

Edward C. Holmes

Curriculum Vitae

Personal Information:

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

Address:

Marie Bashir Institute for Infectious Diseases and Biosecurity,
School of Life and Environmental Sciences and Sydney Medical School,
Charles Perkins Centre,
The University of Sydney, Sydney, NSW 2006, Australia.

- Tel: +61 2 9351 5591; Fax: +61 2 9351 2175
- E-mail: edward.holmes@sydney.edu.au
- Websites:
 - <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
 - <http://sydney.edu.au/science/biology/viralevolution/index.shtml>
 - <https://scholar.google.com.au/citations?user=Syrp1IMAAAAJ&hl=en>

Current Appointments:

- 2018-Present: ARC Australian Laureate Fellow and Professor, The University of Sydney, Australia.
- 2018-Present: Honorary Professor, Shanghai Public Health Clinical Center & Institutes of Biomedical Sciences, 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.

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

- 2018: ASM Microbe, American Society for Microbiology, Atlanta, USA.
- 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. Nature Conference on Viral Infection and Immune Response 2018. Shanghai, China.
- 2018: XXIV Congress of the Latin American Association of Microbiology, Santiago, Chile.
- 2017: 3rd One Health Aotearoa Symposium. Wellington, New Zealand.
- 2017: 12th International Congress on Genomics. Shenzhen, China.
- 2017: 2017 Australian Tropical Health Conference. Cairns, Australia.
- 2017: International Union of Microbiological Societies. Singapore.
- 2016: 4th 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: 8th Australian Virology Society Meeting. Hunter Valley, Australia.
- 2015: 10th 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: 3rd International One Health Congress. Amsterdam, The Netherlands.
- 2014: 12th 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 Experience:

- 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 an 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.

Pending

- 2018-2021: Real-time surveillance and decision support for the Indo-Pacific Region: Developing outbreak genomics and disease models for emerging infectious diseases. Co-CI (CI, Prof. E. McBryde, James Cook University). DFAT. Joint International Calls. APP1153238. \$2,999,882.00.

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. Co-PI. 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-PI (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-PI (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-PI (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. Co-PI. 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-PI (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-PI (PI, Dr. H. Bourhy, Institut Pasteur, Paris, France). Agency National de la Recherche (ANR). No financial support received.
- 2012–2017: Australia Fellowship. Co-PI. 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. Sub-contractor. (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 = 513
- Citations = 51,995
- h-index = 120
- i10-index = 461

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

Published

513. Duchêne S & **Holmes EC.** (2018). Estimating evolutionary rates in giant viruses using ancient genomes. *Virus Evol.* **4**: vey006. doi: 10.1093/ve/vey006.
512. 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.
511. 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.
510. Leopardi S, **Holmes EC**, Gastaldelli M, Tassoni L, Priori P, Scaravelli D, Zamperin G & Benedictis P. (2018). Interplay between co-divergence and cross-species transmission in the evolutionary history of bat coronaviruses. *Infect.Genet.Evol.* **58**, 279-289.
509. 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.
508. 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.
507. 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.
506. 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.
505. 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 16th century mummy. *PLoS Pathog.* **14**:e1006750.
504. 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.
503. 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.
502. 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.
501. Shi M, Zhang Y-Z & **Holmes EC**. (2018). Meta-transcriptomics and the evolutionary biology of RNA viruses. *Virus Res.* **243**, 83-90.
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.
495. Di Giallonardo F, Schlub TE, Shi M & **Holmes EC**. (2017). Dinucleotide composition in RNA viruses is shaped more by virus family than host species. *J.Virol.* **91**:e02381-16.
494. Du Y, Chen M, Yang J, Jia Y, Han S, **Holmes EC** & Cui J. (2017). Molecular evolution and emergence of H5N6 avian influenza virus in central China. *J.Virol.* **91**:e00143-17.
493. Dudas G, Carvalho LM, Bedford T, Tatem AJ, Baele G, Faria N, Park DJ, Ladner J, Arias A, Asogun D, Bielejec F, Caddy S, Cotten M, Dambrozio J, Dellicour S, Di Caro A, Diclaro II JW, Duraffour S, Elmore M, Fakoli L, Gilbert M, Gevao SM, Gire S, Gladden-Young A, Gnirke A, Goba A, Grant DS, Haagmans B, Hiscox JA, Jah U, Kargbo B, Kugelman J, Liu D, Lu J, Malboeuf CM, Mate S, Matthews DA, Matranga CB, Meredith L, Qu J, Quick J, Pas SD, Phan MVT, Poliakis G, Reusken C, Sanchez-Lockhart M, Schaffner SF, Schieffelin JS, Sealfon RS, Simon-Loriere E, Smits SL, Stoecker K, Thorne L, Tobin EA, Vandi MA, Watson SJ, West K, Whitmer S, Wiley MR, Winnicki SM, Wohl S, Wölfel R, Yozwiak NL, Andersen KG, Blyden S, Bolay F, Carroll M, Diallo B, Formenty P, Fraser C, Gao GF, Garry RF, Goodfellow I, Günther S, Happi C, **Holmes EC**, Kargbo B, Kellam P, Koopmans MPG, Loman NJ, Magassouba N, Naidoo D, Nichol ST, Nyenswah T, Palacios G, Pybus OG, Sabeti P, Sall A, Ströeher U, Wury I, Suchard MA, Lemey P & Rambaut A. (2017). Virus genomes reveal factors that spread and sustained the Ebola epidemic. *Nature* **544**, 309-315.
492. Eden J-S, Chisholm R-H, Bull RA, White PA, **Holmes EC** & Tanaka MM. (2017). Persistent infections in immunocompromised hosts are rarely sources of new pathogen variants. *Virus Evol.* **3**:vex018. doi:10.1093/ve/vex018.
491. Eden J-S, Rose K, Ng J, Shi S, Wang Q, Sintchenko V & **Holmes EC**. (2017). *Francisella tularensis* subsp. *holartica* in ringtail possums, Australia. *Emerg.Infect.Dis.* **23**, 1198-1201.
490. Faria NR, Quick J, Morales I, Thézé J, Jesus JG, Giovanetti M, Kraemer MU, Hill SC, Black A, da Costa AC, Franco L, Patroca S, Wu CH, Ragwhani J, Cauchemez S, du Plessis L,

- Verotti M, de Oliveira WK, Carmo EH, Coelho GE, Santelli AS, Vinhal LC, Simpson JT, Loose M, Andersen KG, Grubaugh ND, Somasekar S, Chiu CY, Lewis-Ximenez L, Baylis S, Chieppe AO, Aguiar SF, Fernandes CA, Lemos PS, Nascimento B, Monteiro HAO, Siqueira IC, de Queiroz MG, de Souza TR, Bezerra JF, Lemos MR, Pereira GF, Loudal D, Moura LC, Dhalia R, França RF, Magalhães T, Marques ET Jr., Ayres C, Wallau GL, de Lima, MC, Nascimento V, de Cerqueira EM, de Lima MM, Mascarenhas DL, Moura Neto JP, Levin AS, Tozetto-Mendoza TR, Fonseca SN, Correa CM, Milagres FP, Segurado A, **Holmes EC**, Rambaut A, Bedford T, Nunes MRT, Sabino EC, Alcântara LCJ, Loman N & Pybus OG. (2017). Epidemic establishment and cryptic transmission of Zika virus in Brazil and the Americas. *Nature* **546**, 406-410.
489. Fourment M, Darling AE & **Holmes EC**. (2017). The impact of migratory flyways on the spread of avian influenza virus in North America. *BMC Evol.Biol.* **17**:118.
488. Geoghegan JL, Duchêne S & **Holmes EC**. (2017). Comparative analysis estimates the relative frequencies of co-divergence and cross-species transmission within viral families. *PLoS Pathog.* **13**:e1006215.
487. Geoghegan JL & **Holmes EC**. (2017). Predicting virus emergence amidst evolutionary noise. *Open Biol.* **7**:170189. <http://dx.doi.org/10.1098/rsob.170189>.
486. Hackenbrack N, Rogers MB, Ashley RE, Keel MK, Kubiski SV, Bryan III JA, Ghedin E, **Holmes EC**, Hafenstein SL & Allison AB. (2017). Evolution and cryo-EM capsid structure of a North American bat adenovirus and its relationship to other mastadenoviruses. *J.Virol.* **91**:e01504-16.
485. Kerr PJ, Cattadori IM, Liu J, Sim D, Dodds JW, Brooks JW, Kennett MJ, **Holmes EC** & Read AF. (2017). Next step in the ongoing arms race between myxoma virus and wild rabbits in Australia is a novel disease phenotype. *Proc.Natl.Acad.Sci.USA* **114**, 9397-9402.
484. Kerr PJ, Cattadori IM, Rodgers MB, Liu J, Sim D, Boag B, Eden J-E, Ghedin E, Read AF & **Holmes EC**. (2017). The evolution of myxoma virus: genomic and phenotypic characterization of isolates from Great Britain reveals multiple successful evolutionary pathways distinct from those in Australia. *PLoS Pathog.* **13**:e1006252.
483. Lin X-D, Wang W, Hao Z-Y, Wang Z-X, Guo W-P, Guan X-Q, Wang M-R, Wang H-W, Zhou R-H, Li M-H, Tang G-P, Wu J, **Holmes EC** & Zhang Y-Z. (2017). Extensive diversity of coronaviruses in bats from China. *Virology* **507**, 1-10.
482. Liu J, Cattadori IM, Sim DG, Eden J-S, **Holmes EC**, Read AF & Kerr PJ. (2017). Reverse engineering field isolates of myxoma virus demonstrates that some gene disruptions or loss of function do not explain virulence changes observed in the field. *J.Virol.* **91**:e01289-17.
481. Lu M, Tian J-H, Yu B, Guo W-P, Li M-H, **Holmes EC** & Zhang Y-Z. (2017). Extensive diversity of rickettsiales bacteria in ticks from Wuhan, China. *Ticks Tick.Borne Dis.* **8**, 574-580.
480. Nicholson LJ, Mahar JE, Strive T, Zheng T, **Holmes EC**, Ward V & Duckworth JA. (2017). Discovery and characterisation of a novel rabbit calicivirus in New Zealand. *Appl.Environ.Micro.* **83**:e00090-17.
479. Pettersson JH-O, Shi M, Bohlin J, Eldholm V, Brynildsrud OB, Paulsen KM, Andreassen A & **Holmes EC**. (2017). Characterizing the virome of *Ixodes ricinus* ticks from northern Europe. *Sci.Rep.* **7**:10870.
478. Porter AF, Duggan AT, Poinar HN & **Holmes EC**. (2017). Comment: Characterization of two historic smallpox specimens from a Czech museum. *Viruses* **9**, 276.
477. Remnant EJ, Shi M, Buchmann G, Blacquièrre T, **Holmes EC**, Beekman M & Ashe A. (2017). A diverse range of novel RNA viruses in geographically distinct honey bee populations. *J.Virol.* **91**:e00158-17.
476. Shi M, Neville P, Nicholson J, Eden J-S, Imrie A & **Holmes EC**. (2017). High-resolution metatranscriptomics reveals the ecological dynamics of mosquito-associated RNA viruses in Western Australia. *J.Virol.* **91**:e00680-17.

475. Simon-Loriere E, Faye O, Prot M, Casademont I, Fall G, Fernandez-Garcia MD, Diagne MM, Kipela J-M, Fall IS, **Holmes EC**, Sakuntabhai A & Sall AA. (2017). Autochthonous Japanese encephalitis with Yellow fever coinfection in Africa. *New.Eng.J.Med.* **376**, 1483-1485.
474. Tao Y, Shi M, Chommanard C, Queen K, Zhang J, Markotter W, Kuzmin IV, **Holmes EC** & Tong S. (2017). Surveillance of bat coronaviruses in Kenya identifies relatives of human coronaviruses NL63 and 229E and their recombination history. *J.Virol.* **91**:e01953-16.
473. Voorhees IEH, Glaser AL, Toohey-Kurth K, Newbury S, Dalziel BD, Dubovi EJ, Poulsen K, Leutenegger C, Willgert KJE, Brisbane-Cohen L, Richardson-Lopez J, **Holmes EC** & Parrish CR. (2017). Spread of canine influenza A(H3N2) virus, United States. *Emerg.Infect.Dis.* **23**, 1950-1957.
472. Wang W, Lin X-D, Liao Y, Guan X-Q, Xu J-M, Guo W-P, Xing J-G, **Holmes EC** & Zhang Y-Z. (2017). Discovery of a highly divergent coronavirus in the Asian house shrew from China illuminates the origin of the alphacoronaviruses. *J.Virol.* **91**:e00764-17.
471. Weyrich LS, Duchêne S, Soubrier J, Arriola L, Llamas B, Breen J, Morris AG, Alt KW, Caramelli D, Dresely V, Farrell M, Farrer AG, Francken M, Gully N, Haak W, Hardy K, Harvati K, Held P, **Holmes EC**, Kaidonis J, Krause J, Lalueza-Fox C, de la Rasilla M, Rosas A, Semal P, Soltysiak A, Townsend G, Usai D, Wahl J, Huson DH, Dobney K & Cooper A. (2017). Neanderthal behaviour, diet, and disease inferred from ancient DNA in dental calculus. *Nature* **544**, 357-361.
470. Abbadi M, Fusaro A, Ceolin C, Casarotto C, Quartesan R, Dalla Pozza M, Cattoli G, Toffan A, **Holmes EC** & Panzarin V. (2016). Molecular evolution and phylogeography of co-circulating IHNV and VHSV in Italy. *Front.Microbiol.* **7**, Article 1306. doi:10.3389/fmicb.2016.01306.
469. Allison AB, Organtini LJ, Zhang S, Hafenstein SL, **Holmes EC** & Parrish CR. (2016). Single mutations in the VP2 300 loop of the three-fold spike of the carnivore parvovirus capsid can determine host range. *J.Virol.* **90**, 753-767.
468. Bourhy H, Nakouné E, Hall M, Nouvellet P, le Pelletier A, Talbi C, Watier L, **Holmes EC**, Cauchemez S, Lemey P, Donnelly CA & Rambaut A. (2016). Revealing the micro-scale signature of endemic zoonotic disease transmission in an African urban setting. *PLoS Pathog.* **12**:e1005525.
467. Bos KI, Herbig A, Sahl J, Waglechner N, Fourment M, Forrest SA, Klunk J, Schuenemann VJ, Poinar D, Kuch M, Golding GB, Dutour O, Keim P, Wagner DM, **Holmes EC**, Krause J & Poinar HN. (2016). Eighteenth century *Yersinia pestis* genomes reveal the long-term persistence of an historical plague focus. *eLife* **5**:e12994.
466. Chen L-J, Lin X-D, Guo W-P, Tian J-H, Wang W, Ying X-H, Wang M-R, Yu B, Li M-H, Shi M, **Holmes EC** & Zhang Y-Z. (2016). Diversity and evolution of avian influenza viruses in live poultry markets, free range poultry and wild wetland birds in China. *J.Gen.Virol.* **97**, 844-854.
465. Dill JA, Camus AC, Leary JH, Di Giallonardo F, **Holmes EC** & Ng TFF. (2016). Distinct viral lineages of hepadnavirus from fish and amphibians reveal the complex evolutionary history of hepadnaviruses. *J.Virol.* **90**, 7920-7933.
464. Di Giallonardo F, Geoghegan JL, Docherty DE, McLean RG, Zody MC, Qu J, Yang X, Birren BW, Malboeuf CM, Newman RM, Ip HS & **Holmes EC**. (2016). Fluid spatial dynamics of West Nile virus in the USA: rapid spread in a permissive host environment. *J.Virol.* **90**, 862-872.
463. Duchêne S, Duchêne DA, Di Giallonardo F, Eden J-S, Geoghegan JL, Holt KE, Ho SYW & **Holmes EC**. (2016). Cross-validation to select Bayesian hierarchical models in phylogenetics. *BMC Evol.Biol.* **16**:115.
462. Duchêne S, Holt KE, Weill F-X, Le Hello S, Hawkey J, Edwards DJ, Fourment M & **Holmes EC**. (2016). Genome-scale rates of evolutionary change in bacteria. *Microb.Genom.* doi: 10.1099/mgen.0.000094.

461. Duchêne S, Di Giallonardo F & **Holmes EC**. (2016). Substitution model adequacy and assessing the reliability of estimates of virus evolutionary rates and time scales. *Mol.Biol.Evol.* **33**, 255-267.
460. Duchêne S, Geoghegan JL, **Holmes EC** & Ho SYW. (2016). Estimating evolutionary rates using time-structured data: a general comparison of phylogenetic methods. *Bioinformatics* **32**, 3375-3379.
459. Duggan AT, Perdomo MF, Piombino-Mascali D, Marciniak S, Poinar D, Emery MV, Buchmann JP, Duchêne S, Jankauskas R, Humphreys M, Golding GB, Southon J, Devault AM, Rouillard J-M, Sahl JW, Dutour O, Hedman K, Sanjantila A, Smith GL, **Holmes EC** & Poinar HN. (2016). 17th century variola virus reveals the recent history of smallpox. *Curr.Biol.* **26**, 1-6.
458. Feng KH, Sun M, Iketani S, **Holmes EC** & Parrish CR. (2016). Comparing the functions of equine and canine influenza H3N8 virus PA-X proteins: suppression of reporter gene expression and modulation of global host gene expression. *Virology* **496**, 138-146.
457. Fourment M & **Holmes EC**. (2016). Seqotron: a user-friendly sequence editor for Mac OS X. *BMC Research Notes* **9**:106.
456. Geoghegan JL, Senior AM, Di Giallonardo F & **Holmes EC**. (2016). Virological factors that increase the transmissibility of emerging human viruses. *Proc.Natl.Acad.Sci.USA* **113**, 4170-4175.
455. Geoghegan JL, Senior AM & **Holmes EC**. (2016). Pathogen population bottlenecks and adaptive landscapes: overcoming the barriers to disease emergence. *Proc.R.Soc.Lond.B.* **283** 20160727. doi:10.1098/rspb.2016.0727.
454. Guo W-P, Tian J-H, Lin X-D, Ni X-B, Chen X-P, Liao Y, Yang S-Y, Dumler JS, **Holmes EC** & Zhang Y-Z. (2016). Extensive genetic diversity of Rickettsiales bacteria in multiple mosquito species. *Sci.Rep.* **6**:38770. doi:10.1038/srep38770.
453. **Holmes EC**. (2016). Complexities of estimating evolutionary rates in viruses. *J.Virol.* **90**, 2155.
452. **Holmes EC**, Dudas G, Rambaut A & Andersen KG. (2016). The evolution of Ebola virus: Insights from the 2013-2016 epidemic. *Nature* **358**, 193-200.
451. Huang C, Liu L, Xu W, Jin T, Zhao Y, Song J, Shi Y, Ji W, Jia H, Zhou Y, Wen H, Zhao H, Liu H, Li H, Wang Q, Wu Y, Wang L, Liu D, Liu G, Yu H, **Holmes EC**, Lu L & Gao GF. (2016). A bat-derived putative cross-family recombinant coronavirus with a reovirus gene. *PLoS Pathog.* **12**:e1005883.
450. Lam TT-Y, Zhu H, Guan Y & **Holmes EC**. (2016). Genomic analysis of the emergence, evolution and spread of human respiratory RNA viruses. *Annu.Rev.Genom.Hum.Genet.* **17**, 15.1-15.26.
449. Li K, Lin X-D, Huang K-Y, Shi M, Guo W-P, Wang M-R, Xing J-G, Wang W, Wang K, Li M-H, Cao J-H, Jiang M-L, **Holmes EC** & Zhang Y-Z. (2016). Identification of novel and diverse rotaviruses in rodents and insectivores, and evidence of cross-species transmission to humans. *Virology* **494**, 168-177.
448. Liu W, Pickering P, Duchêne S, **Holmes EC** & Aaskov JG. (2016). Highly divergent dengue virus type 2 in traveller returning from Borneo to Australia. *Emerg.Infect.Dis.* **22**, 2146-2148.
447. Mahar JE, Nicholson L, Eden J-S, Duchêne S, Kerr PJ, Duckworth J, Ward VK, **Holmes EC** & Strive T. (2016). Benign rabbit caliciviruses exhibit similar evolutionary dynamics to those of their virulent relatives. *J.Virol.* **90**, 9317-9329.
446. Marciniak S, Prowse TL, Herring DA, Klunk J, Kuch M, Duggan AT, Bondioli L, **Holmes EC** & Poinar NH. (2016). *Plasmodium falciparum* malaria in 1st-2nd century CE southern Italy. *Curr.Biol.* **26**, 1220-1223.
445. McColl KA, Sunarto A & **Holmes EC**. (2016). Cyprinid herpesvirus 3 and its evolutionary future as a biological control agent for carp in Australia. *Virol.J.* **13**:206. doi:10.1186/s12985-016-0666-4.

444. Poon LLM, Song T, Rosenfeld R, Lin X, Rogers MB, Zhou B, Sebra R, Halpin RA, Guan Y, Twaddle A, DePasse JV, Stockwell TB, Wentworth DE, **Holmes EC**, Greenbaum B, Peiris JSM, Cowling BJ & Ghedin E. (2016). Quantifying influenza virus diversity and transmission in humans. *Nat. Genet.* **48**, 195-200.
443. Rambaut A, Dudas G, de Carvalho LM, Park DJ, Yozwiak NL, **Holmes EC** & Andersen KG. (2016). Comment on “Mutation rate and genotype variation of Ebola virus from Mali case sequences”. *Science* **353**, 658.
442. Sabir JSM, Lam TT-Y, Ahmed MMA, Li L, Shen Y, Abo-Aba SEM, Qureshi MI, Abu-Zaid M, Zhang Y, Khiyami MA, Alharbi NS, Hajrah NH, Sabir MJ, Mutwakil MHZ, Kabli SA, Alsulaimany FAS, Obaid AY, Zhou B, Smith DK, **Holmes EC**, Zhu H & Guan Y. (2016). Co-circulation of three camel coronavirus species and recombination of MERS-CoV in Saudi Arabia. *Science* **351**, 81-84.
441. Shi M, Lin X-D, Tian J-H, Chen L-J, Chen X, Li C-X, Qin X-C, Li J, Cao J-P, Eden J-S, Buchmann JP, Wang W, Xu J, **Holmes EC** & Zhang Y-Z. (2016). Redefining the invertebrate virosphere. *Nature* **540**, 539-543.
440. Shi M, Lin X-D, Vasilakis N, Tian J-H, Li C-X, Chen L-J, Eastwood J, Diao X-N, Chen M-H, Chen X, Qin X-X, Widen SG, Wood TG, Tesh RB, Xu J, **Holmes EC** & Zhang Y-Z. (2016). Divergent viruses discovered in arthropods and vertebrates revise the evolutionary history of the *Flaviviridae* and related viruses. *J. Virol.* **90**, 659-669.
439. Tan Y, Hassan F, Schuster JE, Simenauer A, Selvarangan R, Halpin RA, Lin X, Fedorova N, Stockwell TB, Lam TT-Y, Chappell JD, Hartert TV, **Holmes EC** & Das SR. (2016). Molecular evolution and intraclade recombination of Enterovirus D68 during the 2014 outbreak in the United States. *J. Virol.* **90**, 1997-2007.
438. Troupin C, Dacheux L, Tanguy M, Sabeta C, Blanc H, Bouchier C, Vignuzzi M, Duchêne S, **Holmes EC** & Bourhy H. (2016). Large-scale phylogenomic analysis reveals the complex evolutionary history of rabies virus in multiple carnivore hosts. *PLoS Pathog.* **12**:e1006041.
437. Urbanowicz RA, McClure CP, Sakuntabhai A, Sall AA, Kobinger G, Müller MA, **Holmes EC**, Rey F, Simon-Loriere E & Ball JK. (2016). Human adaptation of Ebola virus during the West African outbreak. *Cell* **167**, 1079-1087.
436. Valastro V, **Holmes EC**, Fusaro A, Britton P, Jackwood MW, Cattoli G & Monne I. (2016). S1 gene-based phylogeny of Infectious Bronchitis Virus: an attempt to harmonize virus classification. *Infect. Genet. Evol.* **39**, 349-364.
435. Allison AB, Ballard JR, Tesh RB, Brown JD, Ruder MG, Keel MK, Munk BA, Mickley RM, Travassos da Rosa APA, Ellis JC, Ip H, Shem-Bochsler VI, Rodgers MB, Ghedin E, **Holmes EC**, Parrish CR & Dwyer C. (2015). Cyclic avian mass mortality in the northeastern United States is associated with a novel orthomyxovirus. *J. Virol.* **89**, 1389-1403.
434. Allison AB, Stallknecht DE & **Holmes EC**. (2015). Evolutionary genetics and vector adaptation of recombinant viruses of the western equine encephalitis antigenic complex provides new insights into alphavirus diversity and host switching. *Virology* **474**, 154-162.
433. Blasdel KR, Guzman H, Widen SG, Firth C, Wood TG, **Holmes EC**, Tesh RB, Vasilakis N & Walker PJ. (2015). *Ledantavirus*: a proposed new genus in the *Rhabdoviridae* has a strong ecological association with bats. *Am. J. Trop. Med. Hyg.* **92**, 405-410.
432. Buchmann J & **Holmes EC**. (2015). Cell walls and the convergent evolution of the viral envelope. *Microbiol. Mol. Biol. Rev.* **79**, 403-418.
431. Di Giallonardo F & **Holmes EC**. (2015). Virus biocontrol: grand experiments in disease emergence and evolution. *Trends Microbiol.* **23**, 83-90.
430. Di Giallonardo F & **Holmes EC**. (2015). Exploring host-pathogen interactions through biological control. *PLoS Pathog.* **11**:e1004865.
429. Duchêne DA, Duchêne S, **Holmes EC** & Ho SYW. (2015). Evaluating the adequacy of molecular clock models using posterior predictive simulations. *Mol. Biol. Evol.* **32**, 2986-2995.

428. Duchêne S, Duchêne DA, **Holmes EC** & Ho SYW. (2015). The performance of the date-randomisation test in phylogenetic analyses of time-structured virus data. *Mol.Biol.Evol.* **32**, 1895-1906.
427. Duchêne S, Ho SYW & **Holmes EC**. (2015). Declining transition/transversion ratios through time reveal limitations to the accuracy of nucleotide substitution models. *BMC Evol.Biol.* **15**:36.
426. Eden J-S, Kovaliski J, Duckworth JA, Swain G, Maher JE, Strive T & **Holmes EC**. (2015). Comparative phylodynamics of rabbit haemorrhagic disease virus (RHDV) in Australia and New Zealand. *J.Virol.* **89**, 9548-9558.
425. Eden J-S, Read AJ, Duckworth JA, Strive T & **Holmes EC**. (2015). Resolving the origin of rabbit haemorrhagic disease virus: insights from an investigation of the viral stocks released in Australia. *J.Virol.* **89**, 12217-12220.
424. Ernst T, McCarthy S, Chidlow G, Luang-Suarkia D, **Holmes EC**, Smith DW & Imrie A. (2015). Emergence of a new lineage of dengue virus type 2 in travellers entering Western Australia from Indonesia, 2010-2012. *PLoS Negl.Trop.Dis.* **9**:e0003442.
423. Feng KH, Gonzalez G, Deng L, Yu H, Tse VL, Huang L, Huang K, Wasik BR, Zhou B, Wentworth DE, **Holmes EC**, Chen X, Varki A, Murcia PR & Parrish CR. (2015). Equine and canine influenza viruses H3N8 viruses show minimal biological differences despite phylogenetic divergence. *J.Virol.* **89**, 6860-6873.
422. Fourment M & **Holmes EC**. (2015). Avian influenza virus exhibits distinct evolutionary dynamics in poultry and wild birds. *BMC Evol.Biol.* **15**:120.
421. Geoghegan JL, Tan LV, Kuhnert D, Halpin RA, Lin X, Simenauer A, Akopov A, Das SR, Stockwell TB, Ngoc NM, Uyen LTT, Tuyen NTK, Thanh TT, Hang VTT, Qui PT, Hung NT, Khanh TH, Thinh LQ, Nhan LNT, Van HMT, Viet DC, Tuan HM, Viet HL, Chau NVV, Thwaites G, Grenfell BT, Stadler T, Wentworth DE, **Holmes EC** & Van Doorn R. (2015). Phylodynamics of enterovirus 71-associated hand, foot and mouth disease in Viet Nam. *J.Virol.* **89**, 8871-8879.
420. Guo W-P, Lin X-D, Chen Y-P, Liu Q, Wang W, Wang C-Q, Li M-H, Sun X-Y, Shi M, **Holmes EC** & Zhang Y-Z. (2015). Fourteen types of co-circulating recombinant enterovirus were associated with hand, foot, and mouth disease in children from Wenzhou, China. *J.Clin.Virol.* **70**, 29-38.
419. Hall RN, Mahar JE, Haboury S, Stevens V, **Holmes EC** & Strive T. (2015). Emerging Rabbit Hemorrhagic Disease Virus RHDV2 (RHDVb), Australia. *Emerg.Infect.Dis.* **21**, 2276-2278.
418. **Holmes EC** & Zhang Y-Z. (2015). The evolution and emergence of hantaviruses. *Curr.Opin.Virol.* **10**, 27-33.
417. Katzelnick LC, Fonville JM, Gromowski G, Arriaga JB, Green A, James SL, Lau L, Montoya M, Wang C, VanBlargan LA, Russell CA, Thu HM, Pierson TC, Buchy P, Aaskov JG, Muñoz-Jordán JL, Vasilakis N, Gibbons RV, Tesh RB, Osterhaus ADME, Fouchier RAM, Durbin A, Simmons CP, **Holmes EC**, Harris E, Whitehead SS & Smith DJ. (2015). Dengue viruses cluster antigenically but not as discrete serotypes. *Science* **349**, 1338-1343.
416. Kerr PJ, Liu J, Cattadori I, Ghedin E, Read AF & **Holmes EC**. (2015). Myxoma virus and the leporipoxviruses: an evolutionary paradigm. *Viruses* **7**, 1029-1061.
415. Lam TT-Y, Zhou B, Wang J, Chai Y, Shen Y, Chen X, Ma C, Hong W, Duan L, Chen P, Jiang J, Zhang Y, Li L, Smith DK, Leung GM, Peiris JSM, **Holmes EC**, Guan Y & Zhu H. (2015). Dissemination, divergence and establishment of H7N9 influenza viruses in China. *Nature* **522**, 102-105.
414. Lam TT-Y, Zhu H, Chong LY, **Holmes EC** & Guan Y. (2015). Puzzling origins of the Ebola outbreak in the Democratic Republic of Congo, 2014. *J.Virol.* **89**, 10130-10132.
413. Lambrechts L, Ferguson NM, Harris E, **Holmes EC**, McGraw EA, O'Neill SL, Ooi EE, Ritchie SA, Ryan PA, Scott TW, Simmons CP & Weaver SC. (2015). Assessing the epidemiological effect of wolbachia for dengue control. *Lancet Infect.Dis.* **15**, 862-866.

412. Li C-X, Shi M, Tian J-H, Lin X-D, Kang Y-J, Qin X-C, Chen L-J, Xu J, **Holmes EC** & Zhang Y-Z. (2015). Unprecedented RNA virus diversity in arthropods reveals the ancestry of negative-sense RNA viruses. *eLife* **4**:e05378.
411. Li K, Lin X-D, Wang W, Shi M, Guo W-P, Zhang X-H, Xing J-G, He J-R, Wang K, Li M-H, Cao J-H, Jiang M-L, **Holmes EC** & Zhang Y-Z. (2015). Isolation and characterization of a novel arenavirus harbored by rodents and shrews in Zhejiang, China. *Virology* **476**, 37-42.
410. Lopes AM, Dalton K, Magalhães MJ, Parra F, Esteves PJ, **Holmes EC** & Abrantes J. (2015). Full genomic analysis of new variant Rabbit Hemorrhagic Disease Virus (RHDVb) revealed multiple recombination events. *J.Gen. Virol.* **96**, 1309-1319.
409. Nelson MI, Viboud C, Vincent AL, Culhane MR, Detmer SE, Wentworth DE, Rambaut A, Suchard MA, **Holmes EC** & Lemey P. (2015). Global migration of influenza A viruses in swine. *Nat. Commun.* **6**:6696 doi:10.1038/ncomms7696.
408. Park DJ, Dudas G, Wohl S, Goba A, Whitmer SLM, Andersen KG, Sealfon RS, Ladner JT, Kugelman JR, Matranga CB, Winnicki SM, Qu J, Gire SK, Gladden-Young A, Jalloh S, Nosamiefan D, Yowziak NL, Moses L, Jiang P-P, Lin AE, Schaffner SF, Bird B, Towner J, Mamoh M, Gbakie M, Kanneh L, Kargbo D, Massally JLB, Kamara FK, Konuwa E, Sellu J, Jalloh AA, Mustapha I, Foday M, Yillah M, Erickson BR, Sealy T, Blau D, Paddock C, Brault A, Amman B, Basile J, Bearden S, Belser J, Bergeron E, Campbell S, Chakrabarti A, Dodd K, Flint M, Gibbons A, Goodman C, Klena J, McMullan L, Morgan L, Russell B, Salzer J, Sanchez A, Wang D, Jungreis I, Tomkins-Tinch C, Kislyuk A, Lin MF, Chapman S, MacInnis B, Matthews A, Bochicchio J, Hensley LE, Kuhn JH, Nusbaum C, Scheiffelin JS, Birren BW, Forget M, Nichol ST, Palacios GF, Ndiaye D, Happi C, Gevao SM, Vandt MA, Kargbo B, **Holmes EC**, Bedford T, Gnirke A, Ströher U, Rambaut A, Garry RF & Sabeti PC. (2015). Ebola virus epidemiology, transmission, and evolution during seven months in Sierra Leone. *Cell* **161**, 1516–1526.
407. Parrish CR, Murcia PR & **Holmes EC**. (2015). Influenza A virus reservoirs: dogs, horses, and new possibilities for human infections. *J. Virol.* **89**, 2990-2994.
406. Patterson Ross Z, Komadina N, Mo DY, Spirason N, Kelly H, Sullivan SG, Barr IG & **Holmes EC**. (2015). Inter-seasonal influenza is characterized by extended virus transmission and persistence. *PLoS Pathog.* **11**:e1004991.
405. Pollett S, Nelson MI, Kasper M, Tinoco Y, Simons M, Romero C, Silva M, Wentworth D, **Holmes EC** & Bausch DG. (2015). Phylogeography of H3N2 influenza virus in Peru: absence of persistence and 'source-sink' dynamics in a tropical region. *Emerg.Infect.Dis.* **21**, 1330-1338.
404. Rogers MB, Song T, Sebra R, Greenbaum BD, Hamelin M-E, Fitch A, Twaddle A, Cui L, **Holmes EC**, Boivin G & Ghedin E. (2015). Intra-host dynamics of antiviral resistance in influenza A virus reflect complex patterns of segment linkage, reassortment and natural selection. *mBio* **6**, e02464-14.
403. Simmons HE, Prendeville HR, Dunham JP, Ferrari MJ, Earnest JD, Pilson D, Munkvold GP, **Holmes EC** & Stephenson AG. (2015). Transgenic virus resistance in crop-wild *Cucurbita pepo* does not prevent vertical transmission of *Zucchini yellow mosaic virus*. *Plant Dis.* **99**, 1616-1621.
402. Simon-Loriere E, Faye O, Faye O, Koivogui L, Magassouba N, Keita S, Thiberge J-M, Diancourt L, Bouchier C, Vandebogaert M, Caro V, Fall G, Buchmann JP, Matranga CB, Sabeti PC, Manuguerra J-C, **Holmes EC** & Sall AA. (2015). Distinct lineages of Ebola virus in Guinea during the 2014 West African epidemic. *Nature* **524**, 102-105. [Joint corresponding author].
401. Sintchenko V & **Holmes EC**. (2015). The role of pathogen genomics in assessing disease transmission. *BMJ.* **350**, h1314.
400. Tan LV, Tuyen NTK, Thanh TT, Ngan TT, Van HMT, Sabanathan S, Van TTM, Thanh LTM, Nguyet LA, Geoghegan JL, Chai OK, Hang VTT, Ny NTH, Anh NT, Ha DQ, Qui PT, Viet DC, Tuan HM, Wong TK, **Holmes EC**, Chau NVV, Thwaites G & van Doorn HR. (2015). A generic

- assay for whole-genome amplification and deep sequencing of Enterovirus 71. *J.Virol.Meth.* **215-216**, 30-36.
399. Thomas JM, Allison AB, **Holmes EC**, Phillips JE, Bunting EM, Yabsley MJ & Brown JD. (2015). Molecular surveillance for Lymphoproliferative Disease Virus in wild turkeys (*Meleagris gallopavo*) from the eastern United States. *PLoS One* **10**:e0122644.
398. Vijaykrishna D, **Holmes EC**, Joseph U, Fourment M, Su YCF, Halpin R, RTC Lee, Deng Y-M, Gunalan V, Lin X, Stockwell TB, Federova NB, Zhou B, Spirason N, Kühnert D, Bošková V, Stadler T, Costa A-M, Dwyer DE, Huang QS, Jennings LC, Rawlinson W, Sullivan SG, Hurt A, Maurer-Stroh S, Wentworth DE, Smith GJD & Barr IG. (2015). The contrasting phylodynamics of human influenza B viruses. *eLife* **4**:e05055.
397. Walker PJ, Firth C, Widen SG, Blasdel KR, Guzman H, Wood TG, Paradkar PN, **Holmes EC**, Tesh RB & Vasilakis N. (2015). Evolution of genome size and complexity in the *Rhabdoviridae*. *PLoS Pathog.* **11**:e1004664.
396. Wang M, Barasheed O, Rashid H, Booy R, El Bashir H, Haworth E, Ridda I, **Holmes EC**, Dwyer DE, Nguyen-Van-Tam J, Memish ZA & Heron L. (2015). A cluster-randomised controlled trial to test the effectiveness of facemasks in preventing respiratory virus infection among Hajj pilgrims. *J.Epidemiol.Global Health* **5**, 181-189.
395. Wang W, Lin X-D, Guo W-P, Zhou R-H, Wang M-R, Wang C-Q, Ge S, Mei S-H, Li M-H, Shi M, **Holmes EC** & Zhang Y-Z. (2015). Discovery, diversity and evolution of novel coronaviruses sampled from rodents in China. *Virology* **474**, 19-27.
394. Wang W, Yu B, Lin X-D, Kong D-G, Wang J, Tang W-F, Tian J-H, Li M-H, **Holmes EC** & Zhang Z-Y. (2015). Reemergence and autochthonous transmission of dengue virus, eastern China, 2014. *Emerg.Infect.Dis.* **21**, 1670-1673.
393. Allison AB, Keel MK, Philips JE, Cartoceti AN, Munk BA, Nemeth NM, Welsh TI, Thomas JM, Crum JM, Lichtenwalner AB, Bunting EM, Fadly AM, Zavala G, **Holmes EC** & Brown JD. (2014). Avian oncogenesis induced by lymphoproliferative disease virus: a neglected or emerging retroviral pathogen? *Virology* **450-451**, 2-12.
392. Allison AB, Kohler DJ, Ortega A, Hoover EA, Grove DM, **Holmes EC** & Parrish CR. (2014). Host-specific parvovirus evolution in nature is recapitulated by *in vitro* adaptation to different carnivore species. *PLoS Pathog.* **10**:e1004475.
391. Allison AB, Mead DG, Palacios GF, Tesh RB & **Holmes EC**. (2014). Gene duplication and phylogeography of the North American members of the Hart Park serogroup of avian rhabdoviruses. *Virology* **448**, 284-292.
390. Barasheed O, Rashid H, Alfelali M, Tashani M, Azeem M, Bokhary M, Kalantan N, Samkari J, Heron L, Kok J, Taylor J, El Bashir H, Memish ZA, Haworth E, **Holmes EC**, Dwyer DE, Asghar A, Booy R & Hajj Research Team. (2014). Viral respiratory infections among Hajj pilgrims in 2013. *Virologica Sinica* **29**, 364-371.
389. Blasdel KR, Widen SG, Diviney SM, Firth C, Wood TG, **Holmes EC**, Tesh RB, Vasilakis N & Walker PJ. (2014). Koolpinyah and Yata viruses: two newly recognised ephemeroviruses from tropical regions of Australia and Africa. *Vet.Microbiol.* **174**, 547-553.
388. Chen Z-H, Qin X-C, Song R, Shen Y, Chen X-P, Wang W, Zhao Y-X, Zhang J-S, He J-R, Li M-H, Zhao X-H, Liu D-W, Fu X-K, Tian D, Li X-W, Xu J, Plyusnin A, **Holmes EC** & Zhang Y-Z. (2014). Co-circulation of multiple hemorrhagic fever diseases with distinct clinical characteristics in Dandong, China. *PLoS One* **9**:e89896.
387. Cui J, Schlub T & **Holmes EC**. (2014). An allometric relationship between the genome length and virion volume of viruses. *J.Virol.* **88**, 6403-6410.
386. Cui J, Zhao W, Huang Z, Jarvis ED, Gilbert MTP, Walker PJ, **Holmes EC** & Zhang G. (2014). Low frequency of paleoviral infiltration across the avian phylogeny. *Genome Biol.* **15**, 539.
385. Dalziel BD, Huang K, Geoghegan JL, Arinaminpathy N, Dubovi EJ, Grenfell BT, Ellner SP, **Holmes EC** & Parrish CR. (2014). Contact heterogeneity, rather than low transmission efficiency, limits the emergence and spread of canine influenza virus. *PLoS Pathog.* **10**: e1004455.

384. Devault AM, Golding GB, Waglechner N, Enk JM, Kuch M, Tien JH, Shi M, Fisman DN, Dhody AN, Forrest S, Bos KI, Earn DJD, **Holmes EC** & Poinar HN. (2014). Second-pandemic strain of *Vibrio cholerae* from the Philadelphia cholera outbreak of 1849. *New Eng.J.Med.* **370**, 334-340.
383. Duchêne S, **Holmes EC** & Ho SYW. (2014). Analyses of evolutionary dynamics in viruses are hindered by a time-dependent bias in rate estimates. *Proc.Roy.Soc.Lond.B.* **281**:20140732. doi: 10.1098/rspb.2014.0732.
382. Dunham JP, Simmons HE, **Holmes EC** & Stephenson AG. (2014). Analysis of viral (zucchini yellow mosaic virus) genetic diversity during systemic movement through a *Cucurbita pepo* vine. *Virus Res.* **191**, 172-179.
381. Eden J-S, Hewitt J, Lim KL, Boni MF, Merif J, Greening G, Ratcliff RM, **Holmes EC**, Tanaka MM, Rawlinson WD & White PA. (2014). The emergence and evolution of the novel epidemic norovirus GII.4 variant Sydney 2012. *Virology* **450-451**, 106-113.
380. Elsworth P, Cooke BD, Kovaliski J, Sinclair R, **Holmes EC** & Strive T. (2014). Increased virulence of Rabbit Haemorrhagic Disease Virus associated with genetic resistance in wild Australian rabbits (*Oryctolagus cuniculus*). *Virology* **464-465**, 415-423.
379. Fourment M & **Holmes EC**. (2014). Novel non-parametric models to estimate evolutionary rates and divergence times from heterochronous sequence data. *BMC Evol.Biol.* **14**:163.
378. Geoghegan JL, Walker PJ, Duchemin J-B, Jeanne I & **Holmes EC**. (2014). Seasonal drivers of the epidemiology of arthropod-borne viruses in Australia. *PLoS Negl.Trop.Dis.* **8**:e3325.
377. Kang Y-J, Diao X-N, Zhao G-Y, Chen M-H, Xiong Y, Shi M, Fu W-M, Guo Y-J, Pan B, **Holmes EC**, Gillespie JJ, Dumler SJ & Zhang Y-Z. (2014). Extensive diversity of Rickettsiales bacteria in two species of ticks from China and the evolution of the Rickettsiales. *BMC Evol.Biol.* **14**:167.
376. Kovaliski J, Sinclair R, Mutze G, Peacock D, Strive T, Abrantes J, Esteves PJ & **Holmes EC**. (2014). Molecular epidemiology of Rabbit Haemorrhagic Disease Virus (RHDV) in Australia; when one became many. *Mol.Ecol.* **23**, 408-420.
375. Lin X-D, Zhou R-H, Fan F-N, Ying X-H, Sun X-Y, Wang W, **Holmes EC** & Zhang Y-Z. (2014). Biodiversity and evolution of Imjin virus and Thottapalayam virus in *Crocidurinae* shrews in Zhejiang Province, China. *Virus Res.* **189**, 114-120.
374. Lopes AM, Capucci L, Gavier-Widén D, Le Gall-Reculé G, Brocchi E, Barbieri I, Quéméner A, Pendu JL, Geoghegan JL, **Holmes EC**, Esteves PJ & Abrantes J. (2014). Molecular evolution and antigenic variation of European brown hare syndrome virus (EBHSV). *Virology* **468-470**, 104-112.
373. Monne I, Fusaro A, Nelson MI, Bonfanti L, Mulatti P, Hughes J, Murcia PR, Schivo A, Valastro V, Moreno A, **Holmes EC** & Cattoli G. (2014). Emergence of a highly pathogenic avian influenza virus from a low pathogenic progenitor. *J.Virol.* **88**, 4375-4388.
372. Nelson MI, Njouom R, Viboud C, Niang MND, Kadjo H, Ampofo W, Adebayo A, Tarnagda Z, Miller MA, **Holmes EC** & Diop OM. (2014). Multi-year persistence of two pandemic A/H1N1 influenza virus lineages in West Africa. *J.Infect.Dis.* **210**, 121-125.
371. Nelson MI, Wentworth DE, Culhane MR, Vincent AL, Viboud C, LaPoint MP, Lin X, **Holmes EC** & Detmer SE. (2014). Introductions and evolution of human-origin seasonal influenza A viruses in multinational swine populations. *J.Virol.* **88**, 10110-10119.
370. Qin X-C, Shi M, Tian J-H, Lin X-D, Gao D-Y, He J-R, Wang J-B, Li C-X, Kang Y-J, Yu B, Zhou D-J, Xu J, Plyusnin A, **Holmes EC** & Zhang Y-Z. (2014). A tick-borne segmented RNA virus contains genome segments derived from unsegmented viral ancestors. *Proc.Natl.Acad.Sci.USA* **111**, 6744-6749.
369. Trinidad L, Blasdel KR, Joubert DA, Davis SS, Melville L, Kirkland PD, Coulibaly F, **Holmes EC** & Walker PJ. (2014). Evolution of bovine ephemeral fever virus in the Australian episystem. *J.Virol.* **88**, 1525-1525.
368. Vasilakis N, Castro F, Widen S, Aguilar PA, Guzman H, Guevara C, Wood TG, Popov V, Ghedin E, Halsey ES, **Holmes EC**, Walker PJ & Tesh RB. (2014). Arboretum and Puerto

- Almendras viruses: two novel rhabdoviruses isolated from mosquitoes in Peru. *J.Gen.Virol.* **95**, 787-792.
367. Wagner DM, Keim PS, Scholz HC, **Holmes EC** & Poinar H. (2014). *Yersinia pestis* and the three plague pandemics: Authors' reply. *Lancet Infect. Dis.* **14**, 919.
366. Wagner DM, Klunk J, Harbeck M, Devault A, Waglechner N, Sahl JW, Enk J, Birdsell DN, Kuch M, Lumibao C, Poinar D, Pearson T, Fourment M, Golding B, Earn DJD, DeWitte S, Rouillard J-M, Grupe G, Wiechmann I, Bliska JB, Keim PS, Scholz HC, **Holmes EC** & Poinar H. (2014). *Yersinia pestis* and the Plague of Justinian 541-543 AD: a genomic analysis. *Lancet Infect.Dis.* **14**, 319-326.
365. Wang C-Q, Gao J-H, Li M, Guo W-P, Lu M-Q, Wang W, Hu M-X, Li M-H, Yang J, Hui JL, **Holmes EC** & Zhang Y-Z. (2014). Co-Circulation and Evolution of Hantaan, Kenkeme, and Khabarovsk Hantaviruses in Bolshoy Ussuriysky Island, Heilongjiang Province, China. *Virus Res.* **191**, 51-58.
364. Zhang G, Li C, Li Q, Li B, Larkin DM, Lee C, Storz JF, Antunes A, Greenwold MJ, Meredith RW, Ödeen A, Cui J, Zhou Q, Xu L, Pan H, Wang Z, Jin L, Zhang P, Hu H, Yang W, Hu J, Xiao J, Yang Z, Liu Y, Xie Q, Yu H, Lian J, Wen P, Zhang F, Li H, Zeng Y, Xiong Z, Liu S, Zhou L, Huang Z, An N, Wang J, Zheng Q, Xiong Y, Wang G, Wang B, Wang J, Fan Y, da Fonseca RR, Alfaro-Núñez A, Campos P, Schubert M, Orlando L, Mourier T, Howard J, Ganapathy G, Pfenning A, Whitney O, Rivas MV, Hara E, Smith J, Farré M, Narayan J, Slavov G, Romanov MN, Borges R, Machado JP, Khan I, Springer MS, Gatesy J, Hoffmann FG, Opazo JC, Håstad O, Sawyer RH, Kim H, Kim K-W, Kim HJ, Cho S, Li N, Huang Y, Bruford MW, Zhan X, Dixon A, Bertelsen MF, Derryberry E, Warren W, Li S, Ray DA, Green RE, O'Brien SJ, Griffin D, Johnson WE, Haussler D, Ryder OA, Willerslev E, Graves GR, Alström P, Fjeldså J, Mindell D, Edwards SV, Braun EL, Rahbek C, Burt DW, Houde P, Zhang Y, Yang H, Wang J, **Avian Genome Consortium***, Jarvis ED, M Gilbert MTP & Wang J. (2014). Comparative genomics reveal insights into avian genome evolution and adaptation. *Science* **346**, 1311-1320. [*Consortium member]
363. Zhang Y-Z & **Holmes EC**. (2014). What is the time-scale of hantavirus evolution? *Infect.Genet.Evol.* **25**, 144-145.
362. Allison AB, Kohler DJ, Fox KA, Brown JD, Gerhold RW, Shearn-Bochsler VI, Dubovi EJ, Parrish CR & **Holmes EC**. (2013). Frequent cross-species transmission of parvoviruses among diverse carnivore hosts. *J.Virol.* **87**, 2342-2347.
361. Bhatt S, Lam TT, Lycett SJ, Leigh Brown AJ, Bowden TA, **Holmes EC**, Guan Y, Wood JLN, Brown IH, Kellam P, Combating Swine Influenza Consortium & Pybus OG. (2013). The evolutionary dynamics of influenza A virus adaptation to mammalian hosts. *Phil.Trans.Roy.Soc.Lond.B.* **368** 20120382; doi:10.1098/rstb.2012.0382.
360. Cheng X, Tan Y, He M, Lam TT-Y, Lu X, Viboud C, He J, Zhang S, Lu J, Wu C, Fang S, Wang X, Xie X, Ma H, Nelson MI, Kung H-F, **Holmes EC** & Cheng J. (2013). Epidemiological dynamics and phylogeography of influenza virus in southern China. *J.Infect.Dis.* **207**, 106-114.
359. Cui J, Eden J-S, **Holmes EC** & Wang L-F. (2013). Adaptive evolution of bat dipeptidyl peptidase 4 (DDP4): Implications for the origin and emergence of Middle East Respiratory Syndrome Coronavirus. *Viol.J.* **10**:304.
358. Fusaro A, Monne I, Salomoni A, Angot A, Trolese M, Ferrè N, Mutinelli F, **Holmes EC**, Capua I, Lemey P, Cattoli G & De Benedictis P. (2013). The introduction of fox rabies into Italy (2008-2011) was due to two viral genetic groups with distinct phylogeographic patterns. *Infect.Genet.Evol.* **17**, 202-209.
357. Ghedin E, Rogers MB, Widen SG, Guzman H, Travassos da Rosa APA, Wood TG, Fitch A, Popov V, **Holmes EC**, Walker PJ, Vasilakis N & Tesh RB. (2013). Kolenté virus, a rhabdovirus species isolated from ticks and bats in the Republic of Guinea. *J.Gen.Virol.* **94**, 2609-2615.
356. Guo W-P, Lin X-D, Wang W, Tian J-H, Cong M-L, Zhang H-L, Wang M-R, Wang J-B, Zhou R-H, Wang J-B, Li M-H, Xu J, **Holmes EC** & Zhang Y-Z. (2013). Phylogeny and origins of hantaviruses harbored by bats, insectivores, and rodents. *PLoS Pathog.* **9**:e1003159.

355. Hayward JA, Tachedjian M, Cui J, Field H, **Holmes EC**, Wang L-F & Tachedjian G. (2013). Identification of diverse full-length endogenous betaretroviruses in megabats and microbats. *Retrovirology* **10**:35.
354. **Holmes EC**. (2013). What can we predict about viral evolution and emergence? *Curr.Opin.Virol.* **3**, 180-184.
353. Ke R, Aaskov J, **Holmes EC** & Lloyd-Smith JO. (2013). Phylodynamic analysis of the emergence and epidemiological impact of transmissible defective dengue viruses. *PLoS Pathog.* **9**:e1003193.
352. Kerr PJ, Rogers MB, Fitch A, DePasse JV, Cattadori IM, Hudson PJ, Tscharke DC, **Holmes EC** & Ghedin E. (2013). Comparative analysis of the complete genome sequence of the Californian MSW strain of myxoma virus reveals potential host adaptations. *J.Virol.* **87**, 12080-12089.
351. Kerr PJ, Rogers M, Fitch A, DePasse JV, Cattadori IM, Twaddle AC, Hudson PJ, Tscharke DC, Read AF, **Holmes EC** & Ghedin E. (2013). Genome scale evolution of myxoma virus (MYXV) reveals host-pathogen adaptation and rapid geographic spread. *J.Virol.* **87**, 12900-12915.
350. Lam TT-Y, Chong YL, Shi M, Hon C-C, Li J, Martin DP, Tang JW-T, Mok C-K, Shih S-R, Yip C-W, Jiang J, Hui RK-H, Pybus OG, **Holmes EC** & Leung FC-C. (2013). Systematic phylogenetic analysis of influenza A viruses reveals many novel mosaic genome segments. *Infect.Genet.Evol.* **18**, 367-378.
349. Levitt AL, Singh R, Cox-Foster DL, Rajotte E, Ostiguy N, Hoover K & **Holmes EC**. (2013). Cross-species transmission of honey bee viruses in associated arthropods. *Virus Res.* **176**, 232-240.
348. Murcia PR, Baillie GJ, Stack JC, Jervis C, Elton E, Mumford JA, Daly J, Kellam P, Grenfell BT, **Holmes EC** & Wood JLN. (2013). Evolution of equine influenza virus in vaccinated horses. *J.Virol.* **87**, 4768-4771.
347. Nougairède A, de Fabritus L, Aubry F, Gould EA, **Holmes EC** & de Lamballerie X. (2013). Random codon re-encoding induces stable reduction of replicative fitness of Chikungunya virus in primate and mosquito cells. *PLoS Pathog.* **9**:e1003172.
346. Nguyen NM, Kien DTH, Trung VT, Quyen NTH, Chau NTB, Long VT, Dui LT, Nguyen HL, Farrar J, **Holmes EC**, Rabaa MA, Wills B, Truong NT, Huong NTC, Lan NTH, Mai PP, Hung NT, Tai LTH, Chau NVV, Wolbers M & Simmons CP. (2013). Host and viral features of human dengue virus infection shape the population of infected and infectious *Aedes aegypti* mosquitoes. *Proc.Natl.Acad.Sci.USA.* **110**, 9072-9077.
345. Quan P-L, Firth C, Conte J, Williams S, Zambranan C, Anthony A, Ellison J, Gilbert A, Kuzmin I, Niezgodna M, Osinubi MOV, Recuenco S, Markotter W, Breiman R, Kalemba L, Malekani J, Lindblade KA, Rostal M, Ojeda-Flores R, Medellin R, Davis LB, Blau DM, Ogunkoya AB, Castillo DAA, Moran D, Ngam S, Akaibe D, Agwanda B, Briese T, Epstein J, Daszak P, Rupprecht CE, **Holmes EC** & Lipkin WI. (2013). Bats are a major natural reservoir for hepaciviruses and pegiviruses. *Proc.Natl.Acad.Sci.USA* **110**, 8194-8199.
344. Pepperell CS, Casto AM, Kitchen A, Granka JM, Cornejo OE, **Holmes EC**, Birren B, Galagan J & Feldman MW. (2013). The role of selection in shaping diversity of natural *M.tuberculosis* populations. *PLoS Pathog.* **9**:e1003543.
343. Rabaa MA, Klunghong C, Yoon I-K, **Holmes EC**, Chinnawirotpisan P, Thaisomboonsuk B, Srikiatkachorn A, Rothman AL, Tannitisupawong D, Aldstadt J, Nisalak A, Mammen MP Jr., Thammapalo S, Gibbons RV, Endy TP, Fansiri T, Scott TW & Jarman RG. (2013). Frequent in-migration and highly focal transmission of dengue viruses among children in Kamphaeng Phet, Thailand. *PLoS Negl.Trop.Dis.* **7**:e1990.
342. Rabaa MA, Simmons CP, Fox A, Le MQ, Nguyen TTT, Le HY, Gibbons RV, Nguyen TX, **Holmes EC** & Aaskov JG. (2013). Dengue virus in sub-tropical northern and central Viet Nam: population immunity and climate shape patterns of viral invasion and maintenance. *PLoS Negl.Trop.Dis.* **7**:e2581.

341. Saira K, Lin X, DePasse JV, Halpin R, Twaddle A, Stockwell T, Angus B, Cozzi-Lepri A, Delfino M, Dugan V, Dwyer D, Freiberg M, Horban A, Losso M, Lynfield R, Wentworth DN, **Holmes EC**, Davey R, Wentworth DE & Ghedin E. (2013). Sequence analysis of *in vivo* defective-interfering (DI)-like RNA of influenza A H1N1 pandemic virus. *J. Virol.* **87**, 8064-8074.
340. Shi M, **Holmes EC**, Brar MS & Leung FC-C. (2013). Recombination is associated with an outbreak of novel Highly Pathogenic Porcine Productive and Respiratory Syndrome viruses in China. *J. Virol.* **87**, 10904-10907.
339. Shi M, Lemey P, Brar MS, Suchard MA, Murtaugh MP, Carman S, D'Allaire S, Delisle B, Lambert M-E, Gagnon CA, Ge L, Qu Y, Yoo D, **Holmes EC** & Leung FC-C. (2013). The spread of type 2 porcine reproductive and respiratory syndrome virus (PRRSV) in North America: a phylogeographic approach. *Virology* **447**, 146-154.
338. Simon-Loriere E & **Holmes EC**. (2013). Gene duplication is infrequent in the recent evolutionary history of RNA viruses. *Mol. Biol. Evol.* **30**, 1263-1269.
337. Simon-Loriere E, **Holmes EC** & Pagán I. (2013). The effect of gene overlapping on the rate of RNA virus evolution. *Mol. Biol. Evol.* **30**, 1916-1928.
336. Simons HE, Dunham JP, Zinn KE, Munkvold GP, **Holmes EC** & Stephenson AG. (2013). *Zucchini yellow mosaic virus* (ZYMV, *Potyvirus*): Vertical transmission, seed infection and cryptic infections. *Virus Res.* **176**, 259-264.
335. Stack JR, Murcia PR, Grenfell BT, Wood JLN & **Holmes EC**. (2013). Inferring the inter-host transmission of influenza A virus using patterns of intra-host genetic evolution. *Proc. Roy. Soc. Lond. B.* **280** 20122173; doi:10.1098/rspb.2012.2173.
334. Tan Y, Guan W, Lam TT-Y, Pan S, Wu S, Zhan Y, Viboud C, **Holmes EC** & Yang Z. (2013). Differing epidemiological dynamics of influenza B lineages in Guangzhou, southern China, 2009-2010. *J. Virol.* **87**, 12447-12456.
333. Tao Y, Shi M, Conrardy C, Kuzmin IV, Recuenco S, Agwanda B, Alvarez DA, Ellison JA, Gilbert AT, Moran D, Niezgodna M, Lindblade KA, **Holmes EC**, Breiman RF, Rupprecht CE & Tong S. (2013). Discovery of diverse polyomaviruses in bats and the evolutionary history of the *Polyomaviridae*. *J. Gen. Virol.* **94**, 738-748.
332. Tong S, Zhu X, Li Y, Shi M, Bourgeois M, Zhang J, Recuenco S, Gomez J, Yang H, Chen L-M, Tao Y, Chen X, Dreyfus C, Yu W, McBride R, Carney PJ, Gilbert AT, Chang J, Guo Z, Davis CT, Cox N, Paulson JC, Stevens J, Rupprecht C & **Holmes EC**, Wilson IA, Donis RO. (2013). New World bats harbor diverse influenza A viruses. *PLoS Pathog.* **9**:e1003657.
331. Vasilakis N, Widen S, Mayer SV, Seymour R, Wood TG, Popov V, Guzman H, Travassos da Rosa AAPA, Ghedin E, **Holmes EC**, Walker PJ & Tesh RB. (2013). Niakha virus: A novel member of the family *Rhabdoviridae* isolated from phlebotomine sandflies in Senegal. *Virology* **377**, 80-89.
330. Vasilakis N, Widen S, Travassos da Rosa AAPA, Wood TG, Walker PJ, **Holmes EC** & Tesh RB. (2013). *Malpais Spring virus* is a new species in the genus *Vesiculovirus*. *Viol. J.* **10**:69.
329. Viboud C, Nelson MI, Tan Y & **Holmes EC**. (2013). Contrasting the epidemiological and evolutionary dynamics of influenza spatial transmission. *Phil. Trans. Roy. Soc. Lond. B.* **368** 20120199; doi:10.1098/rstb.2012.0199.
328. Wang L, Yin Q, He G, Rossiter SJ, **Holmes EC** & Cui J. (2013). Ancient invasion of an extinct gammaretrovirus in cetaceans. *Virology* **441**, 66-69.
327. Wang W, Wang M-R, Lin X-D, Guo W-P, Li M-H, Mei S-H, Li Z-M, Cong M-L, Jiang R-L, Zhou R-H, **Holmes EC**, Plyusnin A & Zhang Y-Z. (2013). Ongoing spillover of Hantaan and Gou hantaviruses from rodents is associated with Hemorrhagic Fever with Renal Syndrome (HFRS) in China. *PLoS Negl. Trop. Dis.* **7**:e2484.
326. Allison AB, Harbison CE, Pagán I, Stucker KM, Kaelber JT, Brown JD, Ruder MG, Keel MK, Dubovi EJ, **Holmes EC** & Parrish CR. (2012). Role of multiple hosts in the cross-species transmission and emergence of a pandemic parvovirus. *J. Virol.* **86**, 865-872.
325. Allison AB, **Holmes EC**, Potgieter C, Wright IM, Sailleau C, Breard, E Ruder MG & Stallknecht DE. (2012). Segmental configuration and putative origin of the reassortant

- orbivirus, epizootic hemorrhagic disease virus serotype 6, strain Indiana. *Virology* **424**, 67-75.
324. Bhardwaj G, Ko KD, Hong Y, Zhang Z, Ho NL, Kline LA, Gotlin M, Hartranft DN, Patterson ME, Dave F, Smith EJ, **Holmes EC**, Patterson RL & van Rossum DB. (2012). PHYRN: A novel method for the phylogenetic analysis of highly divergent sequences. *PLoS One* **7**, e34261.
323. Boni MF, Smith GJD, **Holmes EC** & Vijaykrishna D. (2012). No evidence for intra-segment recombination of 2009 H1N1 influenza virus in swine. *Gene* **494**, 242-245.
322. Cook S, Moureau G, Kitchen A, Gould EA, de Lamballerie X, **Holmes EC** & Harbach RE. (2012). Molecular evolution of the insect-specific flaviviruses. *J.Gen.Virol.* **93**, 223-234.
321. Cui J & **Holmes EC**. (2012). Endogenous retroviruses in the ferret genome. *J.Virol.* **86**, 3383-3385.
320. Cui J & **Holmes EC**. (2012). Endogenous RNA viruses of plants in insect genomes. *Virology* **427**, 77-79.
319. Cui J & **Holmes EC**. (2012). Evidence for an endogenous papillomavirus-like element in the platypus genome. *J.Gen.Virol.* **93**,1362-1366.
318. Cui J & **Holmes EC**. (2012). Endogenous hepadnaviruses in the genome of the budgerigar (*Melopsittacus undulatus*) and the evolution of avian hepadnaviruses. *J.Virol.* **86**, 7688-7691.
317. Cui J, Tachedjian G, Tachedjian M, **Holmes EC**, Zhang S & Wang L-F. (2012). Identification of diverse groups of endogenous gammaretroviruses in mega and microbats. *J.Gen.Virol.* **93**, 2037-2045.
316. Ghedin E, **Holmes EC**, DePasse JV, Pinilla LT, Fitch A, Hamelin M-E, Papenburg J & Boivin G. (2012). Presence of oseltamivir-resistant pandemic A/H1N1 minor variants before drug therapy with subsequent selection and transmission. *J.Infect.Dis.* **206**, 1504-1511.
315. Holt KE, Baker S, Weill F-X, **Holmes EC**, Kitchen A, Yu J, Sangal V, Brown DJ, Coia JE, Kim DW, Choi SY, Kim SH, da Silveira WD, Pickard DJ, Farrar JJ, Parkhill J, Dougan G & Thomson NR. (2012). *Shigella sonnei* genome sequencing and phylogenetic analysis indicate recent global dissemination from Europe. *Nat.Genet.* **44**, 1056-1059.
314. Hughes J, Allen RC, Baguelin M, Hampson K, Baillie GJ, Elton D, Newton JR, Kellam P, Wood JLN, **Holmes EC** & Murcia PR. (2012). Transmission of equine influenza virus during an outbreak is characterized by frequent mixed infections and loose transmission bottlenecks. *PLoS Pathog.* **8**:e1003081.
313. Kerr PJ, Ghedin E, DePasse JV, Fitch A, Cattadori IM, Hudson PJ, Tschärke DC, Read AF & **Holmes EC**. (2012). Evolutionary history and attenuation of myxoma virus on two continents. *PLoS Pathog.* **8**:e1002950.
312. Lam TT-Y, Hon C-C, Lemey P, Pybus OG, Shi M, Tun HM, Li J, Jiang J, **Holmes EC** & Leung FC-C. (2012). Phylodynamics of H5N1 highly pathogenic avian influenza virus in Indonesia. *Mol.Ecol.* **21**, 3062-3077.
311. Lam TT-Y, Ip HS, Ghedin E, Wentworth DE, Halpin RA, Stockwell TB, Spiro DJ, Dusek RJ, Bortner JB, Bales BD, Yparraguirre DR & **Holmes EC**. (2012). Migratory flyway and geographical distance are barriers to the gene flow of influenza virus among North American birds. *Ecol.Lett.* **15**, 24-33.
310. Lam TT-Y, Zhu H, Smith DK, Guan Y, **Holmes EC** & Pybus OG. (2012). The recombinant origin of emerging human norovirus GII.4/2008: intra-genic exchange of the capsid P2 domain. *J.Gen.Virol.* **93**, 817-822.
309. Murcia PR, Hughes J, Battista P, Lloyd L, Baillie GJ, Ramirez-Gonzalez RH, Ormond D, Oliver K, Elton D, Mumford JA, Caccamo M, Kellam P, Grenfell BT, **Holmes EC** & Wood JLN. (2012). Evolution of an Eurasian avian-like influenza virus in naïve and vaccinated pigs. *PLoS Pathog.* **8**:e1002730.
308. Nelson MI, Detmer SE, Wentworth DE, Tan Y, Schwartzbard A, Halpin RA, Stockwell TB, Lin X, Vincent AL, Gramer MR & **Holmes EC**. (2012). Genomic reassortment of influenza A virus in North American swine, 1998-2011. *J.Gen.Virol.* **93**, 2584-2589.

307. Nelson MI, Gramer MR, Vincent AL & **Holmes EC**. (2012). Global transmission of influenza viruses from humans to swine, 2009-2011. *J.Gen.Virol.* **93**, 2195-2203.
306. Nelson MI, Vincent AL, Kitikoon P, **Holmes EC** & Gramer MR. (2012). Evolution of novel reassortant A/H3N2 influenza viruses in North American swine and humans, 2009-2011. *J.Virol.* **86**, 8872-8878.
305. Nielsen ACY, Gyhrs ML, **Holmes EC** & Cui J. (2012). Co-circulation and persistence of genetically distinct Saffold viruses, Denmark. *Emerg.Infect.Dis.* **18**, 1694-1696.
304. Pagán I, **Holmes EC** & Simon-Loriere E. (2012). Level of gene expression is a major determinant of protein evolution in the viral order *Mononegavirales*. *J.Virol.* **86**, 5253-5263.
303. Panzarin V, Fusaro A, Monne I, Cappelozza E, Patarnello P, Bovo G, Capua I, **Holmes EC** & Cattoli G. (2012). Molecular epidemiology and evolutionary dynamics of betanodavirus in southern Europe. *Infect.Genet.Evol.* **12**, 63-70.
302. Shi M, Jagger BW, Wise HM, Digard P, **Holmes EC** & Taubenberger JK. (2012). Evolutionary conservation of the PA-X open reading frame in segment 3 of influenza A virus. *J.Virol.* **86**, 12411-12413.
301. Simmons HE, Dunham JP, Stack JC, Dickins BJA, Pagán I, **Holmes EC** & Stephenson AG. (2012). Deep sequencing reveals persistence of intra- and inter-host diversity in natural and greenhouse populations of *Zucchini yellow mosaic virus*. *J.Gen.Virol.* **93**, 1831-1840.
300. Stucker KM, Pagán I, Cifuentes JO, Kaelber JT, Lillie TD, Hafenstein S, **Holmes EC** & Parrish CR. (2012). The role of evolutionary intermediates in the host adaptation of canine parvovirus. *J.Virol.* **86**, 1514-1521.
299. Thai KTD, Henn MR, Zody MC, Tricou V, Nguyet NM, Charlebois P, Lennon NJ, Green L, de Vries PJ, Hien TT, Farrar J, van Doorn HR, de Jong MD, Birren BW, **Holmes EC** & Simmons CP. (2012). High-resolution analysis of intrahost genetic diversity in dengue virus serotype 1 identifies mixed infections. *J.Virol.* **86**, 835-843.
298. Bahl J, Nelson MI, Chan KH, Chen R, Vijaykrishna D, Halpin R, Stockwell T, Lin X, Wentworth DE, Ghedin E, Guan Y, Peiris M, Riley S, Rambaut A, **Holmes EC** & Smith GJD. (2011). Temporally structured metapopulation dynamics and persistence of influenza A H3N2 virus in humans. *Proc.Natl.Acad.Sci.USA* **108**, 19359-19364.
297. Bhatt S, **Holmes EC** & Pybus OG. (2011). The genomic rate of molecular adaptation of the human influenza A virus. *Mol.Biol.Evol.* **28**, 2443-2451.
296. Cattoli G, Fusaro A, Monne I, Coven F, Joannis F, Abd El-Hamid HS, Amarin NM, Mancin M, **Holmes EC** & Capua I. (2011). Evidence for differing evolutionary dynamics of A/H5N1 viruses among countries applying or not applying avian influenza vaccination in poultry. *Vaccine* **29**, 9368-9375.
295. Fusaro A, Monne I, Salviato A, Valastro V, Schivo A, Amarin NM, Gonzalez C, Ismail MM, Al-anakari R-A, Al-Bowi MH, Khan OA, Ali ASM, Hedayati A, Garcia JG, Ziay GM, Shoushtari A, Al Qahtani KN, Capua I, **Holmes EC** & Cattoli G. (2011). Phylogeography and evolutionary history of reassortant H9N2 viruses with potential human health implications. *J.Virol.* **85**, 8413-8421.
294. Ghedin E, Laplante J, DePasse J, Wentworth DE, Santos RP, Lepow ML, Porter J, Stellrecht K, Lin X, Operario D, Griesemer S, Fitch A, Halpin RA, Stockwell TB, Spiro DJ, **Holmes EC** & St. George K. (2011). Deep sequencing reveals mixed infection with pandemic influenza A (H1N1) virus strains and the emergence of oseltamivir resistance. *J.Infect.Dis.* **203**, 168-174.
293. **Holmes EC**. (2011). What does virus evolution tell us about virus origins? *J.Virol.* **85**, 5247-5251.
292. **Holmes EC**. (2011). The evolution of endogenous viral elements. *Cell Host & Microbe* **10**, 368-377.
291. **Holmes EC**, Ghedin E, Halpin RA, Stockwell TB, Zhang X-Q, Fleming R, Davey R, Benson CA, Mehta S, Taplitz R, Liu Y-T, Brouwer KC, Wentworth DE, Lin X, INSIGHT FLU002 Study Group & Schooley RT. (2011). Extensive geographical mixing of human H1N1/09 influenza A virus in a single university community. *J.Virol.* **85**, 6923-6929.

290. Kitchen A, Shackelton L & **Holmes EC**. (2011). Family level phylogenies reveal modes of macroevolution in RNA viruses. *Proc.Natl.Acad.Sci.USA* **108**, 238-243.
289. Lam TT-Y, Zhu H, Wang J, Smith DK, **Holmes EC**, Webster RG, Webby R, Peiris JM & Guan Y. (2011). Reassortment events among swine influenza A viruses in China: Implications for the origin of the 2009 influenza pandemic. *J.Virol.* **85**, 10279-10285.
288. Liu W, Rourke M, **Holmes EC** & Aaskov J. (2011). Persistence of multiple genetic lineages within intra-host populations of Ross River Virus. *J.Virol.* **85**, 5674-5678.
287. Morens DM, **Holmes EC**, Davis AS & Taubenberger JK. (2011). Rinderpest eradication: why humans should celebrate too. *J.Infect.Dis.* **204**, 502-505.
286. Murcia PR, Wood JLN, **Holmes EC**. (2011). Genome-scale evolution and phylodynamics of equine H3N8 influenza A virus. *J.Virol.* **85**, 5312-5322.
285. My PVT, Rabaa MA, Vinh H, **Holmes EC**, Hoang NVM, Vinh NT, Phuong LT, Tham NT, Bay PVB, Campbell JI, Farrar J & Baker S. (2011). The emergence of rotavirus G12 and the prevalence of enteric viruses from hospitalised pediatric diarrheal patients in southern Vietnam. *Am.J.Trop.Med.Hyg.* **85**, 768-775.
284. Nelson MI, Lemey P, Tan Y, Vincent A, Lam TT-Y, Detmer S, Viboud C, Suchard MA, Rambaut A, **Holmes EC** & Gramer M. (2011). Spatial dynamics of human-origin H1 influenza A virus in North American swine. *PLoS Pathog.* **7**:e1002077.
283. Nelson MI, Tan Y, Ghedin E, Wentworth DE, St. George K, Edelman L, Beck ET, Fan J, Lam TT-Y, Kumar S, Spiro DJ, Simonsen L, Viboud C, **Holmes EC**, Henrickson KJ & Musser JM. (2011). Phylogeography of the spring and fall waves of the H1N1/09 pandemic influenza virus in the United States. *J.Virol.* **85**, 828-834.
282. Raghwani J, Rambaut A, **Holmes EC**, Hang VT, Hien TT, Farrar J, Wills B, Lennon NJ, Birren BW, Henn MR & Simmons CP. (2011). Endemic dengue associated with the co-circulation of multiple viral lineages and localized density-dependent transmission. *PLoS Pathog.* **7**:e1002064.
281. Simmons HE, **Holmes EC**, Gildow FE, Bothe-Goralczyk ME & Stephenson AG. (2011). Experimental verification of seed transmission in *Zucchini yellow mosaic virus*. *Plant Dis.* **95**, 751-754.
280. Simmons HE, **Holmes EC** & Stephenson AG. (2011). Rapid turnover of intra-host genetic diversity in *zucchini yellow mosaic virus*. *Virus Res.* **155**, 389-396.
279. Simon-Loriere E & **Holmes EC**. (2011). Why do RNA viruses recombine? *Nat.Rev.Micro.* **9**, 617-626.
278. Torres-Pérez F, Palma RE, Hjelle B, **Holmes EC** & Cook JA. (2011). Spatial but not temporal co-divergence of a virus and its mammalian host. *Mol.Ecol.* **20**, 4109-4122.
277. Vasilakis N, Cardoso J, Hanley KA, **Holmes EC** & Weaver SC. (2011). Fever from the forest: prospects for continued emergence of sylvatic dengue virus and impact on public health. *Nat.Rev.Micro.* **9**, 532-541.
276. Balmaseda A, Standish K, Mercado JC, Matute JC, Tellez Y, Saborío S, Hammond SN, Nuñez A, Avilés W, Henn MR, **Holmes EC**, Gordon A, Coloma J, Kuan G & Harris E. (2010). Trends in patterns of dengue transmission over four years of a pediatric cohort study in Nicaragua. *J.Infect.Dis.* **201**, 5-14.
275. Boni MF, de Jong MD, van Doorn HR & **Holmes EC**. (2010). Guidelines for identifying homologous recombination events in influenza A virus. *PLoS One* **5**:e10434.
274. Bennett SN, Drummond AJ, Kapan DD, Muñoz JL, Pybus OG, **Holmes EC** & Gubler DJ. (2010). Epidemic dynamics revealed in dengue evolution. *Mol.Biol.Evol.* **27**, 811-818.
273. Carpi G, **Holmes EC** & Kitchen A. (2010). The evolutionary dynamics of bluetongue virus. *J.Mol.Evol.* **70**, 583-592.
272. Carrillo-Valenzo K, Danis-Lozano R, Velasco-Hernández JX, Sanchez-Burgos G, Alpuche C, Lopez I, Rosales C, Baronti C, de Lamballerie X, **Holmes EC** & Ramos-Castañeda J. (2010).

- Evolution of dengue virus in México is characterized by frequent lineage replacement. *Arch. Virol.* **155**, 1401-1412.
271. Chen R & **Holmes EC**. (2010). Hitchhiking and the population genetic structure of avian influenza virus. *J.Mol.Evol.* **70**, 98-105.
270. Dacheux L, Berthet N, Dissard G, **Holmes EC**, Delmas O, Larrous F, Guigon G, Dickinson P, Faye O, Sall AA, Old IG, Kong K, Kennedy GC, Manuguerra J-C, Cole ST, Caro V, Gessain A & Bourhy H. (2010). Application of broad-spectrum resequencing microarray for genotyping rhabdoviruses. *J.Virol.* **84**, 9557-9574.
269. Firth C, Kitchen A, Shapiro B, Suchard MA, **Holmes EC** & Rambaut A. (2010). Using time-structured data to estimate evolutionary rates of double-stranded DNA viruses. *Mol.Biol.Evol.* **27**, 2038-2051.
268. Fusaro A, Nelson MI, Joannis T, Bertolotti L, Monne I, Salviato A, Capua I, **Holmes EC** & Cattoli G. (2010). Evolutionary dynamics of multiple sublineages of H5N1 influenza viruses in Nigeria, 2006-2008. *J.Virol.* **84**, 3239-3247.
267. Ghedin E, Wentworth DE, Halpin RA, Lin X, Bera J, DePasse J, Fitch A, Griesemer S, Hine E, Katzel DA, Overton L, Proudfoot K, Sitz J, Szczypinski B, St. George K, Spiro DJ & **Holmes EC**. (2010). Unseasonal transmission of H3N2 Influenza A virus during the swine-origin H1N1 pandemic. *J.Virol.* **84**, 5715-5718.
266. Grard G, Moureau G, Charrel RN, **Holmes EC**, Gould EA & de Lamballerie X. (2010). Genomics and evolution of Aedes-borne flaviviruses and related viruses. *J.Gen.Virol.* **91**, 87-94.
265. Hayward JJ, Dubovi EJ, Scarlett JM, Janeczko S, **Holmes EC** & Parrish CR. (2010). Microevolution of canine influenza virus in shelters and its molecular epidemiology in the United States. *J.Virol.* **84**, 12636-12645.
264. Hoelzer K, Murcia PR, Baillie GJ, Wood JLN, Metzger S, Osterrieder K, Dubovi EJ, **Holmes EC** & Parrish CR. (2010). Intra-host evolutionary dynamics of canine influenza virus in naïve and partially immune dogs. *J.Virol.* **84**, 5329-5335.
263. **Holmes EC**. (2010). The comparative genomics of viral emergence. *Proc.Natl.Acad.Sci.USA.* **107**, 1742-1746.
262. **Holmes EC**. (2010). Does hepatitis C virus really form quasispecies? *Infect.Genet.Evol.* **10**, 431-432.
261. **Holmes EC**. (2010). The RNA virus quasispecies: fact or fiction? *J.Mol.Biol.* **400**, 271-273.
260. Jahnke M, **Holmes EC**, Kerr PJ, Wright JD & Strive T. (2010). Evolution and phylogeography of the non-pathogenic calicivirus RCV-A1 in wild rabbits in Australia. *J.Virol.* **84**, 12397-12404.
259. Jones A, Lowry K, Aaskov J, **Holmes EC** & Kitchen A. (2010). Molecular evolutionary dynamics of Ross River virus and implications for vaccine efficacy. *J.Gen.Virol.* **91**, 182-188.
258. Murcia PR, Baillie GJ, Daley J, Elton D, Jervis C, Mumford JA, Newton R, Parrish CR, Hoelzer K, Dougan G, Parkhill J, Lennard N, Ormond D, Moule S, Whitwham A, McKinley TJ, McCauley JW, **Holmes EC**, Grenfell BT & Wood JLN. (2010). The intra- and inter-host evolutionary dynamics of equine influenza virus. *J.Virol.* **84**, 6943-6954.
257. Pagán I, Firth C & **Holmes EC**. (2010). Phylogenetic analysis reveals rapid evolutionary dynamics in the plant RNA virus genus *Tobamovirus*. *J.Mol.Evol.* **71**, 298-307.
256. Pagán I & **Holmes EC**. (2010). Long-term evolution of the *Luteoviridae*: time-scale and mode of virus speciation. *J.Virol.* **84**, 6177-6187.
255. Rabaa M, Ty Hang VT, Wills B, Farrar J, Simmons CP & **Holmes EC**. (2010). Phylogeography of DENV-2 in southern Viet Nam: anthropogenic aspects of viral dispersal. *PLoS Negl.Trop.Dis.* **4**:e766.
254. Romano CM, Mello IMG de C, Pinho JRP, Melo FR, Motoki M, Jamal L, **Holmes EC**, Zanotto PM de A & the VGDN Consortium. (2010). Social networks shape the transmission dynamics of hepatitis C virus. *PLoS One* **5**:e11170.

253. Sall AA, Faye O, Diallo M, Firth C, Kitchen A & **Holmes EC**. (2010). Yellow fever virus exhibits slower evolutionary dynamics than dengue virus. *J. Virol.* **84**, 765-772.
252. Singh R, Levitt AL, Rajotte EG, **Holmes EC**, Ostiguy N, van Engelsdorp D, Lipkin WI, de Pamphilis CW, Toth AL & Cox-Foster DL. (2010). RNA viruses in hymenopteran pollinators: evidence of inter-taxa virus transmission via pollen and potential impact on non-*Apis* hymenopteran species. *PLoS One* **5**:e14357.
251. Talbi C, Lemey P, Suchard MA, Abdelatif E, Elharrak M, Jalal N, Faouzi A, Echevarría JE, Morón SV, Rambaut A, Campiz N, Tatem AJ, **Holmes EC** & Bourhy H. (2010). Phylodynamics and human-mediated dispersal of a zoonotic virus. *PLoS Pathog.* **6**:e1001166.
250. Ty Hang VT, **Holmes EC**, Veasna D, Nguyen TQ, Hien TT, Quail M, Churcher C, Parkhill J, Cardoso J, Farrar J, Willis B, Lennon NJ, Birren BW, Buchy P, Henn MR & Simmons CP. (2010). Emergence of the Asian I genotype of dengue virus serotype 2 in Viet Nam: *In vivo* fitness advantage and selectively mediated lineage replacement across South-East Asia. *PLoS Negl. Trop. Dis.* **4**:e757.
249. Vasilakis N, Cardoso J, Diallo M, Sall AA, **Holmes EC**, Hanley KA & Weaver SC. (2010). Sylvatic dengue viruses share the pathogenic potential of urban/endemic dengue viruses. *J. Virol.* **84**, 3726-3728.
248. Volk SM, Chen R, Tsetsarkin KA, Adams AP, Garcia TI, Sall AA, Nasar F, Schuh AJ, **Holmes EC**, Higgs S, Maharaj PD, Brault AC & Weaver SC. (2010). Genome scale phylogenetic analyses of chikungunya virus reveal independent emergences of recent epidemics and varying evolutionary rates. *J. Virol.* **84**, 6497-6504.
247. Bahl J, Vijaykrishna D, **Holmes EC**, Smith GJD & Guan Y. (2009). Gene flow and competitive exclusion of avian influenza A in the natural reservoir hosts. *Virology* **390**, 289-297.
246. Botosso VF, Zanotto PM de A, Ueda M, Arruda E, Gilio AE, Vieira SE, Stewien KE, Peret TC, Jamal LF, de M C Pardini MI, Pinho JR, Massad E, Sant'anna OA, **Holmes EC**, Durigon EL & the VGDN Consortium. (2009). Positive selection results in frequent reversible amino acid replacements in the G protein gene of human respiratory syncytial virus. *PLoS Pathog.* **5**:e1000254.
245. Cardoso J, Ooi MH, Tio PH, Perera D, **Holmes EC**, Bibi K & Manap ZA. (2009). Dengue virus serotype 2 from a sylvatic lineage isolated a patient with dengue haemorrhagic fever. *PLoS Negl. Trop. Dis.* **3**:e423.
244. Chen R & **Holmes EC**. (2009). Frequent inter-species transmission and geographic subdivision in avian influenza viruses from wild birds. *Virology* **383**, 156-161.
243. Cook S, Moureau G, Harbach RE, Mukwaya L, Goodger K, Ssenfuka F, Gould EA, **Holmes EC** & de Lamballerie X. (2009). Isolation of a novel species of flavivirus and a novel strain of *Culex flavivirus* (*Flaviviridae*) from a natural mosquito population in Uganda. *J. Gen. Virol.* **90**, 2669-2678.
242. Dorji T, Yoon I-K, **Holmes EC**, Wangchuk S, Tobgay T, Nisalak A, Chinnawirotpisan P, Sangkachantaranon K, Gibbons RV & Jarman RG. (2009). Diversity and origin of dengue serotypes 1, 2 and 3 in Bhutan. *Emerg. Infect. Dis.* **5**, 1630-1632.
241. Duffy S & **Holmes EC**. (2009). Validation of high rates of nucleotide substitution in geminiviruses: Phylogenetic evidence from *East African cassava mosaic viruses*. *J. Gen. Virol.* **90**, 539-1547.
240. Dunham EJ, Dugan VG, Kaser EK, Perkins SE, Brown IH, **Holmes EC** & Taubenberger JK. (2009). Different evolutionary trajectories of European avian-like and classical swine H1N1 influenza A viruses. *J. Virol.* **83**, 5485-5494.
239. Firth C, Charleston MA, Duffy S, Shapiro B & **Holmes EC**. (2009). Insights into the evolutionary history of an emerging livestock pathogen: porcine circovirus 2. *J. Virol.* **83**, 12813-12821.

238. Ghedin E, Fitch A, Boyne A, DePasse J, Bera J, Halpin RA, Griesemer S, Smit M, Jennings L, St. George K, **Holmes EC** & Spiro DJ. (2009). Mixed infection and the genesis of influenza diversity. *J.Virol.* **83**, 8832-8841.
237. **Holmes EC**. (2009). The evolutionary genetics of emerging viruses. *Annu.Rev.Ecol.Evol.Syst.* **40**, 353-372.
236. **Holmes EC**. (2009). RNA virus genomics: a world possibilities. *J.Clin.Invest.* **119**, 2488-2495.
235. **Holmes EC** & Grenfell BT. (2009). Discovering the phylodynamics of RNA viruses. *PLoS Comput.Biol.* **5**:e1000505.
234. **Holmes EC**, Toi P-H, Perera D, Muhi J & Cardoso J. (2009). Importation and co-circulation of multiple serotypes of dengue virus in Sarawak, Malaysia. *Virus Res.* **143**, 1-5.
233. Kerr PJ, Kitchen A & **Holmes EC**. (2009). The origin and phylodynamics of rabbit hemorrhagic disease virus. *J.Virol.* **83**, 12129-12138.
232. Nelson MI, Simonsen L, Miller MA, Viboud C & **Holmes EC**. (2009). The origin and global emergence of adamantane resistant A/H3N2 influenza viruses. *Virology* **388**, 270-278.
231. Nelson MI, Spiro DJ, Wentworth DE, Fan J, Beck ET, St. George K, Halpin RA, Bera J, Hine E, Proudfoot K, Stockwell TB, Lin X, Bose ME, Jurgens L, Kumar S, Viboud C, **Holmes EC** & Henrickson KJ. (2009). The early diversification of influenza A/H1N1pdm. *PLoS Currents: Influenza.* 10.1371/currents.RRN1126.
230. Rambaut A & **Holmes EC**. (2009). The early molecular epidemiology of the swine-origin A/H1N1 human influenza pandemic. *PLoS Currents: Influenza.* 10.1371/currents.RRN1003.
229. Ramsden C, **Holmes EC** & Charleston MA. (2009). Hantavirus evolution in relation to its rodent and insectivore Hosts: No evidence for co-divergence. *Mol.Biol.Evol.* **26**, 143-153.
228. Schreiber MJ, **Holmes EC**, Ong SH, Soh HSH, Liu W, Tanner L, Aw PPK, Tan HC, Ng LC, Leo YS, Low JGH, Ong A, Ooi EE, Vasudevan S & Hibberd ML. (2009). Genomic epidemiology of a dengue virus epidemic in urban Singapore. *J.Virol.* **83**, 4163-4173.
227. Talbi C, **Holmes EC**, de Benedictis P, Faye O, Nakouné E, Gamatié D, Diarra A, Elmamy BO, Sow A, Sangare O, Dundon WG, Capua I, Sall AA & Bourhy H. (2009). The evolutionary history and dynamics of dog rabies virus in West and Central Africa. *J.Gen.Virol.* **90**, 783-791.
226. Boni MF, Zhou Y, Taubenberger JK & **Holmes EC**. (2008). Homologous recombination is very rare or absent in human influenza A virus. *J.Virol.* **82**, 4807-4811.
225. Bourhy H, Reynes J-M, Dunham EJ, Dacheux L, Larouss F, Hong VTQ, Xu G, Yan J, Miranda MEG & **Holmes EC**. (2008). The origin and phylogeography of dog rabies virus. *J.Gen.Virol.* **89**, 2673-2681.
224. Briese T, Palacios G, Lipkin WI, Renwick N, Venter M, Jarman RG, Dominguez SR, Holmes KV & **Holmes EC**. (2008). Prior evidence of putative novel rhinovirus species, Australia response. *Emerg.Infect.Dis.* **14**, 1824-1825.
223. Briese T, Renwick N, van den Berg M, Jarman J, Ghosh D, Köndgen S, Shrestha S, Hoegh AM, Flecha IC, Adjogoua EV, Akoua-Koffi C, Myint KS, Williams D, Chidlow G, Calvo C, Palacios G, Kapoor V, Joseph Villari J, Harnett G, Smith D, Mackenzie J, Ellerbrok H, Schweiger B, Schønning K, Chaddha M, Fabian H, Leendertz FH, Mishra AC, Gibbons R, Venter M, **Holmes EC** & Lipkin WI. (2008). Global distribution of novel rhinovirus genotype. *Emerg.Infect.Dis.* **14**, 944-947.
222. Chang GS, Hoon Y, Ko KD, Bhardwaj G, **Holmes EC**, Patterson RL & van Rossum DB. (2008). Phylogenetic profiles reveal evolutionary relationships within the 'twilight zone' of sequence similarity. *Proc.Natl.Acad.Sci.USA* **105**, 13474-13479.
221. Chen R & **Holmes EC**. (2008). The evolutionary dynamics of human influenza B virus. *J.Mol.Evol.* **66**, 655-663.

220. Cox-Foster DL, Conlan S, **Holmes EC**, Palacios G, Kalkstein AL, Evans JD, Moran NA, Quan P-L, Geiser DM, Briese T, Hornig M, Hui J, van Engelsdorp D, Pettis JS & Lipkin WI. (2008). The latest buzz about colony collapse disorder. *Science* **319**, 724-725.
219. de Graaf M, Osterhaus ADME, Fouchier RAM & **Holmes EC**. (2008). Evolutionary dynamics of human and avian metapneumoviruses. *J.Gen.Virol.* **89**, 2933-2942.
218. Delmas O, **Holmes EC**, Talbi C, Larrous F, Dacheux L, Bouchier C & Bourhy H. (2008). Genomic diversity and evolution of the lyssaviruses. *PLoS One* **3**:e2057.
217. Duffy S & **Holmes EC**. (2008). Phylogenetic evidence for rapid rates of molecular evolution in the single-stranded DNA begomovirus *Tomato Yellow Leaf Curl Virus*. *J.Virol.* **82**, 957-965.
216. Duffy S, Shackelton LA & **Holmes EC**. (2008). Rates of evolutionary change in viruses: Patterns and determinants. *Nat.Rev.Genet.* **9**, 267-276.
215. Dugan VG, Chen R, Spiro DJ, Sengamalay N, Zaborsky J, Ghedin E, Nolting J, Swayne DE, Runstadler JA, Happ GM, Senne DA, Wang R, Slemons RD, **Holmes EC** & Taubenberger JK. (2008). The evolutionary genetics and emergence of avian influenza viruses in wild birds. *PLoS Pathog.* **4**:e1000076.
214. Hoelzer K, Shackelton LA, **Holmes EC** & Parrish CR. (2008). Within-host genetic diversity of endemic and emerging parvoviruses of cats and dogs. *J.Virol.* **82**, 11096-11105.
213. Hoelzer K, Shackelton LA, Parrish CR & **Holmes EC**. (2008). Phylogenetic analysis reveals the emergence, evolution and dispersal of carnivore parvoviruses. *J.Gen.Virol.* **89**, 2280-2289.
212. **Holmes EC**. (2008). The evolutionary history and phylogeography of human viruses. *Annu.Rev.Microbiol.* **62**, 307-328.
211. Jarman RG, **Holmes EC**, Rodpradit P, Klungthong C, Gibbons RV, Nisalak A, Rothman AI, Libraty DH, Ennis FA, Mammen MP Jr. & Endy TP. (2008). Microevolution of dengue viruses circulating among primary school Children in Kamphaeng Phet, Thailand. *J.Virol.* **82**, 5494-5500.
210. Nelson MI, Edelman L, Spiro DJ, Boyne AR, Bera J, Halpin R, Ghedin E, Miller MA, Simonsen L, Viboud C & **Holmes EC**. (2008). Molecular epidemiology of A/H3N2 and A/H1N1 influenza virus during a single epidemic season in the United States. *PLoS Pathog.* **4**:e1000133.
209. Nelson MI, Viboud C, Simonsen L, Bennett RT, Griesemer SB, St. George K, Taylor J, Spiro DJ, Sengamalay NA, Ghedin E, Taubenberger JK & **Holmes EC**. (2008). Multiple reassortment events in the evolutionary history of H1N1 influenza A virus since 1918. *PLoS Pathog.* **4**:e1000012.
208. Palacios G, Hui J, Quan PL, Kalkstein A Honkavuori KS, Bussetti AV, Conlan S, Evans J, Chen YP, VanEngelsdorp D, Efrat H, Pettis J, Cox-Foster D, **Holmes EC**, Briese T & Lipkin WI. (2008). Genetic analysis of Israel Acute Paralysis Virus: Distinct clusters are circulating in the United States. *J.Virol.* **82**, 6209-6217.
207. Parrish CR, **Holmes EC**, Morens DM, Park E-C, Burke DS, Calisher CH, Laughlin CA, Saif LJ & Daszak P. (2008). Cross-species viral transmission and the emergence of new epidemic diseases. *Microbiol.Mol.Biol.Rev.* **72**, 457-470.
206. Pomeroy LW, Bjørnstad ON & **Holmes EC**. (2008). The evolutionary and epidemiological dynamics of the *Paramyxoviridae*. *J.Mol.Evol.* **66**, 98-106.
205. Rambaut A, Pybus OG, Nelson MI, Viboud C, Taubenberger JK & **Holmes EC**. (2008). The genomic and epidemiological dynamics of human influenza A virus. *Nature* **453**, 615-619.
204. Ramsden C, Melo FL, Figueiredo LM, **Holmes EC**, Zanotto PM de A and the VGDN Consortium. (2008). High rates of molecular evolution in hantaviruses. *Mol.Biol.Evol.* **25**, 1488-1492.
203. Romano CM, Zanotto PM de A & **Holmes EC**. (2008). Bayesian coalescent analysis reveals a high rate of molecular evolution in GB virus C. *J.Mol.Evol.* **66**, 292-297.

202. Shackelton LA & **Holmes EC**. (2008). The role of alternative genetic codes in virus evolution and emergence. *J.Theor.Biol.* **254**, 128-134.
201. Simmons HE, **Holmes EC** & Stephenson AG. (2008). Rapid evolutionary dynamics of zucchini yellow mosaic virus. *J.Gen.Virol.* **89**, 1081-1085.
200. Aaskov J, Buzacott K, Field E, Berlioz-Arthaud A & **Holmes EC**. (2007). Multiple recombinant dengue type 1 viruses in an isolate from a dengue patient. *J.Gen.Virol.* **88**, 3334-3340.
199. Aulicino PC, **Holmes EC**, Rocco C, Mangano AM & Sen L. (2007). Extremely rapid spread of HIV-1 BF recombinants in Argentina. *J.Virol.* **81**, 427-429.
198. Brault AC, Huang C Y-H, Langevin SA, Kinney RM, Bowen RA, Ramey WN, Panella NA, **Holmes EC**, Powers AM & Miller BR. (2007). A single positively selected West Nile viral mutation confers increased avian virogenesis in American crows. *Nat.Genet.* **39**, 1162-1166.
197. Bryant JE, **Holmes EC** & Barrett ADT. (2007). Out of Africa: A molecular perspective on the introduction of Yellow Fever Virus into the Americas. *PLoS Pathog.* **3**:e75.
196. Cox-Foster DL, Conlan S, **Holmes EC**, Palacios G, Evans JD, Moran NA, Quan P-L, Briese T, Geiser DM, Martinson V, van Engelsdorp D, Kalkstein AL, Drysdale A, Hui J, Zhai J, Cui L, Hutchinson S, Simons JF, Egholm M, Pettis JS & Lipkin WI. (2007). A metagenomic survey of microbes in honey bee colony collapse disorder. *Science* **318**, 283-287.
195. Davis PL, Rambaut A, Bourhy H & **Holmes EC**. (2007). The evolutionary dynamics of canid and mongoose rabies virus in Southern Africa. *Arch.Virol.* **152**, 1251-1258.
194. de Freitas RB, Durigon EL, Oliveira D de S, Romano CM, de Freitas MRC, Linhares A de C, Melo FL, Walshkeller L, Barbosa ML, Huatuco EMM, **Holmes EC** & Zanotto PM de A. (2007). The 'pressure pan' evolution of human erythrovirus B19 in the Amazon, Brazil. *Virology* **369**, 281-287.
193. Duffy S & **Holmes EC**. (2007). Multiple introductions of the Old World begomovirus, tomato yellow leaf curl virus (TYLCV), in the New World. *Appl.Environ.Micro.* **73**, 7114-7117.
192. Dunham EJ & **Holmes EC**. (2007). Inferring the time-scale of dengue virus evolution under realistic models of DNA substitution. *J.Mol.Evol.* **64**, 656-661.
191. Grard G, Moureau G, Charrel RN, Lemasson J-J, Gonzalez J-P, Gallian P, Gritsun T, **Holmes EC**, Gould EA & de Lamballerie X. (2007). Genetic characterisation of tick-borne flaviviruses: New insights into evolution, pathogenetic determinants and taxonomy. *Virology* **361**, 80-92.
190. **Holmes EC**. (2007). Viral evolution in the genomic age. *PLoS Biol.* **5**:e278.
189. **Holmes EC** & Drummond AJ. (2007). The evolutionary genetics of viral emergence. *Curr.Top.Micro.Immunol.* **315**, 51-66.
188. Kalayanarooj S, Rimal HS, Andjaparidze A, Vatcharasaev V, Nisalak A, Jarman RG, Chinnawirotpisan P, Mammen MP, **Holmes EC** & Gibbons RV. (2007). Clinical investigation and molecular characteristics of dengue hemorrhagic fever outbreak in Timor-Leste, 2005. *Am.J.Trop.Med.Hyg.* **77**, 534-537.
187. Nelson MI & **Holmes EC**. (2007). The evolution of epidemic influenza. *Nat.Rev.Genet.* **8**, 196-205.
186. Nelson MI, Simonsen L, Viboud C, Miller MA & **Holmes EC**. (2007). Phylogenetic analysis reveals the global migration of seasonal influenza A viruses. *PLoS Pathog.* **3**:1220-1228.
185. Pybus OG, Rambaut A, Freckleton RP, Belshaw R, Drummond AJ & **Holmes EC**. (2007). Phylogenetic evidence for deleterious mutation load in RNA viruses and its contribution to viral evolution. *Mol.Biol.Evol.* **24**, 845-852.
184. Romano CM, de Melo FL, Corsini MAB, **Holmes EC** & Zanotto PM de A. Demographic histories of ERV-K in humans, chimpanzees and rhesus monkeys. (2007). *PLoS One* **2**:e1026.
183. Sanjuán R, Cuevas JM, Furió V, **Holmes EC** & Moya A. (2007). Selection for robustness in mutagenized RNA viruses. *PLoS Genet.* **3**: e93.

182. Schreiber MJ, Ong SH, Holland RC, Hibberd ML, Vasudevan SG, Mitchell WP & **Holmes EC**. (2007). DengueInfo: A web portal to dengue information resources. *Infect.Genet.Evol.* **7**, 540-541.
181. Shackelton LA, Hoelzer K, Parrish CR & **Holmes EC**. (2007). Comparative analysis reveals frequent recombination in parvoviruses. *J.Gen.Virol.* **88**, 3294-3301.
180. Sharp EL, Farrell HE, Borchers K, **Holmes EC** & Davis-Poynter NJ. (2007). Sequence analysis of the Equid herpesvirus-2 chemokine receptor homologues E1, ORF74 and E6 demonstrates high sequence divergence between field isolates. *J.Gen.Virol.* **88**, 2450-2462.
179. Simonsen L, Viboud C, Grenfell BT, Dushoff J, Jennings L, Smit M, Macken C, Hata M, Gog J, Miller MA & **Holmes EC**. (2007). The genesis and spread of reassortant human influenza A/H3N2 viruses conferring adamantane resistance. *Mol.Biol.Evol.* **24**, 1811-1820.
178. Snapinn KW, **Holmes EC**, Young DS, Bernard KA, Kramer LD & Ebel GD. (2007). Declining growth rate of West Nile virus in North America. *J.Virol.* **81**, 2531-2534.
177. Thümer L, Rethwilm A, **Holmes EC** & Bodem J. (2007). The complete nucleotide sequence of a New World simian foamy virus. *Virology* **369**, 191-197.
176. Vasilakis N, **Holmes EC**, Fokam EB, Faye O, Diallo M, Sall AA & Weaver SC. (2007). Evolutionary processes among sylvatic dengue-2 viruses. *J.Virol.* **81**, 9591-9595.
175. Walker PR, Ketunuti M, Choge IA, Meyers T, Gray G, **Holmes EC** & Morris L. (2007). Polymorphisms in Nef associated with different clinical outcomes in HIV-1 subtype C infected children. *AIDS Res.Hum.Retro.* **23**, 204-215.
174. Zhou Y & **Holmes EC**. (2007). Bayesian estimates of the evolutionary rate and age of hepatitis B virus. *J.Mol.Evol.* **65**, 197-205.
173. Aaskov J, Buzacott K, Thu HM, Lowry K & **Holmes EC**. (2006). Long-term transmission of defective RNA viruses in humans and *Aedes* mosquitoes. *Science* **311**, 236-238.
172. Adams B, **Holmes EC**, Zhang C, Mammen MP Jr, Nimmannitya S, Kalayanarooj S & Boots M. (2006). Cross-protective immunity can account for the alternating epidemic pattern of dengue virus serotypes circulating in Bangkok. *Proc.Natl.Acad.Sci.USA* **103**, 14234-14239.
171. Bennett SN, **Holmes EC**, Chirivella M, Rodriguez DM, Beltran M, Vorndam V, Gubler DJ & McMillan WO. (2006). Molecular evolution of dengue 2 virus in Puerto Rico: positive selection in the viral envelope accompanies clade reintroduction. *J.Gen.Virol.* **87**, 885-893.
170. Chare ER & **Holmes EC**. (2006). A phylogenetic survey of recombination frequency in plant RNA viruses. *Arch.Virol.* **151**, 933-946.
169. Chen R & **Holmes EC**. (2006). Avian influenza virus exhibits rapid evolutionary dynamics. *Mol.Biol.Evol.* **23**, 2336-2341.
168. Cook S, Bennett SN, **Holmes EC**, de Chesse R, Moureau G & de Lamballerie X. (2006). Isolation of a new strain of the flavivirus cell fusing agent virus in a natural mosquito population from Puerto Rico. *J.Gen.Virol.* **87**, 735-748.
167. Cook S & **Holmes EC**. (2006). A multigene analysis of the phylogenetic relationships among the flaviviruses (family *Flaviviridae*) and the evolution of vector transmission. *Arch.Virol.* **151**, 309-325.
166. Davis PL, Bourhy H & **Holmes EC**. (2006). The evolutionary history and dynamics of bat rabies virus. *Infect.Genet.Evol.* **6**, 464-473.
165. Edwards CTT, **Holmes EC**, Pybus OG, Wilson DJ, Viscidi RP, Abrams EJ, Phillips RE & Drummond AJ. (2006). Evolution of the human immunodeficiency virus envelope gene is dominated by purifying selection. *Genetics* **174**, 1441-1453.
164. Edwards CTT, **Holmes EC**, Wilson DJ, Viscidi RP, Abrams EJ, Phillips RE & Drummond AJ. (2006). Population genetic estimation of the loss of genetic diversity during horizontal transmission of HIV-1. *BMC Evol.Biol.* **6**:28.
163. Frater AJ, Edwards CTT, McCarthy N, Fox J, Brown H, Milicic A, Mackie N, Pillay T, Drijfhout JW, Dunstan S, Clarke JR, **Holmes EC**, Zhang HT, Pfafferott K, Goulder PJ,

- McClure MO, Weber J, Phillips RE & Fidler S. (2006). Passive sexual transmission of HIV-1 variants and adaptation in new hosts. *J.Virol.* **80**, 7226-7234.
162. Grard G, Lemasson J-J, Sylla M, Dudot A, Cook S, Molez J-F, Charrel RN, Gonzalez J-P, Munderloh U, **Holmes EC** & de Lamballerie X. (2006). Ngoye virus: A novel evolutionary lineage within the genus *Flavivirus*. *J.Gen.Virol.* **87**, 3273-3277.
161. **Holmes EC**. (2006). Future issues in RNA virus evolution. *Future Virol.* **1**, 243-249.
160. **Holmes EC**, Lipman DJ, Zamarin D & Yewdell JW. (2006). Comment on 'Large-scale analysis of avian influenza isolates'. *Science* **313**, 1573b.
159. Kuiken T, **Holmes EC**, McCauley J, Rimmelzwaan GF, Williams CS & Grenfell BT. (2006). Host species barriers to influenza virus infections. *Science* **312**, 394-397.
158. Nelson MI, Simonsen L, Viboud C, Miller MA, Taylor J, St. George K, Griesemer SB, Ghedin E, Sengamalay NA, Spiro DJ, Volkov I, Grenfell BT, Lipman DJ, Taubenberger JK & **Holmes EC**. (2006). Stochastic processes are key determinants of the short-term evolution of influenza A virus. *PLoS Pathog.* **2**:e125.
157. Shackelton LA & **Holmes EC**. (2006). Phylogenetic evidence for the rapid evolution of human B19 erythrovirus. *J.Virol.* **80**, 3666-3669.
156. Shackelton LA, Parrish CR & **Holmes EC**. (2006). Evolutionary basis of codon usage and nucleotide composition bias in vertebrate DNA viruses. *J.Mol.Evol.* **62**, 551-563.
155. Shackelton LA, Rambaut A, Pybus OG & **Holmes EC**. (2006). JC virus evolution and its association with human populations. *J.Virol.* **80**, 9928-9933.
154. Shapiro B, Rambaut A, Pybus OG, Drummond A & **Holmes EC**. (2006). A phylogenetic method for detecting positive epistasis in gene sequences and its application to RNA virus evolution. *Mol.Biol.Evol.* **23**, 1724-1730.
153. Wolf YI, Viboud C, **Holmes EC**, Koonin EV & Lipman DJ. (2006). Long intervals of stasis punctuated by bursts of positive selection in the seasonal evolution of influenza A virus. *Biol.Direct.* **1**:34.
152. Zhang C, Mammen MP Jr, Chinnawirotpisan P, Klungthong C, Rodpradit P, Nisalak A, Nimmannitya S, Kalayanarooj S, Vaughn DW & **Holmes EC**. (2006). Structure and age of genetic diversity of dengue virus type 2 in Thailand. *J.Gen.Virol.* **87**, 873-883.
151. Zhou Y, Mammen MP Jr, Chinnawirotpisan P, Klungthong C, Vaughn DW, Nimmannitya S, Kalayanarooj S, **Holmes EC** & Zhang C. (2006). Comparative analysis reveals no consistent association between the secondary structure of the 3'UTR of dengue viruses and disease syndrome. *J.Gen.Virol.* **87**, 2595-2603.
150. Bourhy H, Cowley JA, Larrous F, **Holmes EC** & Walker PJ. (2005). Phylogenetic relationships among the rhabdoviruses inferred using the L polymerase gene. *J.Gen.Virol.* **86**, 2849-2858.
149. Carrington CVF, Foster JE, Pybus OG, Bennett SN & **Holmes EC**. (2005). Invasion and maintenance of dengue virus type 2 and type 4 in the Americas. *J.Virol.* **79**, 14680-14687.
148. Cook S, Diallo M, Sall AA, Cooper A & **Holmes EC**. (2005). Mitochondrial markers for the molecular identification of *Aedes* mosquitoes (Diptera: Culicidae) involved in the transmission of arboviral disease in West Africa. *J.Med.Entomol.* **42**, 19-28.
147. Davis PL, **Holmes EC**, Larrous F, Van de Poel WHM, Tjørnehøj K, Alonso WJ & Bourhy H. (2005). Phylogeography, population dynamics, and molecular evolution of European bat lyssaviruses. *J.Virol.* **79**, 10487-10497.
146. Edwards CTT, Pfafferot KJ, Goulder PGR, Phillips RE & **Holmes EC**. (2005). Inpatient escape in the A*0201-restricted epitope SLYNTVATL drives evolution of human immunodeficiency virus type 1 at the population level. *J.Virol.* **79**, 9363-9366.
145. **Holmes EC**, Ghedin E, Miller N, Taylor J, Bao Y, St. George K, Grenfell BT, Salzberg SL, Fraser CM, Lipman DJ & Taubenberger JK. (2005). Whole-genome analysis of human influenza A virus reveals multiple persistent lineages and reassortment among recent H3N2 viruses. *PLoS.Biol.* **3(9)**, e300.

144. Milicic A, Edwards CTT, Hue S, Fox J, Brown H, Pillay T, Drijfhout JW, Weber JN, **Holmes EC**, Fidler SJ, Zhang H-T, & Phillips RE. (2005). Sexual transmission of single human immunodeficiency type 1 virions encoding highly polymorphic multisite cytotoxic T-lymphocyte escape variants. *J.Virol.* **79**, 13953-13962.
143. Pillay T, Zhang H-T, Drijfhout JW, Robinson N, Brown H, Khan M, Moodley J, Adhikari M, Pfafferott K, Feeny ME, St. John A, **Holmes EC**, Coovadia HM, Klenerman P, Goulder PJR & Phillips RE. (2005). Unique acquisition of cytotoxic T-lymphocyte escape mutants in infant human immunodeficiency virus type 1 infection. *J.Virol.* **79**, 12100-12105.
142. Pybus OG, Cochrane A, **Holmes EC** & Simmonds P. (2005). The hepatitis C virus epidemic among injecting drug users. *Infect.Genet.Evol.* **5**, 131-139.
141. Rodríguez-Roche R, Alvarez M, **Holmes EC**, Bernardo L, Kourí G, Gould EA & Guzman MG. (2005). Dengue virus type 3, Cuba 2000-2002. *Emerg.Infect.Dis.* **11**, 773-774.
140. Shackelton LA, Parrish CR, Truyen U & **Holmes EC**. (2005). High rate of viral evolution associated with the emergence of canine parvoviruses. *Proc.Natl.Acad.Sci.USA* **102**, 379-384.
139. Switzer WM, Salemi M, Shanmugam V, Gao F, Cong M-E, Kuiken C, Bhullar V, Beer B, Vallet D, Gautier-Hion A, Tooze A, Villinger F, **Holmes EC** & Heneine W. (2005). Ancient co-speciation of simian foamy viruses and primates. *Nature* **434**, 376-380.
138. Thu HM, Lowry K, Jian L, Hlaing T, **Holmes EC** & Aaskov J. (2005). Lineage extinction and replacement in dengue type 1 virus populations is due to stochastic events rather than natural selection. *Virology* **336**, 163-172.
137. Walker PR, Pybus OG, Rambaut A & **Holmes EC**. (2005). Comparative population dynamics of HIV-1 subtypes B and C: Subtype-specific differences in patterns of epidemic growth. *Infect.Genet.Evol.* **5**, 199-208.
136. Zhang C, Mammen MP Jr, Chinnawirotpisan P, Klungthong C, Rodpradit P, Monkongdee P, Nimmannitya S, Kalayanarooj S & **Holmes EC**. (2005). Clade replacements in dengue virus serotypes 1 and 3 are associated with changing serotype prevalence. *J.Virol.* **79**, 15123-15130.
135. A-Nuegoonpipat A, Berlioz-Arthaud A, Chow V, Endy T, Lowry K, Mai LQ, Ninh TU, Pyke A, Reid M, Reynes J-M, Yun STS, Thu HM, Wong S-S, **Holmes EC** & Aaskov J. (2004). Sustained transmission of dengue virus type 1 in the Pacific due to repeated introduction of different Asian genotypes. *Virology* **329**, 505-512.
134. Barnett OE, Worobey M, **Holmes EC** & Cooper A. (2004). The detection of TT virus among wild chimpanzees via a non-invasive technique. *J.Wildlife Dis.* **40**, 230-237.
133. Chare ER & **Holmes EC**. (2004). Selection pressures in the capsid genes of plant RNA viruses reflect mode of transmission. *J.Gen.Virol.* **85**, 3149-3157.
132. Draenert R, LeGall S, Pfafferott KJ, Leslie AJ, Chetty P, Brander C, **Holmes EC**, Chang SC, Feeney ME, Addo MM, Ruiz L, Ramduth D, Jeena P, Altfeld M, Thomas S, Tang Y, Verrill CL, Dixon C, Prado JG, Kiepiela P, Goldberg AL, Martinez-Picado J, Walker BD & Goulder PJR. (2004). Immune selection for altered antigen processing leads to cytotoxic T lymphocyte escape in chronic HIV-1 infection. *J.Exp.Med.* **199**, 905-915.
131. Grenfell BT, Pybus OG, Gog JR, Wood JLN, Daly JM, Mumford JA & **Holmes EC**. (2004). Unifying the epidemiological and evolutionary dynamics of pathogens. *Science* **303**, 327-332.
130. **Holmes EC**. (2004). The phylogeography of human viruses. *Mol.Ecol.* **13**, 745-756.
129. **Holmes EC** & Rambaut A. (2004). Viral evolution and the emergence of SARS coronavirus. *Phil.Trans.Roy.Soc.Lond.B.* **359**, 1059-1065.
128. Klungthong C, Zhang C, Mammen Jr. MP, Ubol S & **Holmes EC**. (2004). The molecular epidemiology of dengue virus serotype 4 in Bangkok, Thailand. *Virology* **329**, 168-179.

127. Leal E de S, **Holmes EC** & Zanotto PM de A. (2004). Distinct patterns of natural selection in the reverse transcriptase gene of HIV-1 in the presence and absence of antiretroviral therapy. *Virology* **325**, 181-191.
126. Leslie AJ, Pfafferott KJ, Chetty P, Draenert R, Addo MM, Feeney M, **Holmes EC**, Allen T, Prado JG, Altfeld M, Brander C, Dixon C, Ramduth D, Jeena P, Thomas SA, St. John A, Roach TA, Kupfer B, Luzzi G, Edwards A, Taylor G, Lyall H, Tudor-Williams G, Novelli V, Martinez-Picado J, Kiepiela P, Walker BD & Goulder PJR. (2004). HIV evolution: CTL escape mutation and reversion following transmission. *Nat.Med.* **10**, 282-289.
125. Moya A, **Holmes EC** & González-Candelas F. (2004). The population genetics and evolutionary epidemiology of RNA viruses. *Nat.Rev.Microbiol.* **2**, 279-287.
124. Oxenius A, Price DA, Trkola A, Edwards C, Gostick E, Zhang H-T, Easterbrook PJ, Tun T, Johnson A, Waters A, **Holmes EC** & Phillips RE. (2004). Loss of viral control in early HIV-1 infection is temporally associated with decline of HIV-specific CD4⁺ and CD8⁺ T cell frequencies and sequential escape from CTL responses. *J.Infect.Dis.* **190**, 713-721.
123. Priest FG, Barker M, Baillie LWJ, **Holmes EC** & Maiden MCJ. (2004). Population structure and evolution of the *Bacillus cereus* subgroup. *J.Bact.* **186**, 7959-7970.
122. Rambaut A, Crandall KA, Posada D & **Holmes EC**. (2004). The causes and consequences of HIV evolution. *Nat.Rev.Genet.* **5**, 52-61.
121. Shackelton LA & **Holmes EC**. (2004). The evolution of large DNA viruses: Combining genomic information of viruses and their hosts. *Trends Microbiol.* **12**, 458-465.
120. Sheridan I, Pybus OG, **Holmes EC** & Klennerman P. (2004). High resolution phylogenetic analysis of Hepatitis C virus adaptation and its relationship to disease progression. *J.Virol.* **78**, 3447-3454.
119. Urwin R, Russell JE, Thompson EAL, **Holmes EC**, Feavers IM & Maiden MCJ. (2004). Distribution of surface protein variants among hyper-invasive meningococci: Implications for vaccine design. *Infect.Immun.* **72**, 5955-5962.
118. Bennett SN, **Holmes EC**, Chirivella M, Rodriguez DM, Beltran M, Vorndam V, Gubler DJ & McMillan WO. (2003). Selection-driven evolution of emergent dengue virus. *Mol.Biol.Evol.* **20**, 1650-1658.
117. Chare ER, Gould EA & **Holmes EC**. (2003). Phylogenetic analysis reveals a low rate of homologous recombination in negative-sense RNA viruses. *J.Gen.Virol.* **84**, 2691-2703.
116. Craig S, Thu HM, Lowry K, Wang X-F, **Holmes EC** & Aaskov J. (2003). Diverse dengue type 2 virus populations contain recombinant and both parental viruses in a single mosquito host. *J.Virol.* **77**, 4463-4467.
115. Gould EA, de Lamballerie X, Zanotto PM de A & **Holmes EC**. (2003). Origins, evolution, and vector/host co-adaptations within the Genus *Flavivirus*. *Adv.Vir.Res.* **59**, 277-314.
114. Guyatt KJ, Twin J, Davis P, **Holmes EC**, Smith GA, Smith IL, Mackenzie JS & Young PL. (2003). A molecular epidemiological study of Australian bat lyssavirus. *J.Gen.Virol.* **84**, 485-496.
113. **Holmes EC**. (2003). Molecular clocks and the puzzle of RNA virus origins. *J.Virol.* **77**, 3893-3897.
112. **Holmes EC**. (2003). Patterns of intra- and inter-host nonsynonymous variation reveal strong purifying selection in dengue virus. *J.Virol.* **77**, 11296-11298.
111. **Holmes EC**. (2003). Error thresholds and the constraints to RNA virus evolution. *Trends Microbiol.* **11**, 543-546.
110. **Holmes EC**, Roberts A, Staines KA & Ellis SA. (2003). Evolution of major histocompatibility complex class I genes in Cetartiodactyls. *Immunogenetics* **55**, 193-202.
109. **Holmes EC** & Twiddy SS. (2003). The origin, emergence and evolutionary genetics of dengue virus. *Infect.Genet.Evol.* **3**, 19-28.

108. Isobe T, **Holmes EC** & Rudenko G. (2003). The transferrin receptor genes of *Trypanosoma equiperdum* are less diverse in their transferrin binding site than those of the broad host range *Trypanosoma brucei*. *J.Mol.Evol.* **56**, 377-386.
107. Jenkins GM & **Holmes EC**. (2003). The extent of codon usage bias in human RNA viruses and its evolutionary origin. *Virus Res.* **92**, 1-7.
106. Starkman S, MacDonald DM, Lewis JCM, **Holmes EC** & Simmonds P. (2003). Geographic and species association of hepatitis B virus genotypes in non-human primates. *Virology* **314**, 381-393.
105. Twiddy SS & **Holmes EC**. (2003). The extent of homologous recombination in the genus *Flavivirus*. *J.Gen.Virol.* **84**, 429-440.
104. Twiddy SS, **Holmes EC** & Rambaut A. (2003). Inferring the rate and time-scale of dengue virus evolution. *Mol.Biol.Evol.* **20**, 122-129.
103. Twiddy SS, Pybus OG & **Holmes EC**. (2003). Comparative population dynamics of mosquito-borne flaviviruses. *Infect.Genet.Evol.* **3**, 87-95.
102. Uzcategui NY, Comach G, Camacho D, Salcedo M, Cabello de Quintana M, Jimenez M, Sierra G, Cuello de Uzcategui R, James WS, Turner S, **Holmes EC** & Gould EA. (2003). Molecular epidemiology of dengue virus type 3 in Venezuela. *J.Gen.Virol.* **84**, 1569-1575.
101. Walker PR, Worobey M, Rambaut A, **Holmes EC** & Pybus OG. (2003). Sexual transmission of HIV in Africa. *Nature* **422**, 679.
100. Brault AC, Powers AM, **Holmes EC**, Woelk CH & Weaver SC. (2002). Positively charged amino acid substitutions in the E2 envelope glycoprotein are associated with the emergence of Venezuelan equine encephalitis virus. *J.Virol.* **76**, 1718-1730.
99. de Lamballerie X, Crochu S, Billoir F, Neyts J, de Micco P, **Holmes EC** & Gould EA. (2002). Genome sequence analysis of Tamara bat virus and its relationship with the genus *Flavivirus*. *J.Gen.Virol.* **83**, 2443-2454.
98. Fares MA & **Holmes EC**. (2002). A revised evolutionary history of hepatitis B virus (HBV). *J.Mol.Evol.* **54**, 807-814.
97. **Holmes EC** & Moya A. (2002). Is the quasispecies concept relevant to RNA viruses? *J.Virol.* **76**, 460-462.
96. **Holmes EC**, Woelk CH, Kassis R & Bourhy H. (2002). Genetic constraints and the adaptive evolution of rabies virus. *Virology* **292**, 247-257.
95. Jenkins GM, Rambaut A, Pybus OG & **Holmes EC**. (2002). Rates of molecular evolution in RNA viruses: a quantitative phylogenetic analysis. *J.Mol.Evol.* **54**, 152-161.
94. Posada D, Crandall KA & **Holmes EC**. (2002). Recombination in evolutionary genomics. *Annu.Rev.Genet.* **36**, 75-97.
93. Pybus OG, Rambaut A, **Holmes EC** & Harvey PH. (2002). New inferences from tree shape: numbers of missing taxa and population growth rates. *Syst.Biol.* **51**, 881-888.
92. Twiddy SS, Farrar JF, Chau NV, Wills B, Gould EA, Gritsun T, Lloyd G & **Holmes EC**. (2002). Phylogenetic relationships and differential selection pressures among genotypes of dengue-2 virus. *Virology* **298**, 63-72.
91. Twiddy SS, Woelk CH & **Holmes EC**. (2002). Phylogenetic evidence for adaptive evolution of dengue viruses in nature. *J.Gen.Virol.* **83**, 1679-1689.
90. Urwin R, **Holmes EC**, Fox AJ, Derrick JP & Maiden MCJ. (2002). Phylogenetic evidence for frequent positive selection and recombination in the meningococcal surface antigen PorB. *Mol.Biol.Evol.* **19**, 1686-1694.
89. Wittke V, Robb TE, Thu HM, Nimmannitya S, Kalayanrooj S, Vaughn DW, Endy TP, **Holmes EC** & Aaskov JG. (2002). Extinction and rapid emergence of strains of dengue 3 virus during an interepidemic period. *Virology* **301**, 148-156.
88. Woelk CH & **Holmes EC**. (2002). Reduced positive selection in vector-borne RNA viruses. *Mol.Biol.Evol.* **19**, 2333-2336.

87. Woelk CH, Pybus OG, Jin L, Brown DWG & **Holmes EC**. (2002). Increased positive selection pressure in persistent (SSPE) versus acute measles virus infections. *J.Gen.Virol.* **83**, 1419-1430.
86. Ballingall KT, Waibochi L, **Holmes EC**, Woelk CH, MacHugh ND, Lutje V & McKeever DJ. (2001). The CD45 locus in cattle: allelic polymorphism and evidence for exceptional positive selection. *Immunogenetics* **52**, 276-283.
85. Dumpis U, **Holmes EC**, Mendy M, Hill AVS, Thursz M, Hall A, Whittle H & Karayiannis P. (2001). Transmission of hepatitis B virus infection in Gambian families revealed by phylogenetic analysis. *J.Hepatol.* **35**, 99-104.
84. Feil EJ, **Holmes EC**, Enright MC, Bessent D, Day NPJ, Chan M-S, Hood D, Zhou JJ & Spratt BG. (2001). Recombination within natural populations of pathogenic bacteria: short-term empirical estimates and long-term phylogenetic consequences. *Proc.Natl.Acad.Sci.USA* **98**, 182-187. (joint first author).
83. Gould EA, de Lamballerie X, Zanotto PM de A & **Holmes EC**. (2001). Evolution, epidemiology and dispersal of flaviviruses revealed by molecular phylogenies. *Adv.Vir.Res.* **57**, 71-103.
82. Goulder PJR, Pasquier C, **Holmes EC**, Liang B, Tang Y, Rosenberg ES, Burchett SK, McIntosh K, Barnardo M, Bunce M, Walker BD, Brander C & Phillips RE. (2001). Mother-to-child transmission of HIV infection and CTL escape through HLA-A2-SLYNTVATL epitope sequence variation. *Immunol.Let.* **79**, 109-116.
81. Hayman A, Moss T, Simmons G, Arnold C, **Holmes EC**, Naylor-Adamson L, Hawkswell J, Allen K, Radford J, Nguyen-Van-Tam L & Balfe P. (2001). Phylogenetic analysis of multiple heterosexual transmission events of subtype B of HIV-1. *AIDS Res.Hum.Retro.* **17**, 689-695.
80. **Holmes EC**. (2001). On the origin and evolution of the human immunodeficiency virus (HIV). *Biol.Rev.Camb.Philos.Soc.* **76**, 239-254.
79. Jenkins GM, Pagel M, Gould EA, Zanotto P M de A & **Holmes EC**. (2001). Evolution of base composition and codon usage bias in the genus *Flavivirus*. *J.Mol.Evol.* **52**, 383-390.
78. Jenkins GM, Worobey M, Woelk CH & **Holmes EC**. (2001). Evidence for the non-quasispecies evolution of RNA viruses. *Mol.Biol.Evol.* **18**, 987-994.
77. Kelleher AD, Long C, **Holmes EC**, Allen RL, Wilson J, Conlon C, Workman C, Shaunak S, Wulfestieg K, Goulder P, Brander C, Ogg G, Sullivan JS, Dyer W, Jones I, McMichael AJ, Rowland-Jones S & Phillips RE. (2001). Clustered mutations in HIV-1 gag are consistently required for escape from HLA-B27 restricted CTL responses. *J.Exp.Med.* **193**, 375-385.
76. Pybus OG, Charleston MA, Gupta S, Rambaut A, **Holmes EC** & Harvey PH. (2001). The epidemic behaviour of the hepatitis C virus. *Science* **292**, 2323-2325.
75. Rambaut A, Robertson DL, Pybus OG, Peeters M & **Holmes EC**. (2001). Phylogeny and the origin of HIV-1. *Nature* **410**, 1047-1048.
74. Uzcategui NY, Camacho D, Comach G, **Holmes EC** & Gould EA. (2001). Molecular epidemiology of dengue-2 virus in Venezuela: evidence for *in situ* viral evolution and recombination. *J.Gen.Virol.* **82**, 2945-2953.
73. Woelk CH & **Holmes EC**. (2001). Variable immune driven natural selection in the attachment (G) glycoprotein of respiratory syncytial virus (RSV). *J.Mol.Evol.* **52**, 182-192.
72. Woelk CH, Jin L, **Holmes EC** & Brown DWG. (2001). Immune and artificial selection in the hemagglutinin (H) glycoprotein of measles virus. *J.Gen.Virol.* **82**, 2463-2474.
71. Worobey M & **Holmes EC**. (2001). Homologous recombination and the molecular evolution of GB virus C/hepatitis G virus. *Mol.Biol.Evol.* **18**, 254-261.
70. De Michelis S, Sewell H-S, Collares-Pereira M, Santos-Reis M, Schouls LM, Benes V, **Holmes EC** & Kurtenbach K. (2000). Genetic diversity of *Borrelia burgdorferi* sensu lato in ticks from mainland Portugal. *J.Clin.Micro.* **38**, 2128-2133.
69. **Holmes EC** & Burch SS. (2000). The causes and consequences of genetic variation in dengue virus. *Trends Microbiol.* **8**, 74-77.

68. Jenkins GM, Woelk C, Rambaut A & **Holmes EC**. (2000). Testing the extent of sequence similarity among viroids, satellite RNAs and HDV. *J.Mol.Evol.* **50**, 98-102.
67. Macdonald DM, **Holmes EC**, Lewis JCM & Simmonds P. (2000). Detection of hepatitis B virus infection in wild caught chimpanzees (*Pan troglodytes verus*); phylogenetic relationships with human and other primate genotypes. *J.Virol.* **74**, 4253-4257.
66. Mooers AØ & **Holmes EC**. (2000). The evolution of base composition and phylogenetic inference. *Trends Ecol.Evol.* **15**, 365-369.
65. Bollyky PL & **Holmes EC**. (1999). Reconstructing the complex evolutionary history of hepatitis B virus. *J.Mol.Evol.* **49**, 130-141.
64. Bourhy H, Kissi B, Audry L, Smreczak M, Sadkowska-Todys M, Kulonen K, Tordo N, Zmudzinski JF & **Holmes EC**. (1999). Ecology and evolution of rabies virus in Europe. *J.Gen.Virol.* **80**, 2545-2558.
63. Ellis SA, **Holmes EC**, Staines KA, Smith KB, Stear MJ, McKeever DJ, MacHugh ND & Morrison WI. (1999). Variation in the number of expressed MHC genes in different cattle class I haplotypes. *Immunogenetics* **50**, 319-328.
62. Grassly NC, Harvey PH & **Holmes EC**. (1999). Population dynamics of HIV-1 inferred from gene sequences. *Genetics* **151**, 427-438.
61. **Holmes EC** & Ellis SA. (1999). Evolutionary history of MHC class I genes in the mammalian order Perissodactyla. *J.Mol.Evol.* **49**, 316-324.
60. **Holmes EC**, Urwin R & Maiden MCJ. (1999). The influence of recombination on the population structure and evolution of the human pathogen *Neisseria meningitidis*. *Mol.Biol.Evol.* **16**, 741-749.
59. **Holmes EC**, Worobey M & Rambaut A. (1999). Phylogenetic evidence for recombination in dengue virus. *Mol.Biol.Evol.* **16**, 405-409.
58. Proutski V, Gritsun TS, Gould EA & **Holmes EC**. (1999). Biological consequences of deletions within the 3'-UTR of flaviviruses may be due to rearrangements of RNA secondary structure. *Virus Res.* **64**, 107-123.
57. Pybus OG, **Holmes EC** & Harvey PH. (1999). The mid-depth method and HIV-1: a practical approach to testing hypotheses of viral epidemic history. *Mol.Biol.Evol.* **16**, 953-959.
56. Smith NH, **Holmes EC**, Donovan GM, Carpenter GA & Spratt BG. (1999). Networks and groups within the genus *Neisseria*: analysis of *argF*, *recA*, *rho* and 16S rRNA sequences from human *Neisseria* species. *Mol.Biol.Evol.* **16**, 773-783.
55. Worobey M & **Holmes EC**. (1999). Evolutionary aspects of recombination in RNA viruses. *J.Gen.Virol.* **80**, 2535-2544.
54. Worobey M, Rambaut A & **Holmes EC**. (1999). Widespread intra-serotype recombination in natural populations of dengue virus. *Proc.Natl.Acad.Sci.USA* **96**, 7352-7357.
53. Zanutto PM de A, Kallas EG, de Souza RF & **Holmes EC**. (1999). Genealogical evidence for positive selection in the *nef* gene of HIV-1. *Genetics* **153**, 1077-1089.
52. **Holmes EC**. (1998). Human immunodeficiency virus, DNA and statistics. *J.Roy.Stat.Soc.A* **161**, 199-208.
51. **Holmes EC**. (1998). Molecular epidemiology and evolution of emerging infectious diseases. *Brit.Med.Bull.* **54**, 531-541.
50. **Holmes EC**. (1998). The molecular epidemiology of dengue virus: the time for big science. *Trop.Med.Int.Health.* **3**, 855-856.
49. **Holmes EC** & Zanutto PM de A. (1998). Genetic drift of human immunodeficiency virus type 1? *J.Virol.* **72**, 886-887.
48. McGuire K, **Holmes EC**, Gao GF, Reid HW & Gould EA. (1998). Tracing the origins of Louping-ill virus by molecular phylogenetic analysis. *J.Gen.Virol.* **79**, 981-988.
47. Proutski V & **Holmes EC**. (1998). SWAN: sliding window analysis of nucleotide sequence variability. *Bioinformatics* **14**, 467-468.

46. Gao GF, Zanotto PM de A, **Holmes EC**, Reid HW & Gould EA. (1997). Molecular variation, evolution and geographical distribution of Louping ill virus. *Acta Virol.* **41**, 259-268.
45. Grassly NC & **Holmes EC**. (1997). A likelihood method for the detection of selection and recombination using nucleotide sequences. *Mol.Biol.Evol.* **14**, 239-247.
44. Gritsun TS, Venugopal K, Zanotto PM de A, Mikhailov MV, Sall AA, **Holmes EC**, Polkinghorne I, Frolova TV, Pogodina VV, Lashkevich VA & Gould EA. (1997). Complete sequence of two tick-borne flaviviruses isolated from Siberia and the United Kingdom: analysis and significance of the 5'UTR and 3'UTR's. *Virus Res.* **49**, 27-39.
43. Proutski V, Gaunt MW, Gould EA & **Holmes EC**. (1997). Secondary structure of the 3'-untranslated region of yellow fever virus: implications for virulence, attenuation and vaccine development. *J.Gen.Virol.* **78**, 1543-1549.
42. Proutski V, Gould EA & **Holmes EC**. (1997). Secondary structure of the 3'-untranslated region of flaviviruses: similarities and differences. *Nuc.Acids Res.* **25**, 1194-1202.
41. Bollyky PL, Rambaut A, Harvey PH & **Holmes EC**. (1996). Recombination between sequences of hepatitis B virus from different genotypes. *J.Mol.Evol.* **42**, 97-102.
49. Garnett GP & **Holmes EC**. (1996). The ecology of emergent infectious disease. *Bioscience* **46**, 127-135.
39. Kearsey SE, Maiorano D, **Holmes EC** & Todorov IT. (1996). The role of MCM proteins in the cell cycle control of genome duplication. *BioEssays* **18**, 183-190.
38. Proutski V & **Holmes EC**. (1996). Primer Master: A new program for the design and analysis of PCR primers. *CABIOS* **12**, 253-255.
37. Simmonds P, Mellor JM, Sakuldamrongpanich T, Nuchaprayoon C, Tanprasert S, **Holmes EC** & Smith DB. (1996). Evolutionary analysis of variants of hepatitis C virus found in South East Asia: comparison with classification based on sequence similarity. *J.Gen.Virol.* **77**, 3013-3024.
36. Zanotto PM de A, Gibbs MJ, Gould EA & **Holmes EC**. (1996). A reevaluation of the higher taxonomy of viruses based on RNA polymerases. *J.Virol.* **70**, 6083-6096.
35. Zanotto PM de A, Gould EA, Gao GF, Harvey PH & **Holmes EC**. (1996). Population dynamics of flaviviruses revealed by molecular phylogenies. *Proc.Natl.Acad.Sci.USA* **93**, 548-553.
34. Zanotto PM de A, Gould EA & **Holmes EC**. (1996). The limits of molecular phylogeny: the case of the genus *Flavivirus* in the family *Flaviviridae*. *Virus Rev.Res.* **1**, 29-38.
33. Boner W, Schlicht H-J, Hanrieder K, **Holmes EC** & Carman WF. (1995). Further characterisation of two types of precore variant HBV isolates from Hong Kong. *J.Infect.Dis.* **171**, 1461-1467.
32. Bonhoeffer S, **Holmes EC** & Nowak MA. (1995). Causes of HIV diversity. *Nature* **376**, 125.
31. Ellis SA, Martin AJ, **Holmes EC** & Morrison WI. (1995). At least four MHC class I genes are transcribed in the horse: phylogenetic analysis suggests an unusual evolutionary history for the MHC in this species. *Eur.J.Immunogenet.* **22**, 249-260.
30. Gritsun TS, **Holmes EC** & Gould EA. (1995). Analysis of flavivirus envelope proteins reveals domains that may determine their antigenicity, tropism and pathogenesis. *Virus Res.* **35**, 307-321.
29. Healey CJ, Smith DB, Walker J, **Holmes EC**, Fleming KA, Chapman RWG & Simmonds P. (1995). Acute hepatitis C infection following sexual exposure. *Gut* **36**, 148-150.
28. **Holmes EC**, Nee S, Rambaut A, Garnett GP & Harvey PH. (1995). Revealing the history of infectious disease epidemics using phylogenetic trees. *Phil.Trans.Roy.Soc.Lond.B* **349**, 33-40.
27. **Holmes EC**, Zhang LQ, Robertson P, Cleland A, Harvey E, Simmonds P & Leigh Brown AJ. (1995). The molecular epidemiology of HIV-1 in Edinburgh. *J.Infect.Dis.* **171**, 45-53.

26. Kasper P, Simmonds P, Schneeweis KE, Kasier R, Matz B, Oldenburg J, Brackmann H-H & **Holmes EC**. (1995). The genetic diversification of the HIV-1 *gag* p17 gene in patients infected from a common source. *AIDS Res.Hum.Retro.* **11**, 1197-1201.
25. McClure MO, Bieniasz PD, Weber JN, Tedder RS, O'Shea S, Banatvala JE, Tudor-Williams G, Simmonds P & **Holmes EC**. (1995). HIV clearance in an infant? *Nature* **375**, 637.
24. Mellor J, **Holmes EC**, Jarvis LM, Yap PL, Simmonds P & The International HCV Collaborative Study Group. (1995). Investigation of the pattern of hepatitis C virus sequence diversity in different geographical regions: implications for virus classification. *J.Gen.Virol.* **76**, 2493-2507.
23. Nee S, **Holmes EC**, Rambaut A & Harvey PH. (1995). Inferring population history from molecular phylogenies. *Phil.Trans.Roy.Soc.B.* **349**, 25-31.
22. Power JP, Lawlor E, Davidson F, **Holmes EC**, Yap PL & Simmonds P. (1995). Molecular epidemiology of an outbreak of infection with hepatitis C virus in recipients of anti-D immunoglobulin. *Lancet* **345**, 1211-1213.
21. Ball JK, **Holmes EC**, Whitwell H & Desselberger U. (1994). Genomic variation of HIV-1: molecular analyses of HIV-1 in sequential blood samples and various organs obtained at autopsy. *J.Gen.Virol.* **75**, 867-879.
20. Donaldson YK, Bell JE, **Holmes EC**, Hughes ES, Brown HK & Simmonds P. (1994). *In vivo* distribution and cytopathology of variants of HIV-1 showing restricted sequence variability in the V3 loop. *J.Virol.* **68**, 5991-6005.
19. Harvey PH, **Holmes EC** & Nee S. (1994). Model phylogenies to explain the real world. *BioEssays* **16**, 767-770.
18. **Holmes EC** & Garnett GP. (1994). Genes, trees and infections: molecular evidence in epidemiology. *Trends Ecol.Evol.* **9**, 256-260.
17. Jeffs PS, **Holmes EC** & Ashburner M. (1994). The molecular evolution of the *Alcohol dehydrogenase* and *Alcohol dehydrogenase*-related genes in the *Drosophila melanogaster* species subgroup. *Mol.Biol.Evol.* **11**, 287-304.
16. Leigh Brown AJ & **Holmes EC**. (1994). The evolutionary biology of human immunodeficiency virus. *Annu.Rev.Ecol.Syst.* **25**, 127-165.
15. Nee S, **Holmes EC**, May RM & Harvey PH. (1994). Extinction rates can be estimated from molecular phylogenies. *Phil.Trans.Roy.Soc.B.* **344**, 77-82.
14. Simmonds P, Alberti A, Alter HJ, Bonino F, Bradley DW, Brechot C, Brouwer JT, **Holmes EC et al.** (1994). A proposed system for the nomenclature of genotypes of hepatitis C virus genotypes. *Hepatology* **19**, 1321-1324.
13. Simmonds P, Smith DB, McOmish F, Yap PL, Kolberg J, Urdea MS & **Holmes EC**. (1994). Identification of genotypes of hepatitis C virus by sequence comparisons in the core, E1 and NS-5 regions. *J.Gen.Virol.* **75**, 1053-1061.
12. **Holmes EC**, Simmonds P & Leigh Brown AJ. (1993). Sequence data as evidence. *Nature* **364**, 766.
11. **Holmes EC**, Zhang LQ, Simmonds P, Rogers AS, & Leigh Brown AJ. (1993). Molecular investigation of HIV infection in a patient of an HIV-infected surgeon. *J.Infect.Dis.* **167**, 1411-1414.
10. Rice PS, Simmonds P, Smith DB & **Holmes EC**. (1993). Heterosexual transmission of hepatitis C virus. *Lancet.* **342**, 1052-1053.
9. Rigby MA, **Holmes EC**, Pistello M, Mackay N, Leigh Brown AJ & Neil J. (1993). Evolution of structural proteins of feline immunodeficiency virus; molecular epidemiology and evidence of selection for change. *J.Gen.Virol.* **74**, 425-436.
8. Rogers AS, Froggatt JW, Townsend T, Gordon T, Leigh Brown AJ, **Holmes EC**, Zhang LQ & Moses H. (1993). Investigation of potential HIV transmission to the patients of an HIV-infected surgeon. *JAMA* **269**, 1795-1801.

7. Simmonds P, **Holmes EC**, Cha TA, Chan S-W, McOmish F, Irvine B, Beall E, Yap PL, Kolberg J & Urdea MS. (1993). Classification of hepatitis C virus into 6 major genotypes and a series of subtypes by phylogenetic analysis of the NS-5 region. *J.Gen.Virol.* **74**, 2391-2399.
6. Simmonds P, McOmish F, Yap PL, Chan S-W, Lin CK, Dusheiko G, Saeed AA & **Holmes EC**. (1993). Sequence variability in the 5' non-coding region of hepatitis C virus: identification of a new virus type and restrictions on sequence diversity. *J.Gen.Virol.* **74**, 661-668.
5. Zhang LQ, Leigh Brown AJ, **Holmes EC**, Cleland A, Mckenzie P & Simmonds P. (1993). Selection for specific sequences in the external envelope protein of HIV-1 upon primary infection. *J.Virol.* **67**, 3345-3356.
4. Chan S-W, McOmish F, **Holmes EC**, Dow B, Peutherer JF, Follet E, Yap PL & Simmonds P. (1992). Analysis of a new hepatitis C virus type and its phylogenetic relationship to existing variants. *J.Gen.Virol.* **73**, 1131-1141.
3. **Holmes EC**, Zhang LQ, Simmonds P, Ludlam CA & Leigh Brown AJ. (1992). Convergent and divergent sequence evolution in the surface envelope glycoprotein of human immunodeficiency virus type 1 within a single infected patient. *Proc.Natl.Acad.Sci.USA* **89**, 4835-4839.
2. **Holmes EC**. (1991). Different rates of substitution may produce different phylogenies of the eutherian mammals. *J.Mol.Evol.* **33**, 209-215.
1. **Holmes EC**, Pesole G & Saccone C. (1989). Stochastic models of molecular evolution and the estimation of phylogeny and rates of nucleotide substitution in the hominoid primates. *J.Hum.Evol.* **18**, 775-794.

Book Chapters

23. **Holmes EC**. (2016). Evolution of RNA viruses. In *Encyclopedia of Evolutionary Biology*. (Ed. RI Kliman). pp. 476-483. Elsevier Inc.
22. **Holmes EC**. (2013). Virus evolution. In *Fields Virology, 6th Edition*. (Ed. DM Knipe & PM Howley). pp. 286-313. Lippincott Williams & Wilkins, Philadelphia.
21. **Holmes EC**. (2008). Comparative studies of RNA virus evolution. In *Origin and Evolution of Viruses, 2nd Edition*. (Ed. E. Domingo, CR Parrish & JJ Holland). pp. 119-134. Academic Press, London, UK.
20. **Holmes EC**. (2007). The evolution of viral emergence. In *Novel and Re-Emerging Respiratory Viral Diseases*. Novartis Symposium 290. pp. 17-31. John Wiley & Sons, Chichester, UK.
19. **Holmes EC**. (2006). The evolutionary biology of dengue virus. In *New Treatment Strategies for Dengue and other Flaviviral Diseases*. Novartis Symposium 277. pp. 177-187 (Discussion 187-192). John Wiley & Sons, Chichester, UK.
18. **Holmes EC** & Rambaut A. (2005). Evolutionary genetics and the emergence of SARS coronavirus. In *SARS: A Case Study in Emerging Infections*. (Ed. AR McLean, RM May, J Pattison & RA Weiss). pp 16-23. Oxford University Press, Oxford.
17. **Holmes EC**. The evolution of virulence in AIDS viruses. (2004). In *Evolution: From Molecules to Ecosystems*. (Ed. A Moya & E. Font). pp. 69-81. Oxford University Press, Oxford.
16. **Holmes EC**. (2003). Evolutionary genetics and emergence of RNA virus diseases. In *The Evolution of Population Biology*. (Ed. RS Singh & MK Uyenoyama). pp. 391-410. Cambridge University Press, Cambridge.
15. **Holmes EC**. (2002). Acquired Immune Deficiency Syndrome: Origins and Phylogeny of HIV. In *Encyclopedia of Evolution*. (Ed. M Pagel). pp. 1-6. Oxford University Press, New York.
14. **Holmes EC**. (2002). Viruses. In *Encyclopedia of Evolution*. (Ed. M Pagel). pp. 1136-1141. Oxford University Press, New York.

13. Ellis SA, **Holmes EC**, Staines KA & Morrison WI. (2000). The evolution of MHC class I genes in cattle. In *Major Histocompatibility Complex*. (Ed. M Kasahara). pp. 273-278. Springer-Verlag, Tokyo.
12. **Holmes EC** & Zanotto PM de A. (2000). The ecology and evolution of human hepatitis viruses. In *Molecular Epidemiology of Infectious Diseases* (Ed. RCA Thompson). pp. 181-193. Arnold Publishers, London.
11. **Holmes EC**. (1999). Molecular phylogenies and the genetic structure of viral populations. In *Evolution in Health & Disease*. (Ed. S Stearns). pp. 173-182. Oxford University Press.
10. **Holmes EC**, Pybus OG & Harvey PH. (1999). The molecular population dynamics of HIV-1. In *The Evolution of HIV*. (Ed. KA Crandall). pp. 177-207. John Hopkins University Press.
9. Read AF, Aaby P, Antia R, Ebert D, Ewald PW, Gupta S, **Holmes EC**, Sasaki A, Shields D, Taddei F & Moxon R. (1999). What can evolutionary biology contribute to understanding virulence? In *Evolution in Health & Disease*. (Ed. S Stearns). pp. 205-215. Oxford University Press.
8. **Holmes EC**, Bartley LM & Garnett GP. (1998). The emergence of dengue: past, present and future. In *Emerging Infections* (Ed. RM Krause). pp. 301-325. Academic Press.
7. Gould EA, Zanotto PM de A & **Holmes EC**. (1997). The genetic evolution of flaviviruses. In *Factors in the Emergence of Arbovirus Disease*. (Ed. JF Saluzzo & B Dodet). pp. 51-63. Elsevier, Paris.
6. **Holmes EC**, Bollyky PL, Nee S, Rambaut A, Garnett GP & Harvey PH. (1996). Using phylogenetic trees to reconstruct the history of infectious disease epidemics. In *New Uses for New Phylogenies* (Ed. PH Harvey, AJ Leigh Brown, J Maynard Smith & S Nee). pp. 169-186. Oxford University Press.
5. **Holmes EC**, Gould EA & Zanotto PM de A. (1996). An RNA virus tree of life? In *Evolution of Microbial Life* (Ed. DMcL Roberts, P Sharp, G Alderson & MA Collins). pp. 127-144. *Society for General Microbiology Symposium 54*, Cambridge University Press.
4. Nee S, **Holmes EC**, Rambaut A & Harvey PH. (1996). Inferring population history from molecular phylogenies. In *New Uses for New Phylogenies* (Ed. PH Harvey, AJ Leigh Brown, J Maynard Smith & S Nee). pp. 66-80. Oxford University Press.
3. Nee S, **Holmes EC**, May RM & Harvey PH. (1995). Estimating extinction from molecular phylogenies. In *Estimating Extinction Rates*. (Ed. JL Lawton & RM May). pp. 164-182. Oxford University Press.
2. Harvey PH, **Holmes EC**, Mooers AØ & Nee S. (1994). Inferring evolutionary processes from molecular phylogenies. In *Models in Phylogeny Reconstruction*. (Ed. RW Scotland, DJ Siebert & DM Williams). Systematics Association Special Volume Series **52**, 313-333.
1. **Holmes EC**, Simmonds P, Cha T-A, Chan S-W, McOmish F, Irvine B, Beall E, Yap PL, Kolberg J & Urdea MS. (1994). Derivation of a rational nomenclature for hepatitis C virus by phylogenetic analysis of the NS-5 region. In *Viral Hepatitis and Liver Disease*. (Ed. K Nishioka, H Suzuki, S Mishiro & T Oda). Springer-Verlag.

Commentaries & Other Publications

26. **Holmes EC**, Rambaut A & Andersen KG. The pandemic prediction delusion. (Submitted to *Nature*).
25. Zhang Y-Z, Shi M & **Holmes EC**. (2018). Using metagenomics to characterize an expanding virosphere. *Cell* **172**, 1168-1172.
24. **Holmes EC**. (2017). V is for virosphere. *Cell* **169**, 770.
23. **Holmes EC**. (2016). The expanding virosphere. *Cell Host & Microbe* **20**, 279-280.
22. **Holmes EC**. (2014). Freezing viruses in time. *Proc.Natl.Acad.Sci.USA* **111**, 16643-16644.
21. **Holmes EC**. (2011). Genomics: Plague's progress (News & Views). *Nature* **478**, 465-466.
20. **Holmes EC**. (2010). Emerging Viruses: Past, Present and Future. *medicSA (Magazine of the Australian Medical Association (South Australia) Inc.* Nov/Dec. 2010, 19-20.

19. **Holmes EC.** (2010). Malaria: The gorilla connection (News & Views). *Nature* **467**, 404-405.
18. **Holmes EC.** (2010). Perspectives: Helping the resistance. *Science* **328**, 1243-1244.
17. Halloran ME & **Holmes EC.** (2009). Invited commentary: Evaluating vaccination programs using genetic sequence data. *Am.J.Epi.* **170**, 1464-1466.
16. **Holmes EC.** (2009). Preface to *The Phylogenetic Handbook: A Practical Approach to Phylogenetic Analysis and Hypothesis Testing, 2nd Edition*. Edited by P. Lemey, M. Salemi & A-M Vandamme. Cambridge University Press.
15. Pardini MI de MC, Jamal JF, Durigon EJ, Massad E, Perez JF, Pinho JRR, **Holmes EC** & Zanotto PM de A. (2008). Boosting virology in Brazil. *PLoS Biol.* **6**:e57.
14. **Holmes EC.** (2007). When HIV spread afar. *Proc.Natl.Acad.Sci.USA.* **104**, 18351-18352.
13. **Holmes EC.** (2007). Ancient lentiviruses leave their mark. *Proc.Natl.Acad.Sci.USA* **104**, 6095-6096.
12. **Holmes EC.** (2006). The evolution of viral emergence. *Proc.Natl.Acad.Sci.USA* **103**, 4803-4804.
11. **Holmes EC.** (2005). On being the right size (News & Views). *Nat.Genet.* **37**, 923-924.
10. **Holmes EC**, Taubenberger JK & Grenfell BT. (2005). Editorial: Heading off an influenza pandemic. *Science* **309**, 989.
9. **Holmes EC.** (2004). Adaptation and immunity. *PLoS Biol.* **2**, 1267-1269.
8. **Holmes EC.** (2004). Los virus emergentes (in Spanish). *Pasajes* **14**, 5-12.
7. **Holmes EC.** (2004). Virology: 1918 and all that (Perspectives). *Science* **303**, 1787-1788.
6. **Holmes EC.** (2001). Human immunodeficiency virus (In 'Evolution in the century of biology'). *Am.Nat.* **158**, S13.
5. **Holmes EC.** (1999). Genomics, phylogenetics and epidemiology. *Microbiology Today* **26**, 162-163.
4. **Holmes EC.** (1998). The molecular archaeology of infectious disease. *SGM Quart.* **25**, 56-57.
3. **Holmes EC.** (1996). Reconstructing the history of viral epidemics. *Biologist* **43**, 54-57.
2. **Holmes EC** & Harvey PH. (1994). Spinning the web of life. *Current Biol.* **4**, 841-843.
1. **Holmes EC** & Harvey PH. (1993). Fitting the bill. *Current Biol.* **3**, 776-777.

Book Reviews

10. *Pandemics: What Everyone Needs to Know.* (2014). By PC Doherty. *PLoS Biol.* **12**: e1001780.
9. *The Viral Storm: The Dawn of a New Pandemic Age.* (2011). By N Wolfe. *Nature* **478**, 319-320.
8. *Inferring Phylogenies.* (2004). By J Felsenstein. *Quart.Rev.Biol.*
7. *Japanese Encephalitis and West Nile Viruses. Current Topics in Microbiology and Immunology*, vol. 267. (2002). Edited by JS Mackenzie, ADT Barrett & V Deubel. *Microbiol.Today.*
6. *Evolution: An Introduction.* (2001). By SC Stearns & RF Hoekstra. *J.Biogeog.*
5. *Origin and Evolution of Viruses.* (2000). Edited by E Domingo, R Webster & JH Holland. *Quart.Rev.Biol.*
4. *Molecular Basis of Virus Evolution.* (1995). Edited by A Gibbs, CH Calisher & F García-Arenal. *SGM Quarterly.*
3. *The Evolutionary Biology of Viruses.* (1995). Edited by SS Morse. *Quart.Rev.Biol.*
2. *Molecular Ecology In Focus.* (1992). By AR Hoezel & GA Dover. *Genetical.Res.Camb.*
1. *The Fundamentals of Molecular Evolution.* (1991). By W-H Li & D Graur. *Am.J.Phys.Anth.*

Conference Abstracts & Proceedings

25. Saavedra A, Wood S, Geoghegan JL, **Holmes EC** & Durrant-Whyte H. (2015). Modelling the spread of influenza in Western Australia. *First International Workshop on Population Informatics for Big Data (ACM-SIGKDD PopInfo'15)*. Association for Computing Machinery (ACM), Sydney.
24. **Holmes EC**. (2013). RNA virus evolution: a guide for the perplexed. *Antiviral Therapy* **18** S1, A5-A5.
23. Simmons HE, **Holmes EC**, Gildow FE *et al.* (2012). The incidence of seed transmission of Zucchini yellow mosaic virus (ZYMV) over two generations. *Phytopathol.* **102** S1, 7-7.
22. Balmaseda A, Juan CM, Yolanda T, **Holmes EC et al.** (2009). Trends in patterns of dengue transmission over four years of a pediatric cohort study in Nicaragua. *Am.J.Trop.Med.Hyg.* **81**, S27.
21. **Holmes EC**. (2009). The evolutionary genomics of dengue virus. In *Arbovirus Research in Australia* (Ed. P Ryan, J Aaskov & R Russell). Vol. **10**, 69.
20. Jarman RG, Klungthong C, **Holmes EC**, Chinnawirotpisan P, Rodpradit P, Pimgate C, Scott TW, Rothman AL, Yoon IK & Gibbons RV. (2008). Genetic analysis of dengue viruses collected from mosquitoes and humans during dengue cluster investigations in Thailand. *Am.J.Trop.Med.Hyg.* **79**, S37.
19. Allicock OM, Auguste AJ Dunham EJ, Pybus OG, **Holmes EC** & Carrington CV. (2007). Genetic diversity and positive selection in Eastern equine encephalitis virus. *Am.J.Trop.Med.Hyg.* **77**, S176.
18. Auguste AJ, Dunham EJ, Pybus OG, **Holmes EC** & Carrington CV. (2007). Migration and transmission history of St. Louis encephalitis virus. *Am.J.Trop.Med.Hyg.* **77**, S197.
17. Holmes EC. (2007). The evolution and epidemiology of dengue virus. *Salud Pública de México* **49**, E296-E300.
16. Rodriguez-Roche R, Alvarez M, **Holmes EC**, Bernardo L, Flores GK, Halstead SB & Guzman MG. (2006). Dengue hemorrhagic fever caused by sequential dengue 1-3 infections at a long interval: Havana epidemic, 2001-2002. *Am.J.Trop.Med.Hyg.* **75**, S30.
15. Zhang C, Mammen MP, Klungthong C, Chinnawirotpisan P, Rodpradit P, Kalayanaroj S & **Holmes EC**. (2005). The structure of genetic diversity and the evolutionary processes of dengue viruses circulating in Thailand. *Am.J.Trop.Med.Hyg.* **73**, S5.
14. Kurtenbach K, De Michelis S, Sewell HS, Etti S, Schafer SM, **Holmes EC**, Hails R, Collares-Pereira M, Santos-Reis M, Hanincova K, Labuda M, Bormane A & Donaghy M. (2002). The key roles of selection and migration in the ecology of Lyme borreliosis. *Int.J.Med.Micro.* **291** (Suppl. 33.), 152-154.
13. Dingle KE, Colles F, Urwin R, **Holmes EC et al.** (2001). The population structure of *Campylobacter jejuni* is shaped by genetic recombination in combination with selection. *IJMM Int.J.Med.Micro.* **291** S31, 63.
12. Grassly NC & **Holmes EC**. (1998). The use of Monte Carlo simulation to infer population dynamic history from DNA sequence data. In *Proceedings of the Trinational Workshop on Molecular Evolution*. (Ed. MK Uyenoyama, N Takahata & A von Haeseler). pp. 91-112. Duke Publications Group, Durham, NC.
11. Bollyky PL, Rambaut A, Grassly N, Carman WF & **Holmes EC**. (1997). Hepatitis B virus has a recent new world evolutionary origin. *Hepatology* **26**, 765.
10. Bollyky PL, Yasmin M, **Holmes EC**, Trautwein C, Fagan EA & Carman WF. (1997). Viruses from unrelated fulminant hepatitis B cases cluster in phylogenetically distinct lineages, each containing unique motifs of nucleotide and Hbx variants which have increased transcriptional activity in vitro. *J.Hepatology* **26** (Suppl. 1), 67.
9. Yasmin M, Bollyky PL, **Holmes EC**, Carman WF & Fagan EA. (1997). Genotype D variants with high replication efficiency predict good prognosis in fulminant hepatitis B. *J.Hepatol.* **26**, S761.

8. Bonhoeffer S, **Holmes EC** & Nowak MA. (1995). Varying selection pressure in HIV-1 infection. *J.Acquir.Immun.Def.Synd.Hum.Retro.* **10**, 85.
7. Harvey PH, **Holmes EC**, Rambaut A & Nee S. (1995). How to reveal viral population history from gene sequence data. In *Immunobiology of Viral Infection. Proceedings 3rd International Congress of Veterinary Virology.* (Ed. M Schwyzer, M Ackermann, G Bertoni, R Kocherhans, K McCullough, M Engels, R Wittek & R Zanoni).
6. Simmonds P, Hughes ES, Livingstone WJ, Donaldson YK, **Holmes EC**, Brown HK & Bell JE. (1995). Restricted sequence variability of the HIV-1 V3 loop in vivo. *J. Cell. Biochem.* **S21**, 244.
5. **Holmes EC.** (1993). The pattern and process of base substitution in immunodeficiency viruses. *Binary* **5**, 189.
4. Leigh Brown AJ, Zhang LQ, **Holmes EC** & Simmonds P. (1993). Selection on V3 loop sequences in early HIV infection. *AIDS Res.Hum.Retro.* **9 (S1)**, 100.
3. Leigh Brown AJ, Zhang LQ, Robertson P, Cleland A, **Holmes EC** & Simmonds P. (1993). Studies on virus load and sequence in HIV transmission. *J.Cell.Biochem.* **S17**, 4.
2. Leigh Brown AJ, Zhang LQ, **Holmes EC** & Simmonds P. (1992). Selection for specific V3 loop sequences on transmission of HIV. *J.Cell.Biochem.* **S16**, 51.
1. **Holmes EC.** (1987). The phylogenetic position of the primates within the eutheria: molecular evidence. (Abstract issue for XXII congress of the International Primatological Society) *Int.J.Primat.* **8**, 235.