

# Edward C. Holmes

## *Curriculum Vitae*

### Personal Information

- Full Name: Edward Charles Holmes
- Date of Birth: 26<sup>th</sup> February 1965
- Nationality: Dual British and Australian citizen

### Address

Marie Bashir Institute for Infectious Diseases and Biosecurity,  
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  - <http://sydney.edu.au/medicine/people/academics/profiles/edward.holmes.php>
  - <http://sydney.edu.au/charles-perkins-centre/our-research/research-groups/pathogen-discovery-diversity-and-evolution.html>
  - [https://en.wikipedia.org/wiki/Edward\\_C.\\_Holmes](https://en.wikipedia.org/wiki/Edward_C._Holmes)
  - <http://sydney.edu.au/science/biology/viralevolution/index.shtml>
  - <https://scholar.google.com.au/citations?user=Syrp1IMAAAJ&hl=en>

### Current Appointments

- 2018-Present: ARC Australian Laureate Fellow and Professor, The University of Sydney, Australia.
- 2018-Present: Visiting Professor, Fudan University, Shanghai, China.
- 2015-Present: Adjunct Member, The Westmead Institute for Medical Research, Sydney, Australia.
- 2014-Present: Guest Professor, Chinese Center for Disease Control and Prevention, Beijing, China.
- 2009-Present: Member, The Center for Infection and Immunity, Columbia University, New York, NY, USA.

### Previous Appointments

- 2012-2017: NHMRC Australia Fellow and Professor, The University of Sydney, Australia.
- 2012: Verne M. Willaman Chair in the Life Sciences, The Pennsylvania State University, University Park, PA, USA.
- 2007-2012: Eberly College of Science Distinguished Senior Scholar, The Pennsylvania State University, University Park, PA, USA.
- 2006-2013: Affiliate member, Fogarty International Center, National Institutes of Health, Bethesda, MD, USA.
- 2005-2012: (Full) Professor of Biology, The Pennsylvania State University, University Park, PA, USA.
- 1999-2004: University Lecturer in Evolutionary Biology, University of Oxford, UK.
- 1999-2004: Tutorial Fellow in Biological Sciences, New College, Oxford, UK.
- 1994-2002: Royal Society University Research Fellow, University of Oxford, UK.
- 1994-1998: Fellow by Special Election of St. Catherine's College, Oxford, UK.

- 1994-1997: Wellcome Trust Fellow in Biodiversity Research, University of Oxford, UK.
- 1993-1994: Postdoctoral research (SERC funded) with Prof. PH Harvey, FRS, Department of Zoology, University of Oxford, UK.
- 1991-1993: Postdoctoral research (MRC funded) with Dr. AJ Leigh Brown, Institute of Cell, Animal and Population Biology, University of Edinburgh, UK.
- 1990-1991: Postdoctoral research with Dr. CH Langley, Department of Genetics, University of California, Davis, USA.

### Qualifications

- 1990: *Ph.D.*, Department of Zoology, University of Cambridge, UK; Thesis entitled '*Pattern and Process in the Molecular Evolution of the Order Primates*'. Supervisor: Dr. AE Friday.
- 1986: *B.Sc.* in Anthropology, University of London (University College), UK. First Class Honours.

### Awards and Honours

- 2017: Fellow, The Royal Society (FRS).
- 2017: Australian Laureate Fellow, Australian Research Council (ARC).
- 2017: NSW Premier's Prize for Science and Engineering (Biological Sciences).
- 2017: Fellow, The Royal Society of New South Wales.
- 2015: Fellow, Australian Academy of Science (FAA).
- 2011: Australia Fellow, National Health and Medical Research Council (NHMRC).
- 2010: Fogarty International Center Director's Merit Award to the Multinational Influenza Seasonal Mortality Study Team (MISMS). National Institutes of Health, USA.
- 2010: Faculty Scholars Medal in the Life and Health Sciences. The Pennsylvania State University, USA.
- 2008: Kavli Fellow, National Academy of Sciences, USA.
- 2003: Scientific Medal. Zoological Society of London, UK.

### Seminars (Selected; Invited Speaker, Keynote Speaker, Plenary Lecturer), 2013-2018

- 2018: XXIV Congress of the Latin American Association of Microbiology. Santiago, Chile.
- 2018. Nature Conference on Viral Infection and Immune Response 2018. Shanghai, China.
- 2018: Institut Pasteur conference on Emerging Infections and Pandemic Risk. Institut Pasteur, Paris, France.
- 2018. Influenza 2018: Centenary of the 1918 Pandemic. Francis Crick Institute, London, UK.
- 2018: ASM Microbe, American Society for Microbiology. Atlanta, USA.
- 2018: ASID Annual Scientific Meeting 2018. Gold Coast, Australia.
- 2017: 3<sup>rd</sup> One Health Aotearoa Symposium. Wellington, New Zealand.
- 2017: 12<sup>th</sup> International Congress on Genomics. Shenzhen, China.
- 2017: 2017 Australian Tropical Health Conference. Cairns, Australia.
- 2017: International Union of Microbiological Societies. Singapore.
- 2016: 4<sup>th</sup> International One Health Congress. Melbourne, Australia.
- 2016: 16th Asia Pacific Congress of Clinical Microbiology and Infection. Melbourne, Australia.
- 2016: 12th Mosquito Control Association of Australia and 9th Arbovirus Research in Australia. Gold Coast, Australia.
- 2016: Wellcome Trust Scientific Conference on Virus Genomics and Evolution. Wellcome Genome Campus, Hinxton, UK.
- 2015: 8<sup>th</sup> Australian Virology Society Meeting. Hunter Valley, Australia.
- 2015: 10<sup>th</sup> International Conference on Bioinformatics: Genomics and Evolution of Pathogens and Hosts. Atlanta, Georgia, USA.
- 2015: 20th International Bioinformatics Workshop on Virus Evolution and Molecular Epidemiology. Trinidad and Tobago.
- 2015: Australian Society for Microbiology 2015. Canberra, Australia.

- 2015: 3<sup>rd</sup> International One Health Congress. Amsterdam, The Netherlands.
- 2014: 12<sup>th</sup> International Conference on Molecular Epidemiology and Evolutionary Genetics of Infectious Diseases. Bangkok, Thailand.
- 2014: Australian Institute of Medical Scientists. National Scientific Meeting, Sydney.
- 2014: Multinational Influenza Seasonal Mortality Study conference. NIH, Bethesda, Maryland, USA.
- 2014: Lorne Infection & Immunity Conference, 2014. Lorne, Australia.
- 2014: Symposium on Influenza Transmission and Control. Hong Kong.
- 2013: Australian Influenza Symposium, 2013. Sydney, Australia.
- 2013: International Workshop on HIV & Hepatitis Virus Drug Resistance and Curative Strategies. Toronto, Canada.
- 2013: Molecular Microbiology Meeting, 2013. Sydney, Australia.
- 2013: Multinational Influenza Seasonal Mortality Study conference. Padua, Italy.

### Teaching and Mentoring

- 2009: Taught module on 'Evolutionary Inference and Infectious Disease Phylodynamics' as part of the 'Summer Institutes in Statistics and Modelling in Infectious Diseases', University of Washington, Seattle.
- 2007, 2009, 2011: Contributed lectures on viral evolution to 'The Rockefeller University Virology Course'. The Rockefeller University, New York.
- 2005-2012: Course organiser – 'The Evolution of Infectious Disease' at The Pennsylvania State University.
- 1994-2004: Lecturer, and eventually course organiser – 'Evolution & Systematics', University of Oxford.
- 1999-2004: Tutorial Fellow in Biological Sciences, New College, Oxford. Tuition in many aspects of biological science, most notably evolutionary biology and infectious disease biology.
- 1994-Present: Supervision of 27 graduate students (BBSRC, NSERC, Rhodes Trust, Wellcome Trust, NIH, NSF, NHMRC, ARC, APA and start-up grant funded).
- 1989-Present: Lecturing, particularly in evolutionary biology, population genetics, the ecology and evolution of infectious disease and virology, to undergraduate, masters and postgraduate students at the universities of Cambridge, California (Davis), Edinburgh, Oxford, Penn State and Sydney.

### Professional Service

- Editor, *Oxford Bibliographies in Evolutionary Biology* (2012-2014).
- Editor, *Epidemics* (2007-2008).
- Associate Editor and Section Editor, *PLoS Pathogens* (2006-2009).
- Associate Editor, *Molecular Biology & Evolution* (2000-2009).
- Editorial Board, *One Health* (2015-2017)
- Editorial Board, *Philosophical Transactions of the Royal Society Series B* (2013-present).
- Editorial Board (and founding member), *Annual Reviews of Virology* (2012-2013).
- Editorial Board, *Evolutionary Medicine and Public Health* (2012-2014).
- Editorial Board, *Current Opinion in Virology* (2010-present).
- Editorial Board, *Journal of Virology* (2007-present).
- Editorial Board, *Virology* (2006-present).
- Editorial Board, *Journal of General Virology* (1997-2002; 2007-2012).
- Editorial Board, *Journal of Evolutionary Biology* (1995-2000).
- Honorary Editor, *Evolutionary Bioinformatics* (2005-2008).
- Chief Moderator (and co-founder), *PLoS Currents: Influenza* (2009-2012).
- Member, *American Society for Microbiology* (2005-present).
- Member, Scientific Advisory Board, 'Area of Excellence on the Control of Pandemic and Inter-Pandemic Influenza'. University of Hong Kong (2008).

- Member, Advisory Council, Department of Ecology & Evolution, Princeton University.
- Member, *Faculty of 1000 Biology* (2006-2008; resigned).
- Member of Royal Society working group on the safety of GM plants for food use (2001).
- Organizing Committee, 'Options for the Control of Influenza' conference (meetings VII and VIII).
- Scientific Advisory Committee, NHMRC CRE in Infectious Diseases Modelling to Inform Policy (2015-present).
- Steering Committee, Ramaciotti Centre for Genomics (2013-present).
- Chair, NSW Public Health Pathogen Genomics Core Group (2016-2017).
- Expert witness, Strathboss Kiwifruit versus Attorney-General, New Zealand. High Court, Wellington, New Zealand.
- Peer review for *Nature*, *Science*, *Nature Genetics*, *Nature Medicine*, *Nature Microbiology*, *Nature Reviews Genetics*, *Nature Reviews Microbiology*, *PLoS Biology*, *PLoS Computational Biology*, *PLoS Genetics*, *PLoS Pathogens*, *Proceedings of the National Academy of Sciences USA*, *Journal of Virology*, *Genetics*, *Genome Research*, *Molecular Biology & Evolution*, *Molecular Microbiology*, *EMBO J*, *Journal of Molecular Evolution*, *Virology*, *Journal of General Virology*, *AIDS Research and Human Retroviruses*, *American Journal of Tropical Medicine & Hygiene*, *Proceedings of the Royal Society of London Series B*, *Bioinformatics*, *mBio*, *Virus Research*, *Archives of Virology*, *Trends in Genetics*, *Trends in Microbiology*, *Trends in Ecology & Evolution*.

## Research Grants

### Active

- 2018–2022: Redefining virus ecology and evolution. CI. ARC. Australia Laureate Fellowship. FL170100022. \$3,402,903.
- 2018–2020: Using metagenomics to determine the causative agent(s) of tick-borne disease in Australia. CI. NHMRC. Project Grant. GNT1139473. \$639,428.
- 2016–2021: The evolutionary and biological bases of host switching in viruses. Co-CI (CI, Prof. C. Parrish, Cornell University). National Institutes of Health (NIGMS). Grant 2 R01 GM080533. \$1,768,591 USD.
- 2016-2021. Centre of research excellence in protecting the public from emerging infectious diseases. Co-CI (CI, Prof. T. Sorrell, University of Sydney). NHMRC. Centre of Research Excellence. GNT1102962. \$2,500,000.
- 2016-2020: The genetic basis of pathogen blocking: elucidating the contributions of the *Wolbachia*, dengue virus and mosquito genomes. Co-CI (CI, Dr. E. McGraw, Monash University). NHMRC. Project Grant. GNT1103804. \$736,338.80.
- 2016-2019: Genomic dissection and prevention of bacterial transmissions events. Co-CI (CI, Dr. V. Sintchenko, University of Sydney). NHMRC. Project Grant. GNT1103804. \$891,290.
- 2016-2019: The phylodynamics of human enteroviruses: informing vaccine effectiveness and outbreak preparedness. CI. NHMRC. Project Grant. GNT1103804. \$564,867.70.
- 2016-2019: Revealing the evolutionary and ecological dynamics of avian influenza virus. CI. ARC. Discovery Project. DP160102146. \$534,100.
- 2016-2019: Making Green Guard® greener: enhancing the efficacy of a biopesticide. Co-CI (CI, Prof. S. Simpson, University of Sydney). ARC. Linkage Project. LP150100479. \$385,000.

### Completed

- 2014-2017: Defining the evolution of pathogen virulence to enhance rabbit control. CI. ARC. Discovery Project. DP140103362. \$595,000.
- 2014-2016: Cluster-randomised controlled trial to test the effectiveness of facemasks in preventing influenza, corona and other respiratory viruses among Hajj pilgrims. Co-CI (CI, Dr. H. Rashid, The Children's Hospital at Westmead). The Qatar National Research Fund. \$782,812.28.

- 2012–2016: Genomic analysis of the canonical case of virulence evolution: myxomatosis in Australia. CI. National Institutes of Health (NIAID). Grant R01 AI093804-01A1. \$2,806,103 USD.
- 2016. Zika: Open genomic surveillance of Zika virus in Brazil using a novel portable real-time sequencing device. Co-CI (CI, Dr. N. Loman, University of Birmingham, UK). Medical Research Council (UK). (ZK/16-078). £100,000 UKP.
- 2015: PacBio long read sequencer for the Ramaciotti Genomics Consortium of NSW. Co-CI (CI, Dr. M. Wilkins, University of New South Wales). ARC. Linkage Infrastructure. LE150100031. \$630,000.
- 2015. Exploiting genomics to understand pathogen evolution in external infection transmission/evolution and within the normal, obese and immunosuppressed host. Co-CI (CI, Dr. T. Cunningham, University of Sydney). University of Sydney HMR+ Implementation Fund. \$153,913.
- 2014-2017: Black Death genomics and the evolution of pathogen virulence. CI. NHMRC. Project Grant. GNT1065106. \$510,129.50.
- 2014-2015: Towards a real time data sharing to support patient-centred care, quality health delivery, improvement programmes, performance management and research. Co-CI (CI, Dr. J. Morris, The Kolling Institute, Royal North Shore Hospital). Office for Health and Medical Research, Government of New South Wales. \$500,000.
- 2014–2015: Genomic sequencing centers for infectious diseases. Subcontractor (PI, The J. Craig Venter Institute). National Institutes of Health (NIAID). Contract U19AI110819. \$16,200 USD.
- 2013–2016: Genetic variability of non-segmented negative-sense RNA virus populations and host adaptation. Co-CI (PI, Dr. H. Bourhy, Institut Pasteur, Paris, France). Agency National de la Recherche (ANR). No financial support received.
- 2012–2017: Australia Fellowship. CI. NHMRC. GNT1037231. \$4,000,000.
- 2012–2016: The evolutionary and biological bases of host switching in viruses. PI. National Institutes of Health (NIGMS). Grant 2 R01 GM080533. \$1,004,763 USD.
- 2010–2013: Genomic sequencing centers for infectious diseases. Subcontractor (PI, The J. Craig Venter Institute). National Institutes of Health (NIAID). Contract HHSN272200900007C. \$37,752 USD.
- 2010–2012: ARRA: Penn State: ABSL-3 Facility Construction. Consortium investigator. NIH/NCRR (American Recovery and Reinvestment Act). \$14,830,000 (total, all investigators) USD.
- 2009–2012: Detecting homology in the ‘twilight zone’ of sequence similarity. Co-PI (PI, Dr. R. Patterson, University of California, Davis). National Institutes of Health (NIGMS). Grant R01 GM087410. \$157,070 USD.
- 2009–2013: Fitness and virulence of dengue virus in the context of changing host immunity. Co-PI (PI, Dr. E. Harris, The University of California, Berkeley). National Institutes of Health (NIGMS). Grant R01 GM087405. \$135,040 USD.
- 2008–2013: Dengue vaccine and viral evolution in rural Thailand. Co-PI (PI, Dr. T.P. Endy, The State University of New York). National Institutes of Health (NIAID). Grant R01 GM083224. \$89,988 USD.
- 2008–2013: Evaluation of candidate vaccine technologies using computational models. Subcontractor. (PI, Dr. D. Burke, The University of Pittsburgh). Bill & Melinda Gates Foundation. Grant 705580-04. No financial support received.
- 2008–2012: Synthesizing the evolutionary and ecological dynamics of acute RNA viruses: comparative analyses and method development. Co-PI (PI, Prof. B.T. Grenfell, Princeton University). National Institutes of Health (NIGMS). Grant R01 GM083983. No financial support received.
- 2008–2012: Emergence of human pathogens in the genus *Bordetella*. Co-PI (PI, Dr. E.T. Harvill, The Pennsylvania State University). National Institutes of Health (NIGMS). Grant R01 GM083113. No financial support received

- 2008–2011: Population dynamics of arboviruses. Co-PI (PI, Dr. J. Aaskov, Queensland University of Technology). National Health and Medical Research Council, Australia. Grant 497203. No financial support received.
- 2007–2012: The evolutionary and biological bases of host switching in viruses. PI. National Institutes of Health (NIGMS). Grant R01 GM080533. \$1,364,796 USD.
- 2006–2010: Intergovernmental Personnel Act (IPA) from National Institutes of Health (FIC). \$146,794 USD.
- 2004–2007: A comparative genomics approach to investigating the origins and evolution of RNA viruses. The Wellcome Trust. (Advanced Training Fellowship for Dr. B. Shapiro). Grant 74717. £158,999 UKP.
- 2003–2006: An experimental and phylogenetic approach to understanding RNA virus evolution. The Wellcome Trust. Grant 71979. £242,643 UKP.
- 2003–2004: The evolutionary epidemiology of sylvatic yellow fever and dengue viruses. The Wellcome Trust. Grant 69552. £120,906 UKP.
- 2002–2005: A bioinformatics analysis of immune escape and viral persistence in hepatitis C virus (with Dr. P. Klenerman). The Wellcome Trust. (Prize studentship). Grant 68610. £105,521 UKP.
- 2002–2005: The population genetics of molecular adaptation in viral pathogens. The Wellcome Trust. (Biodiversity Junior Fellowship for Dr. O. Pybus). Grant 66889. £147,469 UKP.
- 2002–2005: A comparative study of HIV-1 subtypes B and C and the evolution of viral fitness and co-receptor usage (with Dr. L. Morris). The Wellcome Trust. (Biodiversity studentship). Grant 67502. £76,443 UKP.
- 2001–2004: Antigenic evolution in acute human immunodeficiency virus infection: impact of potent anti-viral drugs (with Prof. R.E. Phillips). The Wellcome Trust. (Prize studentship). Grant 65997. £116,541 UKP.
- 2001–2004: The molecular epidemiology of bat lyssaviruses in Europe. The Wellcome Trust (Biodiversity studentship). Grant 64398. £67,279 UKP.
- 2000–2003: The molecular archaeology of *Yersinia pestis* (with Dr. A. Cooper). The Wellcome Trust (Bioarchaeology studentship). Grant 61610. £80,022 UKP.
- 1999–2001: Revealing evolutionary processes from bacterial gene sequences (with Prof. B.G. Spratt). The Wellcome Trust (Prize studentship). Grant 58789. £57,231 UKP.
- 1999–2002: Understanding primate lentivirus (HIV/SIV) diversity. The Wellcome Trust. (Biodiversity Junior Fellowship for Dr. D.L. Robertson). Grant 57073. £105,000 UKP.
- 1998–2001: Evolutionary aspects of recombination in RNA viruses. The Wellcome Trust (Prize studentship). Grant 55819. £54,000 UKP.
- 1998–2001: Revealing the population genetic structure of dengue virus in Viet Nam. The Wellcome Trust (Biodiversity studentship). Grant 54231. £72,000 UKP.
- 1997–2002: Inferring epidemic processes from gene sequences (with Prof. P.H. Harvey). The Wellcome Trust (programme grant). Grant 50275. £430,000 UKP.
- 1995–1998: Automated analysis of gene sequence data banks to reveal the evolutionary and population processes responsible for genetic diversity (with Prof. P.H. Harvey & Dr. S. Nee). BBSRC (Bioinformatics initiative). £125,000 UKP.
- 1995–1998: Inferring population processes from phylogenetic trees (with Dr. S. Nee & Prof. P.H. Harvey). BBSRC (UK). £100,000 UKP.
- 1995: The molecular epidemiology of HIV and HCV in Thailand. The Royal Society. £9,500 UKP.
- 1994–1998: The development of a phylogenetic approach to the molecular epidemiology of viruses. The Wellcome Trust. Grant 41888. £110,000 UKP.
- 1991–1993: Phylogenetic analysis of HIV sequence change within a local infected community (with Dr. A.J. Leigh Brown). Medical Research Council (UK).

## Publications

### *Metrics Summary* (Google Scholar)

- Peer reviewed papers = 522
- Citations = 53,019
- h-index = 122
- i10-index = 464

### **Books**

- **Holmes EC.** (2009). *The Evolution and Emergence of RNA Viruses*. Oxford Series in Ecology and Evolution (OSEE). Series edited by PH Harvey & RM May. Oxford University Press, Oxford. ISBN. 978-0-19-921112-8.
- Page RDM & **Holmes EC.** (1998). *Molecular Evolution: A Phylogenetic Approach*. Blackwell Science Ltd, Oxford. ISBN 0-86542-889-1.

### **Peer Reviewed Journal Articles**

522. Aghazadeh M, Shi M, Barrs VR, McLuckie AJ, Lindsay SA, Jameson B, Hampson B, **Holmes EC** & Beatty JA. (2018). A novel hepadnavirus identified in an immunocompromised domestic cat in Australia. *Viruses* **10**, 269.
521. Buchmann JP, Fourment M & **Holmes EC.** (2018). The Biological Notation (BON): a structured file format for biological data. *Sci.Rep.* **8**, 9644.
520. Cobbin JCA, Britton P, Burrell R, Thosar D, Selvakumar K, Eden J-S, Jones CA & **Holmes EC.** (2018). A complex mosaic of enteroviruses shapes community-acquired hand, foot and mouth disease transmission and evolution within a single hospital. *Virus Evol.* **4**, vey020.
519. Di Giallonardo F, Audsley M, Shi M, Young PR, McGraw EA & **Holmes EC.** Complete genome of *Aedes aegypti* anphevirus in the Aag2 mosquito cell line. *J.Gen.Virol.* **99**, 832-836.
518. Duchêne S & **Holmes EC.** (2018). Estimating evolutionary rates in giant viruses using ancient genomes. *Virus Evol.* **4**, vey006.
517. Fukuto HS, Vadyvaloo V, McPhee JB, Poinar HN, **Holmes EC** & Bliska JB. (2018). A single amino acid change in the response regulator PhoP acquired during *Yersinia pestis* evolution affects PhoP target gene transcription and polymyxin B susceptibility. *J.Bact.* **200**, e00050-18.
516. Geoghegan JL, Pirota V, Harvey E, Smith A, Buchmann JP, Ostrowski M, Eden J-S, Harcourt R & **Holmes EC.** (2018). Virological sampling of inaccessible wildlife with drones. *Viruses* **10**, 300.
515. Geoghegan JL, Saavedra AF, Duchêne S, Sullivan S, Barr I & **Holmes EC.** (2018). Continental synchronicity of human influenza virus epidemics despite climatic variation. *PLoS Pathog.* **14**:e1006780.
514. Leopardi S, **Holmes EC**, Gastaldelli M, Tassoni L, Priori P, Scaravelli D, Zamperin G & De Benedictis P. (2018). Interplay between co-divergence and cross-species transmission in the evolutionary history of bat coronaviruses. *Infect.Genet.Evol.* **58**, 279-289.
513. Liu J, Xu J, Liu L, Wei X, Song Y, Fang B, Yu X, Li X, Ye G, Du Y, Chen M, Shi W, Liu D, **Holmes EC** & Cui J. (2018). Sudden emergence of human infections with H7N9 avian influenza A virus in Hubei province, central China. *Sci.Rep.* **8**:2486.
512. Mahar JE, Hall RN, Peacock D, Kovaliski J, Piper M, Mourant R, Huang N, Campbell S, Gu X, Read A, Urakova N, Cox T, **Holmes EC** & Strive T. (2018). Rabbit hemorrhagic disease virus 2 (RHDV2; GI.2) is replacing endemic strains of RHDV in the Australian landscape within 18 months of its arrival. *J.Virol.* **92**:e01374-17.
511. Mahar JE, Read AJ, Gu X, Urakova N, Mourant R, Piper M, Haboury S, **Holmes EC**, Strive T & Hall RN. (2018). Detection and circulation of a novel rabbit hemorrhagic disease virus in Australia. *Emerg.Infect.Dis.* **24**, 22-31.

510. Nie F-Y, Lin X-D, Hao Z-Y, Chen X-N, Wang Z-X, Wang M-R, Wu J, Wang H-W, Zhao G, Ma R-Z, **Holmes EC** & Zhang Y-Z. (2018). Extensive diversity and evolution of hepadnaviruses in bats in China. *Virology* **514**, 88-97.
509. Panzarin V, **Holmes EC**, Abbadi M, Zamperin G, Quartesan R, Milani A, Schivo A, Bille L, Dalla Pozza M, Monne I & Toffan A. (2018). Low evolutionary rate of infectious pancreatic necrosis virus (IPNV) in Italy is associated with reduced virulence in trout. *Virus Evol.* **4**, vey019.
508. Patterson Ross Z, Klunk J, Fornaciari G, Giuffra V, Duchêne S, Duggan AT, Poinar D, Douglas MW, Eden J-S, **Holmes EC** & Poinar HN. (2018). The paradox of HBV evolution as revealed from a 16<sup>th</sup> century mummy. *PLoS Pathog.* **14**:e1006750.
507. Qi W, Jia W, Liu D, Li J, Bi Y, Xie S, Li B, Hu T, Du Y, Xing L, Zhang J, Zhang F, Wei X, Eden J-S, Li H, Tian H, Li W, Su G, Lao G, Xu C, Xu B, Liu W, Zhang G, Ren T, **Holmes EC**, Cui J, Shi W, Gao GF & Liao M. (2018). Emergence and adaptation of a novel highly pathogenic H7N9 influenza virus in birds and humans from a 2013 human-infecting low pathogenic ancestor. *J. Virol.* **92**:e00921-17.
506. Rodríguez-Navado C, Lam TT-Y, **Holmes EC** & Pagán I. (2018). The impact of host genetic diversity on virus evolution and emergence. *Ecol.Lett.* **21**, 253-263.
505. Russo AG, Eden J-S, Tuipulotu DE, Shi M, Selechnik D, Shine R, Rollins LA, **Holmes EC** & White PA. (2018). Viral discovery in the invasive Australian cane toad (*Rhinella marina*) using metatranscriptomic and genomic approaches. *J. Virol.* Epub 13 June 2018, doi:10.1128/JVI.00768-18.
504. Shi M, Lin X-D, Chen X, Tian J-H, Chen L-J, Li K, Wang W, Eden J-S, Shen J-J, Liu L, **Holmes EC** & Zhang Y-Z. (2018). The evolutionary history of vertebrate RNA viruses. *Nature* **556**, 197-202.
503. Shi M, White VL, Schlub T, Eden J-S, Hoffmann AA & **Holmes EC**. (2018). No detectable effect of *Wolbachia* wMel on the natural RNA virome of *Drosophila melanogaster*. *Proc.R.Soc.Lond.B.* Epub 25 July doi: 10.1098/rspb.2018.1165.
502. Shi M, Zhang Y-Z & **Holmes EC**. (2018). Meta-transcriptomics and the evolutionary biology of RNA viruses. *Virus Res.* **243**, 83-90.
501. Voorhees IEH, Dalziel BD, Glaser A, Dubovi EJ, Murcia PR, Newbury S, Toohey-Kurth K, Shuo S, Kriti D, Van Barkel H, Goodman LB, Leutenegger C, **Holmes EC** & Parrish CR. (2018). Multiple introductions and recurrent epidemic fade-out of H3N2 canine influenza A virus in the United States. *J. Virol.* Epub 6 June 2018, doi:10.1128/JVI.00323-18.
500. Chappell KJ, Brealey JC, Amarilla AA, Watterson D, Hulse L, Palmieri C, Johnston SD, **Holmes EC**, Meers J & Young PR. (2017). Phylogenetic diversity of Koala retrovirus within a wild Koala population. *J. Virol.* **91**:e01820-16.
499. Chen L-J, Lin X-D, Tian J-H, Liao Y, Ying X-H, Shao J-W, Yu B, Guo J-S, Wang M-R, Peng Y, Shi M, **Holmes EC**, Yang Z-Q & Zhang Y-Z. (2017). Diversity, evolution and population dynamics of avian influenza viruses circulating in the live poultry markets in China. *Virology* **505**, 33-41.
498. Cobbin JCA, Alfelali M, Barasheed O, Taylor J, Dwyer DE, Kok J, Booy R, **Holmes EC** & Rashid H on behalf of the Hajj Research Team. (2017). Multiple sources of genetic diversity of influenza A viruses during the Hajj. *J. Virol.* **91**:e00096-17.
497. Devault AM, Mortimer TD, Kitchen A, Kiesewetter H, Enk JM, Golding GB, Southon J, Kuch M, Duggan AT, Aylward W, Gardner SN, Allen JE, King AM, Wright GD, Kuroda M, Kato K, Briggs DEG, Fornaciari G, **Holmes EC**, Poinar HN & Pepperell CS. (2017). A molecular portrait of maternal sepsis from Byzantine Troy. *eLife* **6**:e20983.
496. Dheilly MN, D Bolnick, S Bordenstein, PJ Brindley, C Figueres, **Holmes EC**, Martínez MJ, Phillips AJ, Robert P & Rosario K. (2017). Parasite Microbiome Project: Systematic investigation of microbiome dynamics within and across parasite-host interactions. *mSystems* **2**:e00050-17.



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