

William Harvey

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Employment

- 2017-present MRC and BBSRC UKRI Innovation Fellow, University of Glasgow
Using a comparative One Health approach to investigate the structural basis of antigenic variation among human and avian influenza viruses.
- 2016-2017 PDRA, University of Glasgow. PI: Prof. Louise Matthews.
BBSRC and NSF-funded project on antimicrobial resistance at the human-animal interface.
- 2016 PDRA, University of Glasgow. PI: Dr. Richard Reeve.
Impact award with the Worldwide Influenza Centre, The Francis Crick Institute.
- 2012-2015 Graduate teaching assistant, University of Glasgow.

Education

- 2011-2016 **Ph.D.** in Ecology and Evolutionary Biology, **University of Glasgow**.
Quantifying the genetic basis of antigenic variation among human influenza A viruses. Supervisors: Dr. Richard Reeve, Prof. John McCauley (The Francis Crick Institute, London) & Prof. Dan Haydon.
- 2006-2010 **B.Sc. (Hons)** Biological Sciences (Evolutionary Biology) – First Class, **University of Edinburgh**. Dissertation: *Investigating the cause of sex ratio bias in *Drosophila miranda**. Supervisor: Prof. Brian Charlesworth.

Funding and Awards

- 2017 **MRC/BBSRC** Three-year Skills Development Fellowship, Institute of Health and Wellbeing, University of Glasgow.
- 2016 **British Council Newton Fund** Funded to present at UK-Malaysia Vaccinology Workshop. Putrajaya, Malaysia.
University of Glasgow Knowledge Exchange Award (Co-I – PI: Richard Reeve) to prepare and release the archive of data on human seasonal influenza H1N1 from the Worldwide Influenza Centre at the Francis Crick Institute.
- 2015 **BBSRC/British Council** Funded to present at Food Security: Improving Approaches to Prevent and Control Viral Diseases of Livestock and Poultry. Istanbul, Turkey.
- 2014 **BBSRC Sparking Impact Award** (Co-I – PI: Richard Reeve) to fund organisation of a symposium.
- 2013 **David Searle Prize** for academic writing, University of Glasgow.
- 2011 **MRC** Ph.D. Studentship University of Glasgow.

Publications

- Peacock TP*, **Harvey WT***, Sadeyen JR, Iqbal M & Reeve R (2018) The molecular basis of antigenic variation among A(H9N2) avian influenza viruses. *bioRxiv* doi: 10.1101/312967 *Contributed equally.
- Davies V, **Harvey WT**, Reeve R & Husmeier D (2017) Improving the identification of antigenic sites in the H1N1 Influenza virus through accounting for the experimental structure in a sparse hierarchical Bayesian model. *Arxiv*: 1710.06366.
- Goldstein EJ, **Harvey WT**, Wilkie GS, Shepherd SJ, MacLean AR, Murcia PR & Gunson RN (2017) Integrating patient and whole genome sequencing data to provide insights into the epidemiology of seasonal influenza A(H3N2) viruses. *Microbial Genomics* doi:10.1099/mgen.0.000137.

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Davies V, Reeve R, **Harvey WT**, Maree FF & Husmeier D (2017) A sparse hierarchical Bayesian model for detecting relevant antigenic sites in virus evolution. *Computational Statistics* doi:10.1007/s00180017-0730-6.

Harvey WT, Benton DJ, Gregory V, Hall JPJ, Daniels RS, Bedford T, Haydon DT, Hay AJ, McCauley JW & Reeve R (2016) Identification of low- and high-impact hemagglutinin amino acid substitutions that drive antigenic drift of influenza A(H1N1) viruses. *PLoS Pathogens* 12: e1005526.

Reeve R, Borley DW, Maree FF, Upadhyaya S, Lukhwareni A, Esterhuysen JJ, **Harvey WT**, Blignaut B, Fry EE, Parida S, Paton DJ and Mahapatra M (2016) Tracking the antigenic evolution of foot-and-mouth disease virus. *PLoS ONE* 11: e0159360.

Davies V, Reeve R, **Harvey WT** and Husmeier D (2016) Selecting random effect components in a sparse hierarchical Bayesian model for identifying antigenic variability. In: *Computational Intelligence Methods for Bioinformatics and Biostatistics: CIBB 2015 Lecture Notes in Computer Science*.

Formal reports and data release

Łuksza M, **Harvey WT**, Reeve R & Lässig M (Feb. & Sep. 2016, Feb. & Sep. 2017) Formal reports detailing antigenic analyses and prediction of influenza A/H3N2 evolution contributed to biannual WHO Consultation and Information Meetings on the Composition of Influenza Virus.

Gregory V, **Harvey WT et al.** (2016) Human former seasonal Influenza A(H1N1) haemagglutination inhibition data 1977–2009 from the WHO Collaborating Centre for Reference and Research on Influenza, London, UK. DOI: 10.5525/gla.researchdata.289.

Conference abstracts and invited presentations

2016 British Ecological Society annual meeting, Liverpool, UK.

UK–Malaysia Vaccinology Workshop, Putrajaya, Malaysia.

2015 Food Security: Improving Approaches to Prevent and Control Viral Diseases of Livestock and Poultry in Istanbul, Turkey.

2014 Invited speaker at Symposium on Viral Evolution, University of Cologne, Germany.
EuFMD, Cavtat, Croatia.

Invited speaker at Glasgow Virology Workshop, University of Glasgow.

2013 Epidemics4, Amsterdam, Netherlands.

Professional Development

Organisation/ teamwork Conceived and jointly co-ordinated a symposium ‘*From viral genotype to phenotype*’ with local and international speakers. Developed links with the Pirbright Institute, leading to ongoing collaboration on avian influenza and the NHS West of Scotland Specialist Virology Centre.

Policy/ Outreach Developed ongoing partnership with international collaborators providing reports to biannual WHO-coordinated meetings at which influenza vaccine composition is decided. Participation as STEM ambassador and at Glasgow Science Festival.

Teaching Teaching assistant on L2, L3 and L4 undergraduate biology courses, and Advanced Statistics and R courses for MSc in Quantitative Methods in Biodiversity, Conservation and Epidemiology for IBAHCM.

Technical Skills

Quantitative techniques Model testing using maximum-likelihood and Bayesian inference, Molecular phylogenetics, phylogeography, phylogenetic comparative methods, ecological diversity analysis, epidemiological modelling, descriptive data analysis (e.g. MDS).

Software R, BUGS/JAGS, BEAST, HyPhy, PyMOL, Latex, Python.

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Laboratory Mutagenesis, reverse-genetics, transfection, cell-culture, PCR, sequencing prep., haemagglutinin inhibition assay.