

**BIOGRAPHICAL SKETCH**

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NAME: Gavin James Smith

POSITION TITLE: Associate Professor

EDUCATION/TRAINING (*Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.*)

INSTITUTION AND LOCATION	DEGREE (if applicable)	Completion Date MM/YYYY	FIELD OF STUDY
The University of Melbourne, Australia	BSc	12/1995	Botany and Ecology
The University of Melbourne, Australia	BSc (Hons)	12/1996	Biological Systematics
The University of Hong Kong, Hong Kong SAR	PhD	10/2003	Molecular Systematics

**A. Personal Statement**

My research program focuses on the ecology, genetic and antigenic evolution, molecular diagnostics, pathogen discovery, population dynamics, molecular epidemiology and interspecies transmission of emerging infectious diseases. To achieve this, I conduct field surveillance studies on both human and animal populations aimed at collection and characterization of viruses for disease detection, prevention and control and for use in ecological and evolutionary studies. My research aims to explicitly link surveillance efforts with research into pathogenesis and host response to address the research priorities including the integration of ecological and phenotypic data for evolutionary hypothesis testing; the epidemiological and evolutionary dynamics of human respiratory viruses; evolution and transmission in animal species; and interspecies transmission and disease emergence.

**B. Positions and Honors****Positions and Employment**

2003-2006	<u>Postdoctoral Fellow</u> , Department of Microbiology, The University of Hong Kong, Hong Kong
2006-2010	<u>Research Assistant Professor</u> , State Key Laboratory of Emerging Infectious Diseases, Department of Microbiology, The University of Hong Kong, Hong Kong
2007-2010	<u>Honorary Assistant Professor</u> , Department of Microbiology, The University of Hong Kong, Hong Kong, Hong Kong SAR
2007- 2021	<u>Member</u> , NIAID/NIH Center of Excellence for Influenza Research and Surveillance, St Jude Children's Research Hospital, Memphis, TN, USA
2010- 2012	<u>Honorary Associate Professor</u> , Department of Microbiology, The University of Hong Kong, Hong Kong, Hong Kong SAR
2010-present	<u>Associate Professor</u> , Program in Emerging Infectious Diseases, Duke-NUS Graduate Medical School, Singapore
2011- present	<u>Associate Research Professor</u> , Duke Global Health Institute, Duke University, Durham, NC, United States
2011-present	<u>Visiting Scientist</u> , WHO Collaborating Centre for Reference and Research on Influenza, VIDRL, Melbourne, Australia

**Other Experience and Professional Memberships**

Chair, Orthomyxoviridae Study Group, International Committee on Taxonomy of Viruses, Virology Division of the International Union of Microbiological Sciences, 2014–present

Member, Local Review Panel Member, Clinical Sciences Individual Research Grants (CS-IRG), National Medical Research Council, Ministry of Health, Singapore, February 2014–December 2015

Member, Senate, National University of Singapore, July 2012–present

Member, Local Review Panel, Cooperative Basic Research Grant (CBRG), National Medical Research Council, Ministry of Health, Singapore, February 2012–December 2013

Member, Influenza Research Database ([www.fludb.org](http://www.fludb.org)) Scientific Working Group, 2010–present

Member, Orthomyxoviridae Study Group, International Committee on Taxonomy of Viruses, Virology Division of the International Union of Microbiological Sciences, 2010–2014

Member, National Institutes of Health (NIH), National Institute of Allergy and Infectious Diseases (NIAID), Division of Microbiology and Infectious Diseases (DMID) Blue Ribbon Panel on Genomics Research, February, 2010

Invited Observer, World Health Organization Consultation on the Composition of Influenza Vaccines, 2008–2010

Secretary, International Society for Influenza and other Respiratory Virus Diseases, 2007–2015

Co-Chair, WHO/OIE/FAO Working Group on Evolution and Nomenclature of Influenza A (H5N1) Virus, 2006–present

### **Honors**

2013 Elected Fellow (FASM) of the Australian Society for Microbiology

2012 Research Output Prize 2011–12, Li Ka Shing Faculty of Medicine, The University of Hong Kong, awarded for “Long-term evolution and transmission dynamics of swine influenza A virus” published in *Nature*, 2011

2011 Beijerinck Guest Chair, Beijerinck Virology Fund, Royal Netherlands Academy of Arts and Sciences, Kingdom of the Netherlands

2010 Research Output Prize 2009–10, Li Ka Shing Faculty of Medicine, The University of Hong Kong, awarded for “Origins and evolutionary genomics of the 2009 swine-origin H1N1 influenza A epidemic” published in *Nature*, 2010

2010 NIAID/NIH Selected Science Advances 2009 awarded for Rapid characterization of the 2009 H1N1 influenza virus

2010 DMID/NIAID/NIH Special Recognition Award “In honor of extraordinary work in H1N1 influenza research”

2009 Outstanding Young Researcher Award 2008–2009, The University of Hong Kong, Hong Kong SAR, China

2009–2013 Professional Member (MASM), Australian Society for Microbiology

2008 Runner-up in Life Sciences, 1<sup>st</sup> Annual ASAIHL-Scopus Young Scientist Awards, Association of Southeast Asian Institutions of Higher Learning, ASAIHL International Office, Thailand

2007–2014 Career Development Award for research into the ecology, evolution and population genetics of influenza A (H5N1) virus. Awarded as part of the NIAID Centers of Excellence for Influenza Research and Surveillance, National Institute of Allergy and Infectious Diseases, National Institutes of Health, USA

2007 Chris Baldock Prize for Early Career Researcher, Australian Biosecurity CRC for Emerging Infectious Diseases, Australia

2006 Research Output Prize 2005–06, Li Ka Shing Faculty of Medicine, The University of Hong Kong, awarded for “H5N1 virus outbreak in migratory waterfowl” published in *Nature*, 2005

### **C. Contribution to Science**

My past research has described the molecular epidemiology and evolutionary dynamics of both high and low pathogenic avian influenza A virus, seasonal and pandemic influenza A virus in humans and the spatial dynamics of influenza A virus in wild bird populations. Specifically my group has helped track the spread and characterized the genotypic and phenotypic evolution of H5, H6 and H9 viruses in China and surrounding regions, elucidated the evolutionary dynamics and reassortment history of H5N1 and further described the evolutionary dynamics of virus lineage competition in wild bird populations. From my work a mechanism for the emergence of pandemic influenza was proposed that was validated by the 2009 pandemic and my group has made a significant contribution to determining the global migration and population structure of seasonal influenza. With the emergence of the H1N1/2009 pandemic influenza virus, we described the

swine origins of the current pandemic virus and showed that each segment of the novel virus genome was placed within well-established swine influenza lineages that have been circulating in swine for more than 10 years prior to the current outbreak. Our evolutionary analyses of 12 years of systematic surveillance of swine influenza viruses in Hong Kong, including genetic, antigenic analyses and in vivo swine experiments, described the dynamic changes of influenza A viruses in swine and showed that reassortment was linked in antigenic change in swine influenza viruses. We also recently described the ecological and evolutionary dynamics of avian influenza A virus in wild waterfowl and shorebirds to predict virus movement in the United States using data from over 30 years of continuous virological surveillance. Our results suggest that, after initially being restricted to one flyway, an introduced virus lineage would be able to spread across the United States within months, providing critical information to inform surveillance for pandemic preparedness in the advent of novel virus introduction.

In summary, my studies have played a key role in global efforts to control influenza outbreaks by providing genetic analysis to expert committees' formulating policy in this area, including pre-pandemic vaccine strain selection and by introducing cutting edge methodologies in bioinformatics and molecular evolution analysis into influenza research to provide a greater understanding of the ecology of influenza viruses. Another key part of my work has been in engaging scientists in the region to assist in developing local research and technical capacity for disease detection, prevention and control.

My current research is directed at efforts to better understand viral disease ecosystems in Asia, specifically the animal-human interface, to support rational implementation of disease control and intervention strategies, and integrates ideas from a number of different fields including evolutionary genetics, virology, ecology, and infectious disease epidemiology. My team conducts human and animal disease surveillance isolates and characterizes pathogens (genetic and phenotypic), then we conduct large-scale analyses to generate hypotheses that are tested in the lab using tissue culture and animal models. I am primarily interested in the roles played by mutation, natural selection, recombination/reassortment and host immune response on virus diversity within an individual, during transmission within a population and during inter-species transmission between hosts. My focus will remain on influenza but I am gradually expanding my repertoire to include (mostly) other respiratory viruses, such as parainfluenza and adenovirus, for which relatively little epidemiological and genetic data are available. Currently I have surveillance programs in Singapore (human and animal), Indonesia (human), Cambodia (human and swine) and the Philippines (human) that have been running for at least 2 years and have been yielding respiratory pathogens and associated epidemiological data.

As an example, for the last three years we have been sampling small mammals (e.g. rats, shrews, squirrels) in Singapore in order to characterize both their population structure and ecology and the epidemiological and evolutionary dynamics of small mammal-borne viruses and bacteria with zoonotic potential. Our central hypothesis is that small mammals represent a reservoir harboring infectious agents with the ability to transmit to, and cause disease in, humans. Areas of high human density, such as Singapore, support peridomestic species that are incriminated as pathogen reservoirs and the heightened contact enhances the opportunity for cross-species transmission. Furthermore, studies elsewhere have indicated that biodiversity loss, which has occurred locally with the increasing urbanization of Singapore, increases pathogen prevalence in small mammal populations. Yet little is known about the biology of small mammal populations or their pathogens in highly urbanized areas such as Singapore and what risk they represent for the emergence and re-emergence of human disease. The ultimate aim of this work is to develop spatio-temporal models for the prediction of risk of human disease from small mammal-borne pathogens in urban settings.

#### **Complete List of Published Work in MyBibliography:**

<http://www.ncbi.nlm.nih.gov/sites/myncbi/gavin.smith.1/bibliography/48475573/public/?sort=date&direction=ascending>

#### **D. Research Support**

**2014-04-DTRA Cooperative Biological Engagement Program** Mendenhall (PI) 16/05/15-31/12/15

Sample collection and diagnostics training on Middle East Respiratory Syndrome (MERS-CoV) in camels and bats in Kazakhstan

Role: Co-Investigator

**SingHealth/Duke-NUS/RCG/2015/0007** Low & Gray (PI) 01/10/15-30/09/17

Adenoviral respiratory infections in Singapore: Identifying predictors for virulence

Role: Co-Investigator

**MOH/CDPHRG/0012/2014** Smith (PI) 31/07/14-30/07/17

Epidemiological and evolutionary dynamics of respiratory viruses in Singapore

Role: PI

**2014-04-DTRA Cooperative Biological Engagement Program** Mendenhall (PI) 19/05/14-30/05/14

Bat Borne Virus Surveillance Workshop in Singapore

Role: Co-Investigator

**W911QY-14-C-0040** Rudge (PI) 30/04/14-31/20/15

Determination of the association between livestock systems and influenza prevalence and diversity in swine, Cambodia

Role: Co-Principal Investigator

**HHSN272201400006C** Webby (PI) 31/03/14-31/03/21

NIAID Centers of Excellence for Influenza Research and Surveillance. Evolutionary studies.

Role: Sub-contract Principal Investigator

**MOH/CDPHRG/0005/2013** Smith (PI) 30/09/13-29/09/16

Genetic diversity of human influenza viruses from a community cohort versus sentinel and hospital-based surveillance in Singapore

Role: PI

### Completed Research Support

**MOE2011-T2-2-049** Vijaykrishna (PI) 01/04/12-31/03/15

Evolutionary consequences of reassortment of influenza A viruses

Role: Co-Investigator

**NMRC/GMS/1251/2010** Smith (PI) 20/10/10-30/07/14

Evolutionary genomics of the 2009 swine-origin H1N1 influenza A pandemic virus

**HHSN266200700005C** Webby (PI) 4/01/07-31/03/14

NIAID Centers of Excellence for Influenza Research and Surveillance. Career Development Award "Ecology, evolution and population genetics of influenza A (H5N1) virus".

Role: Sub-contract Principal Investigator