Mutation rate and genotype variation of Ebola virus from Mali case sequences"*, Science 353(6300): 658-658.
- 2016 Arias A, Watson SJ, Asogun D, ..., **Dudas G**, ..., Pybus OG, Rambaut A, Kellam P, Goodfellow I, Cotten M, *Rapid outbreak sequencing of Ebola virus in Sierra Leone identifies transmission chains linked to sporadic cases*, Virus Evolution 2 (1): vew016.
- 2016 Lewis NS, Russell CA, Langat P, ..., **Dudas G**, ..., Watson SJ, Brown IH, Vincent AL, *The global antigenic diversity of swine influenza A viruses*, eLife 5: e12217.
- 2016 Quick J, Loman NJ, Duraffour S, Simpson JT, Severi E, Cowley L ..., **Dudas G**, ..., Günther S, Carroll MW, *Real-time, portable genome sequencing for Ebola surveillance*, Nature 530(7589): 228-232.
- 2016 **Dudas G**, Rambaut A, *MERS-CoV recombination: implications about the reservoir and potential for adaptation*, Virus Evolution 2(1): vev023.
- 2015 Ladner JT, Wiley MR, Mate S, **Dudas G**, ... Palacios G, *Evolution and Spread of Ebola Virus in Liberia, 2014-2015*, Cell Host & Microbe 18(6): 659-669.
- 2015 [Park DJ, **Dudas G**, Wohl S, Goba A, Whitmer SLM], ..., Sabeti PC, *Ebola Virus Epidemiology, Transmission, and Evolution during Seven Months in Sierra Leone*, Cell 161(7): 1516-1526.
- 2015 Carroll MW, Matthews DA, Hiscox JA, ... **Dudas G**, ... Günther S, *Temporal and spatial analysis of the 2014-2015 Ebola virus outbreak in West Africa*, Nature 524(7563): 97-101.

- 2015 **Dudas G**, Obbard DJ, *Are arthropods at the heart of virus evolution?*, eLife 4: e06837.
- 2015 **Dudas G**, Bedford T, Lycett S, Rambaut A, *Reassortment between Influenza B Lineages and the Emergence of a Coadapted PB1–PB2–HA Gene Complex*, Molecular Biology and Evolution 32(1): 162-172.
- 2014 Obbard DJ, **Dudas G**, *The genetics of host–virus coevolution in invertebrates*, Current Opinion in Virology 8: 73-78.
- 2014 Gire SK, Goba A, Andersen KG, ... **Dudas G**, ... Sabeti PC, *Genomic surveillance elucidates Ebola virus origin and transmission during the 2014 outbreak*, Science 345(6202): 1369-1372.
- 2014 **Dudas G**, Rambaut A, *Phylogenetic analysis of Guinea 2014 EBOV Ebolavirus outbreak*, PLOS Currents Outbreaks 6.
- 2013 Bedford T, Suchard MA, Lemey P, **Dudas G**, Gregory V, ..., Rambaut A, *Integrating influenza antigenic dynamics with molecular evolution*, eLife 3: e01914.

## Professional service

- Ad hoc* referee BMC Bioinformatics, PLoS Currents Outbreaks, eLife, PLoS Neglected Tropical Diseases, Molecular Biology and Evolution, Infection, Genetics and Evolution, PLoS Pathogens, PeerJ, Proceedings of the Royal Society B, Scientific Reports, Virology Journal, Virus Evolution.
- Social media editor Virus Evolution.

## Presentations

- London, 2019 Informal presentation at Imperial College London, "Virus genomes reveal the factors that spread and sustained the West African Ebola epidemic"
- Basel, 2019 Invited talk at ETH Zürich, "Beyond (two) button phylogenetics"
- Phoenix, 2019 Invited talk at Arizona State University, "Reconstructing the history and drivers of viral epidemics from genomes of emerging RNA viruses"
- Flagstaff, 2019 Invited talk at Northern Arizona University, "MERS-CoV spillover at the camel-human interface"
- Edinburgh, 2018 Invited talk at ARTIC network meeting, "MERS-CoV spillover at the camel-human interface"
- San Diego, 2018 Invited talk at UC San Diego HIV Institute, "Reconstructing the history and drivers of viral epidemics from genomes of Zika, MERS-CoV, and Ebola viruses"
- San Francisco, 2018 Invited talk at BioHub, "Reconstructing the history and drivers of viral epidemics from virus genomes"
- Bellevue, 2018 Oral presentation at the 6th Annual Disease Modeling Symposium, "Genomic epidemiology and population genetics of emerging RNA viruses"
- Tucson, 2018 Invited talk at BIO5 Institute, "MERS-CoV spillover at the camel-human interface"
- Tucson, 2018 Invited talk at University of Arizona, "Reconstructing the history and drivers of viral epidemics from virus genomes"

- Seattle, 2017 Invited talk at University of Washington Institute for Health Metrics and Evaluation, "MERS-CoV spillover at the camel-human interface"
- Baltimore, 2017 Invited talk at 19<sup>th</sup> Annual International Meeting of the Institute of Human Virology, "Virus genomes reveal factors that spread and sustained the Ebola epidemic"
- Edinburgh, 2017 Oral presentation at ARTIC network meeting, "Reproducible visualisation using Jupyter notebooks"
- Hong Kong, 2017 Oral presentation at Next Generation Informatics for Global Health: Disease Dynamics and Digital Epidemiology, "Virus genomes reveal factors that spread and sustained the Ebola epidemic"
- Cambridge, 2017 Invited talk at Broad Institute, "Virus genomes reveal factors that spread and sustained the Ebola epidemic"
- Boston, 2017 Invited talk at Harvard T.H. Chan School of Public Health, "Virus genomes reveal factors that spread and sustained the Ebola epidemic"
- Atlanta, 2017 Oral presentation at the MIDAS Network Meeting, "Virus genomes reveal factors that spread and sustained the Ebola epidemic"
- Seattle, 2016 Oral presentation for Combi Seminar series, "Virus genomes reveal the factors that spread and sustained the West African Ebola epidemic"
- Cambridge, 2016 Oral presentation at Virus Genomics and Evolution, "Pattern and determinants of the geographic dissemination of Ebola virus in West Africa 2013-2016"
- Zürich, 2015 Invited talk at University of Zürich, "Lessons about virus biology from molecular clocks"
- Vienna, 2015 Oral presentation at SMBE 2015, "Population genetics of Ebola virus in West Africa"
- Lisbon, 2015 Oral presentation at Forecasting Evolution?, "Population genetics of Ebola virus in West Africa"
- Online, 2015 Invited talk at Phyloseminar.org, "Ebola virus epidemiology, transmission, and viral evolution from four months of sequencing in Sierra Leone"
- Seattle, 2015 Invited talk at Fred Hutchinson Cancer Research Center, "Reticulate evolution: unlikely lessons about RNA viruses and their hosts"
- Oxford, 2014 Invited talk at University of Oxford, "Phylodynamics of co-circulating influenza virus lineages"
- London, 2014 Invited talk at Imperial College London, "Phylodynamics of co-circulating influenza virus lineages"
- Amsterdam, 2013 Oral presentation at Epidemics 4, "Inter-subtype reassortment patterns in influenza B reveal selective maintenance of co-reassorting segment complexes"
- Glasgow, 2012 Oral presentation at Popgroup 46, "Antagonistic interactions between co-circulating subtypes of human influenza viruses"
- Dublin, 2012 Poster at SMBE 2012, "Phylodynamics of influenza viruses before, during and after the 2009 swine flu pandemic"

## Awards

- 2018 SciPy John Hunter Excellence in Plotting Prize, 1st place, for "History of Ebola Virus Epidemic in West Africa 2013-2015", a matplotlib-based phylogeographic visualisation.

- 2017 Young Investigator Award to attend “Next Generation Informatics for Global Health: Disease Dynamics and Digital Epidemiology” in Hong Kong.
- 2015 SMBE Young Investigator Travel Award to attend the SMBE 2015 meeting in Vienna.
- 2015 Wellcome Trust Travel Grant to attend the “Forecasting Evolution?” meeting in Lisbon.

## Workshops

- University of Birmingham, 2015 “PoreCamp: A bootcamp to learn about operating the Oxford Nanopore MinION”, attendee.
- University of Zürich, 2015 “Temporal tree calibration in BEAST”, organiser.

## Outreach

- Moteris magazine Ebolos virusą perpratęs Gytis Dudas: "Lietuvoje vis dar jauti, kad gali kažką pakeisti", *Lithuanian language magazine*, interview. 2019 Mar 22
- NYLA podcast Perpratęs ebolą: Gytis Dudas, *Lithuanian language podcast*, interview. 2018 Dec 14
- Hutch News MERS remains primarily a camel virus – for now, *Fred Hutchinson Cancer Research Center newsletter*, interview. 2018 Jan 16
- Vancouver Bioinformatics Users Group Virus genomes reveal factors that spread and sustained the West African Ebola virus epidemic, *bioinformatics users meeting*, invited talk. 2018 Jan 11
- Cascadia Users of Geospatial Open Source Spring Fling Reconstructing the history of the Ebola epidemic, *open source geography and software meeting*, invited talk. 2017 May 20
- The Washington Post The March for Science could save lives, *daily newspaper*, editorial covering research. 2017 Apr 19
- GenomeWeb Ebola Genomes Help Reconstruct Virus’ Spread During West African Outbreak, *online science newsletter*, interview. 2017 Apr 12
- Hutch News A big-picture look at the world’s worst Ebola epidemic, *Fred Hutchinson Cancer Research Center newsletter*, interview. 2017 Apr 12
- BioPOD April 2015 episode, *podcast*, interview. 2015 Apr
- Eu:Sci podcast Episode 101, *podcast*, interview. 2014 Nov 12
- The Scotsman Edinburgh plays a part in solving Ebola crisis, *Local newspaper*, interview. 2014 Oct 31

- NERC news NERC-funded student helps analyse Ebola genome sequence, *Natural Environment Research Council newsletter*, interview.  
2014 Sep 05
- SciDev.net Ongoing Ebola outbreak highlights research shortcomings, *online science news portal*, interview.  
2014 Jun 04