

Gytis Dudas

Curriculum Vitae

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Postgraduate career

- 2021– Senior researcher, *Life Sciences Centre, University of Vilnius*, Vilnius, Lithuania.
- 2020– Remote consultant, *Ring Therapeutics*, Cambridge, MA, USA.
Based at the Gothenburg Global Biodiversity Center in Sweden
- 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

- 2022 Tsitsiklis A, Osborne CM, Kamm J, Williamson K, Kalantar K, **Dudas G**, ..., DeRisi JL, Mourani PM, Langelier CR, *Lower respiratory tract infections in children requiring mechanical ventilation: a multicentre prospective surveillance study incorporating airway metagenomics*, *The Lancet Microbe* (in press).
- 2022 Kaleta T, Kern L, Hong SL, ..., **Dudas G**, ..., Baele G, Panning M, Fuchs J, *Antibody escape and global spread of SARS-CoV-2 lineage A.27*, *Nature Communications* 13: 1152.
- 2021 [¹ Brito AF, Semenova E, **Dudas G**], Hassler GW, Kalinich CC, Kraemer MUG, Hill SC, ..., Suchard MA, Grubaugh ND, Baele G, Faria NR, *Global disparities in SARS-CoV-2 genomic surveillance*, medRxiv: 2021.08.21.21262393.
- 2021 [**Dudas G**], Hong SL, Potter B, Calvignac-Spencer S, Niatou-Singa FS, Tombolomako TB, Fuh-Neba T, ..., Griškevičius L, [**Baele G**], *Emergence and spread of SARS-CoV-2 lineage B.1.620 with variant of concern-like mutations and deletions*, *Nature Communications* 12: 5769.

¹[] denotes equal contribution

- 2021 Chazot N, Condamine FL, **Dudas G**, Peña C, Kodandaramaiah U, Matos-Maraví P, Aduse-Poku K, Elias M, Warren A, Lohman DJ, Penz CM, DeVries P, Fric ZF, Nylin S, Müller C, Kawahara AY, Silva-Brandão KL, Lamas G, Kleckova I, Zubek A, Ortiz-Acevedo E, Vila R, Vane-Wright RI, Mullen SP, Jiggins CD, Wheat C, Freitas AVL, Wahlberg N., *Conserved ancestral tropical niche but different continental histories explain the latitudinal diversity gradient in brush-footed butterflies*, *Nature Communications* 12: 5717.
- 2021 Klitting R, Kafetzopoulou LE, Thiery W, **Dudas G**, Gryseels S, Kotamarthi A, Vrancken B, Gangavarapu K, Momoh M, Sandi JD, Goba A, Alhasan F, Grant DS, Garry RF, Smither AR, Zeller M, Pauthner MG, McGraw M, Hughes LD, Duraffour S, Günther S, Suchard MA, Lemey P, Andersen KG, Dellicour S., *Predicting the evolution of Lassa Virus endemic area and population at risk over the next decades*, *bioRxiv*: 2021.09.22.461380.
- 2021 Zeller M, Gangavarapu K, Anderson C, Smither AR, Vanchiere JA, Rose R, Snyder DJ, **Dudas G**, Watts A, Matteson NL, Robles-Sikisaka R, ..., Kamil JP, Garry RF, Suchard MA, Andersen KG, *Emergence of an early SARS-CoV-2 epidemic in the United States*, *Cell* 184, 4939–4952.
- 2021 Pautienius A, **Dudas G**, Simkute E, Grigas J, Zakiene I, Paulauskas A, Armonaite A, Zienius D, Slyzius E, Stankevicius A, *Bulk Milk Tank Samples Are Suitable to Assess Circulation of Tick-Borne Encephalitis Virus in High Endemic Areas*, *Viruses* 13(9):1772.
- 2021 Arze CA, Springer S, **Dudas G**, Patel S, Bhattacharyya A, Swaminathan H, Brugnara C, Delagrave S, Ong T, Kahvejian A, Echelard Y, Weinstein EG, Hajjar RJ, Andersen KG, Yozwiak NL, *Global genome analysis reveals a vast and dynamic anellovirus landscape within the human virome*, *Cell Host & Microbe* 29(8): 1305-1315.e6.
- 2021 Pirnay JP, Selhorst P, Hong SL, Cochez C, Potter B, Maes P, Petrillo M, **Dudas G**, Claes V, Van der Beken Y, Verbeken G, Degueldre J, Dellicour S, Cuypers L, T'Sas F, Van den Eede G, Verhasselt B, Weuts W, Smets C, Mertens J, Geeraerts P, Ariën KK, André E, Neirinckx P, Soentjens P, Baele G, *Variant Analysis of SARS-CoV-2 Genomes from Belgian Military Personnel Engaged in Overseas Missions and Operations*, *Viruses* 13(7): 1359.
- 2021 [Batson J, **Dudas G**, Haas-Stapleton E, Kistler A, Li LM, Logan P, Ratnasari K, Retallack H]., *Single mosquito metatranscriptomics identifies vectors, emerging pathogens and reservoirs in one assay*, *eLife* 10:e68353.
- 2021 **Dudas G**, Huber G, Wilkinson M, Yllanes D., *Polymorphism of Genetic Ambigrams*, *Virus Evolution* 2021: veab038.
- 2020 Karcher MD, Carvalho LM, Suchard MA, **Dudas G**, Minin VN., *Estimating effective population size changes from preferentially sampled genetic sequences*, *PLoS Comput Biol* 16(10): e1007774.
- 2020 Müller NF, Stolz U, **Dudas G**, Stadler T, Vaughan TG., *Bayesian inference of reassortment networks reveals fitness benefits of reassortment in human influenza viruses*, *PNAS* 117(29): 17104-17111.
- 2019 **Dudas G**, Bedford T., *The ability of single genes vs full genomes to resolve time and space in outbreak analysis*, *BMC Evolutionary Biology* 19(1): 1-17.

- 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 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., *Phylodynamic assessment of intervention strategies for the West African Ebola virus outbreak*, *Nature Communications* 9: 2222.
- 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, Raghwani 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 [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.
- 2017 Black A, Potter B, **Dudas G**, Feldstein L, Grubaugh ND, Andersen KG, Ellis BR, Ellis EM, Bedford T, *Genetic characterization of the Zika virus epidemic in the US Virgin Islands*, *bioRxiv*: 113100.
- 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.
- 2014 Bedford T, Suchard MA, Lemey P, **Dudas G**, Gregory V, ..., Rambaut A, *Integrating influenza antigenic dynamics with molecular evolution*, eLife 3: e01914.

Professional service

- Co-author and chief data analyst Lithuania's pandemic SARS-CoV-2 genomic surveillance project. Since February 2021 >33 000 SARS-CoV-2 genomes were generated by the project accounting for a monthly average of 6.5% (between 0.1% and 20% in a given month) of all COVID-19 cases in Lithuania.
- Member since 2021 Advisory council of independent experts to the Lithuanian government tasked with advising the government on COVID-19 prevention, diagnostics, treatment, and application of other means of epidemic control.
- Ad hoc referee BMC Bioinformatics, Cell Reports, Nature Communications, Nature Ecology & Evolution, Nature Medicine, Nature Microbiology, PLoS Currents Outbreaks, eLife, PLoS Neglected Tropical Diseases, BMC Genome Medicine, Molecular Biology and Evolution, Infection, Genetics and Evolution, The Journal of Infectious Diseases, PLoS Pathogens, PeerJ, Proceedings of the Royal Society B, Scientific Reports, Virology Journal, Virus Evolution.
- Social media editor Virus Evolution.

Postgraduate student supervision

- 2018-2021 Karthik Gangavarapu (PhD)
- 2017-2021 Barney I Potter (research assistant)
- 2016-2018 Sidney M Bell (PhD)

Presentations

- Vilnius, 2021 Invited oral presentation (remote) at Vilnius University Hospital Santaros Klinikos conference "COVID-19 infekcija: iššūkiai, patirtys ir ateities perspektyva"
- Cambridge, 2021 Invited (remote) talk at University of Cambridge Department of Virology, "MERS-CoV spillover at the camel-human interface"
- Seattle, 2020 Invited (remote) talk at University of Washington Department of Genome Sciences, "Single mosquito metatranscriptomics in California"
- 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 19th 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

- Salt Lake City, 2020 BioVis@IEEE Challenges Workshop, part of VIS 2020 virtual conference, domain expert speaker.

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

- Vilnius University “Genominė epidemiologija: kaip atrodo protrūčiai iš virusų perspektyvos”, *a showcase of research carried out at Vilnius University*, invited talk.
2022 Mar 18
- Mokslų Sriuba “Kaip mutuoja virusai?”, *Lithuanian language pop-science show*, consulting.
2022 Feb 28
- LRT / VU “Mokslas be pamokslų. Koronaviruso evoliucija: ko laukti?”, *joint Vilnius University and Lithuanian National Radio and Television podcast*, interview.
2022 Jan 06
- VLE “COVID-19 atmainos”, *online Lithuanian language encyclopedia*, contributed article.
2021 Sep 21
- Nacionalinė Moksleivių Akademija “Evoliucija populiacijos lygmeniu: kartinės idėjos”, “Šiuolaikinis mokslo atsakas į epidemijas”, *a series of lectures for the National Student Academy, a Lithuanian non-profit public education organisation*, lectures.
2021 Feb 19
- LRT Mokslininkas Gytis Dudas apie pačius įdomiausius ir pavojingiausius virusus: mirtiną galima sutikti ir Lietuvoje, *Lithuanian National Radio and Television*, interview.
2021 Jan 24
- Išmani Lietuva Virusų detektyvas: ar galime užkirsti kelią pandemijoms?, *Lithuanian innovation conference*, invited talk.
2020 Oct 14
- NYLA podcast Koronavirusas: ką jau žinome, o ko dar ne, *Lithuanian language podcast*, interview.
2020 Jul 23
- Nature News How countries are using genomics to help avoid a second coronavirus wave, *science news*, background consultant.
2020 May 27
- FiveThirtyEight Genetic Tracking Helped Us Fight Ebola. Why Can't It Halt COVID-19?, *politics and economics news*, interview.
2020 Apr 15
- LRT Dar neseniai pasaulis kovojo su mirtinu Ebolos virusu: kaip pavyko suvaldyti epidemiją neturint veikiančios vakcinos, *Lithuanian National Radio and Television*, interview.
2020 Mar 25
- NYLA podcast Gyventi su COVID-19. Kalba mokslininkai, *Lithuanian language podcast*, interview.
2020 Mar 15
- 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