

Curriculum Vitae of Dr Justin Bahl

Center for Infectious Diseases

The University of Texas School of Public Health

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Career synopsis

My major research focus is on the molecular epidemiology, ecology, genetic and antigenic evolution, population dynamics, and interspecies transmission dynamics of emerging infectious diseases, particularly influenza. My research is directed towards uncovering how population structure, host immune pressure and transmission bottlenecks shape viral genetic diversity. I am currently an Associate Professor (tenure track) at The University of Texas School of Public Health. I have successfully secured research funding as Principal Investigator (~US\$300,000) and am a Co-Investigator/Collaborator with the NIAID/NIH Centers of Excellence in Influenza Research and Surveillance (~US\$58 million).

Publications

I have a >20 peer-reviewed publications in leading journals such as Nature, PNAS, Journal of Virology, and Emerging Infectious Diseases. My H-index is 15 with >1800 citations.

Google Scholar Profile

<http://scholar.google.com/citations?user=VQ5JSeQAAAAJ&hl=en>

Academic Degrees

PhD – 2007 The University of Hong Kong, Hong Kong (Molecular Systematics and Evolution)

BSc (Hons) – 2001 The University of Toronto, Toronto, Canada, (Botany)

Professional Employment:

Mar 2013 – Present Associate Professor The University of Texas Health Science Center at Houston

Mar 2013 – Present Adjunct Assistant Professor Duke-NUS Graduate Medical School, Singapore

Oct 2011 –Feb 2013 Assistant Professor (Non-Tenure Track) Duke-NUS Graduate Medical School, Singapore

Apr 2010 – 2011 Research Fellow Duke-NUS Graduate Medical School, Singapore

- Mar 2010 Visiting Scientist, Infectious Diseases, St Jude Children's Research Hospital, Memphis USA
- 2008 – 2010 Post-Doctoral Fellow, Department of Microbiology, HKU, Hong Kong.
- 2007 – 2008 Senior research Assistant, Department of Microbiology, HKU, Hong Kong.

Honorary Positions

- Mar 2007-Mar 2014 Member, NIAID/NIH Center of Excellence for Influenza Research and Surveillance, St Jude Children's Research Hospital, Memphis, TN, USA
- Jan 2007-present Member, Institute of Infection and Immunity, Shantou University, Guangdong, China
- April 2011-present Visiting Scientist, Influenza Division, Centers for Disease Control and Prevention, Georgia, USA

Collaborators

St Jude, Richard Webby, Robert Webster, Stacey Shultz-Cherry; **CDC**, Ruben Donis, Alexander (Sasha) Klimov, Todd Davis, Rebecca Garten, Sam Sheppard; **Duke-NUS**, Gavin Smith, Vijaykrishna Dhanasekaran, Mathieu Fourment, Ian Mendenhall, Duane Gubler, Eng Eong Ooi, Brett Ellis, Esther Ellis; **Penn State** Edward C Holmes; **Imperial College** Steven Riley; **University of Edinburgh** Andrew Rambaut; **Oxford University** Oliver Pybus; **The University of Auckland**, Alexei Drummond, Denise Kühnert; **FIC** Martha Nelson; **Erasmus Medical University**, Ron Fouchier, Miranda de Graaf; **Cambridge University**, Nicola Lewis; **JCVI**, David Wentworth, Vivien Dugan, Rebecca Halpin

Further details of professional achievements and interests are provided as follows:

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Annex A

Publications

1. **Bahl J**, Krauss S, Kühnert D, Fourment M, Raven G, Pryor SP, Niles LJ, Danner A, Walker D, Mendenhall I, Su YCF, Dugan VG, Halpin RA, Stockwell TB, Wentworth DE, Webby RJ, Drummond AJ, Smith GJD, Webster RG (2013). Spatial diffusion of avian influenza A virus in North America across migratory flyways. *PLoS Pathogens* In Review
2. Manokaran G, Bidet K, **Bahl J**, Gubler DJ, Sessions OM, Ooi EE (2013). Subgenomic Flavivirus RNA-mediated Suppression of the Interferon Response is linked to Dengue Epidemic. *PLoS Pathogens* In Review
3. Duan S, Govorkova EA, **Bahl J**, Zaraket H, Baranovich T, Seiler P, Prevost K, Webster RG, Webby RJ (2013). Multi-step acquisition of neuraminidase molecular determinants explains the spread of oseltamivir-resistant H1N1 influenza viruses during 2008-2009. *Cell Host and Microbe*. In Review
4. Shepard SS, Davis CT, **Bahl J**, Rivaille P, York IA, Donis R (2013). LABEL: fast and accurate lineage assignment with assessment of H5N1 and H9N2 influenza A hemagglutinins *PLoS Computational Biology* In Review
5. Mendenhall IH, **Bahl J**, Blum MJ & Wesson DM (2012). Genetic structure of *Culex erraticus* populations across the Americas. *Journal of Medical Entomology* 49:522-34
6. WHO/OIE/FAO H5N1 Evolution Working Group (2012) Continued evolution of highly pathogenic avian influenza A (H5N1): updated nomenclature. *Influenza and Other Respiratory Viruses* DOI:10.1111/j.1750-2659.2011.00298.x
7. **Bahl J***, Nelson MI, Chen R, Ghedin E, Halpin R, Stockwell T, Lin X, Vijaykrishna D, Chan KH, Peiris JSM, Riley S, Rambaut R, Holmes EC, Smith GJD* (2011) Temporally structured meta-population dynamics of human influenza A H3N2 virus. *Proceedings of the National Academy of Science USA* DOI:10.1073/pnas.1109314108 *corresponding author
8. Vijaykrishna D, Smith GJD, Pybus OG, Zhu H, Bhatt S, Poon LLM, Riley S, **Bahl J**, Ma SK, Cheung CL, Perera RAPM, Chen H, Shortridge KF, Webby RJ, Webster RG, Guan Y, Peiris JSM (2011) Long-term evolution and transmission dynamics of swine influenza A virus. *Nature* 473: 519-522
9. **Bahl J***, Lau MCY*, Smith GJD*, Vijaykrishna D*, Cary SC, Chan Y, Lacap DC, Lee CS, Papke RT, Warren-Rhodes KA, Wong FKY, McKay CP, & Pointing SB (2011) Ancient origins determine global biogeography of hot and cold desert cyanobacteria. *Nature Communications* 25;2:163. [*equal contribution]
10. Ducatez MF, **Bahl J**, Griffin Y, Stigger-Rosser E, Franks J, Barman S, Vijaykrishna D, Webb A, Guan Y, Webster RG, Smith GJD, Webby RJ. (2011). Cross-clade protective vaccine developed from reconstructed ancestral H5N1 influenza viruses. *Proceedings of the National Academy of Science USA* 108: 349-354 doi: 10.1073/pnas.1012457108

11. Huang K*, **Bahl J***, Fan XH, Vijaykrishna D, Cheung CL, Webby RJ, Webster RG, Chen H, Smith GJD, Peiris JSM, Guan Y. (2010) Establishment of an H6N2 influenza virus lineage in domestic ducks in southern China. *Journal of Virology* 84:6978-86 [*equal contribution]
12. Guan Y, Vijaykrishna D, **Bahl J**, Huachen Z, Wang J, Smith GJD. (2010). The emergence of pandemic influenza viruses. *Protein & Cell* 1:9–13.
13. Schrenzel MD, Witte CL, **Bahl J**, Tucker TA, Fabian N, Greger H, Hollis C, Hsia G, Siltamaki E, Rideout BA. (2010). Genetic characterization and epidemiology of Helicobacters in non-domestic animals. *Helicobacter* 15:126-42
14. Smith GJD*, Vijaykrishna D*, **Bahl J***, Lycett SJ*, Worobey M*, Pybus OG*, Ma SK, Cheung CL, Raghvani J, Bhatt, S, Peiris JSM, Guan Y, Rambaut A* (2009). Origins and evolutionary genomics of the 2009 swine-origin H1N1 influenza A epidemic. *Nature* 459:1122-5 [*equal contribution]
15. Smith GJD*, **Bahl J***, Vijaykrishna D*, Zhang JX, Poon LLM, Chen H, Webster RG, Peiris JSM, Guan Y (2009). Dating the emergence of pandemic influenza viruses. *Proceedings of the National Academy of Science USA* 106:11709-12 [*equal contribution]
16. **Bahl J**, Vijaykrishna D, Holmes EC, Smith GJD, Guan Y (2009). Gene flow and competitive exclusion of avian influenza A virus. *Virology*, doi:10.1016/j.virol.2009.05.002.
17. Smith GJD, Vijaykrishna D, Ellis TM, Dyrting KC, Leung YHC, **Bahl J**, Wong CW, Kai H, Chow MKW, Duan L, Chan ASL, Zhang LJ, Chen H, Luk GSM, Peiris JSM, Guan Y (2009). Characterization of Avian Influenza Viruses A (H5N1) from Wild Birds, Hong Kong, 2004-2008. *Emerging Infectious Diseases* 15: 402–407.
18. Vijaykrishna D, **Bahl J**, Riley S, Duan L, Zhang J, Chen H, Peiris JSM, Smith GJD, Guan Y (2008). Evolutionary dynamics and emergence of panzootic H5N1 influenza viruses. *PLoS Pathogens* 4: e1000161.
19. Duan L, **Bahl J**, Smith GJD, Wang J, Vijaykrishna D, Zhang LJ, Zhang JX, Li KS, Fan XH, Cheung CL, Huang K, Poon LLM, Shortridge KF, Webster RG, Peiris JSM, Chen H, Guan Y (2008). The development and genetic diversity of H5N1 influenza virus in China, 1996–2006. *Virology* 380: 243–254.
20. Al-Azemi A, **Bahl J**, Al-Zenki S, Al-Shayji Y, Al-Ahmad S, Chen H, Guan Y, Peiris JSM, & Smith GJD (2008). Avian influenza A virus (H5N1) outbreaks, Kuwait, 2007. *Emerging Infectious Diseases* 14: 958-961
21. Wang J, Vijaykrishna D, Duan L, **Bahl J**, Zhang JX, Webster RG, Peiris JSM, Chen H, Smith GJD, Guan Y (2008). Identification of the progenitors of Indonesia and Vietnam avian influenza A (H5N1) viruses from southern China. *Journal of Virology* 82: 3405-3414.
22. Xu KM, Smith GJD, **Bahl J**, Duan L, Tai H, Vijaykrishna D, Wang J, Zhang JX, Li KS, Webster RG, Chen H, Peiris JSM, Guan Y (2007). The genesis and evolution

of H9N2 influenza viruses in poultry from southern China, 2000 to 2005. *Journal of Virology* 81: 10389-10401.

23. Cheung CL, Vijaykrishna D, Smith GJD, Fan XH, Zhang JX, **Bahl J**, Duan L, Huang K, Tai H, Wang J, Poon LLM, Peiris JSM, Chen H, Guan Y (2007). Establishment of influenza A virus (H6N1) in minor poultry in southern China. *Journal of Virology* 81: 10402-10412.
24. **Bahl J**, Jeewon R, & Hyde KD (2005). Phylogeny of *Rosellinia capetribulensis* sp. nov. and its allies (Xylariaceae). *Mycologia* 97: 1102-1110.

Book chapters / Proceedings

1. Smith GJD, **Bahl J**, Vijaykrishna D (2012). Genetic analysis. In *Influenza: Methods in Molecular Biology* 865:207-27. (eds Kawaoka Y, Neumann G), Humana Press.
2. **Bahl J**, Vijaykrishna D, Smith GJD, Webster RG, Y Guan. Evolutionary dynamics of avian influenza A virus in the natural reservoir. Proceedings of the Options for the Control of Influenza VI, June 17–23, 2007 Toronto, Ontario, Canada.
3. Vijaykrishna D, Smith GJD, **Bahl J**, Wang J, Webster RG, Guan Y (2007). Dating the emergence of influenza A (H5N1) virus. Proceedings of the Options for the Control of Influenza VI, June 17–23, 2007 Toronto, Ontario, Canada.
4. Cheung CL, Vijaykrishna D, Smith GJD, **Bahl J**, Fan XH, Zhang JX, Chen H, Guan Y. Establishment of influenza A virus (H6N1) in minor poultry in southern China. Proceedings of the Options for the Control of Influenza VI, June 17–23, 2007 Toronto, Ontario, Canada.
5. Duan L, Campetelli L, Smith GJD, **Bahl J**, Donatelli I, Webster RG, Shortridge KF, Peiris JSM, Chen H, Guan Y. Characterization of low pathogenic H5 subtype influenza viruses from Eurasia: Implications for the origin of highly pathogenic H5N1 viruses. Proceedings of the Options for the Control of Influenza VI, June 17–23, 2007 Toronto, Ontario, Canada.
6. Wang J, Smith GJD, **Bahl J**, Li KS, Duan L, Vijaykrishna D, Chen H, Guan Y, Identification of precursors of Indonesia and Vietnam Avian Influenza A (H5N1) viruses from southern China. Proceedings of the Options for the Control of Influenza VI, June 17–23, 2007 Toronto, Ontario, Canada.

Annex B**Scholarship and Awards**

- 2013-2014 Principal Investigator. **“Unifying molecular evolution, spatial epidemiology and host adaptation of emerging influenza A viruses”** Pilot Project Grant. NIAID-NIH St Jude Center for Excellence in Influenza Research and Surveillance (US\$ 183,000)
- 2011-2012 Principal Investigator. **“Spatial and temporal dynamics of avian influenza A in wild birds”** NIAID Influenza Genome Sequencing Project (Funding to sequence 700 influenza viral genomes)
- Sept 2011 European Scientific Working group on Influenza, **“Young Scientist Award”** (US\$1,500)
- 2011-2012 Principal Investigator. **“Adaptation and divergence of H1N1/2009 influenza A virus under controlled experimental conditions”** National Medical Research Council – New Investigator Grant. (US\$140,000)
- Sept 2010 Options for the Control of Influenza. Promising Young Investigator Award. **“Source-sink dynamics of H3N2 seasonal influenza.”** (Approximately US\$8,000)
- May 2010 The University of Hong Kong. Faculty Outstanding Research Output Award for **“The origins and evolutionary genomics of the 2009 swine-origin H1N1 influenza epidemic”** published in Nature. (US\$10,000)
- 2010 NIAID/NIH Selected Science Advances 2009 for **“Rapid Characterization of the 2009 H1N1 Influenza Virus”**
- 2002-2006 The University Grants Council **Post-graduate Research Scholarship** The University of Hong, Hong Kong SAR, China (US\$85,000)

Other indirect support

- 2010-2012 Co-Investigator **“Evolutionary genomics of the 2009 swine-origin H1N1 influenza A pandemic virus”** National Medical Research Council. PI – Gavin JD Smith, Duke-NUS Graduate Medical School (US\$850,000)
- 2007-2014 Collaborator **“NIAID Centers of Excellence for Influenza Research and Surveillance”** National Institutes of Health USA. PI – Robert Webster, St Jude Children’s Research Hospital (US\$57,420,278)

Annex C

Professional Membership and Service

- 2012 - Member, Influenza Research Database (www.fludb.org) Scientific Working Group, Appointment Pending
- 2010–2014 *Member*, CEIRS Influenza Research Database Scientific Working Group, DMID/NIAID/NIH Centers of Excellence for Influenza Research and Surveillance
- 2010 - 2011 *Member*, Research and Policy for Infectious Disease Dynamics (RAPIDD), Division of International Epidemiology and Population Studies (DIEPS), Fogarty International Center, National Institutes of Health
- 2010-present *Member*, International Society for Influenza and other Respiratory Virus Diseases
- 2011-present *Member*, World Health Organization Working Group on Evolution and Nomenclature of Highly Pathogenic Avian Influenza A (H5N1) Virus
- 2006–present WHO/OIE/FAO Working Group on Evolution and Nomenclature of Influenza A (H5N1) Virus, 2006–present
- 2009 *Member*, World Health Organisation Working Group on Evolution and Nomenclature of Pandemic Influenza A (H1N1) Virus

Editorial Board Member:

- 2012-2015 *Infection Genetics and Evolution*

Reviewer:

Proceedings of the National Academy of Sciences, Journal of Virology, Molecular Biology and Evolution, Journal of Clinical Microbiology, Clinical Infectious Diseases, Virology, Journal of General Virology, Archives of Virology, Virus Genes

Annex D**Courses Instructed**

- Jan-May 2012 “GMS6904 Introduction to Emerging Infectious Diseases.” Graduate Course (2 Modules)
- Jan-May 2012 “GMS6905 Developments in infectious diseases.” Graduate Seminar Course.
- June 2010 “Phylogenetic and Bioinformatics Workshop for the Analysis of Seasonal, Pandemic and Avian Influenza Virus” Pasteur Institute, Ho Chi Minh City, Vietnam.
- Feb 2009 “Viral phylogenetics” – Pre-Congress workshop on viral phylogenetics & bioinformatics, 8th Asia Pacific Congress of Medical Virology, Hong Kong, February 25-29, 2009.
- Aug 2009 “Molecular evolution” presented in Bioinformatics & Comparative Genome Analysis: An EMBO World Practical Course, HKU-Pasteur Research Centre, Hong Kong, 16-23 Aug 2009
- 2007 - 2009 “Viral phylogenetics & Bioinformatics”, Pasteur-Asia Virology Course, HKU-Pasteur Research Centre, Hong Kong, (Annual short course)
- 2008-2009 “Viral evolution and phylogenetics” – course for Research staff, PhD students and Postdocs at State Key Laboratory of Emerging Infectious Diseases, The University of Hong Kong, Hong Kong.

Annex E

Invited Lectures and Conference Presentations

1. **J Bahl** (2012) Long-term spatial diffusion patterns of avian influenza A virus is independent of migratory flyways. 6th Orthomyxovirus Research Conference. Quebec, Canada [Oral Presentation]
2. **J Bahl** (2012). Long-term evolutionary consequences of viral migration between wild bird populations. NIAID Centers of Excellence for influenza Research and Surveillance, 6th Annual CEIRS Network Meeting. New York, USA [Invited Speaker]
3. **J Bahl** (2012) Global migration, seasonality and persistence of human influenza A H3N2 virus. University of Texas, School of Public Health. Texas, USA [Invited Speaker]
4. **J Bahl** (2011) Source-sink dynamics of H3N2 seasonal influenza. Centers for Disease Control and Prevention, Atlanta Georgia, USA [Invited Speaker]
5. **J Bahl** (2009). Evolutionary genomics and genesis of pandemic influenza. British Columbia Centres for Disease Control. British Columbia, Canada. [Invited Speaker]
6. **J Bahl** (2009). Evolutionary genomics and genesis of pandemic influenza. UGC Area of Excellence Scheme “Control of Pandemic and Inter-Pandemic Influenza” Hong Kong [Invited Speaker]
7. **J Bahl**, YHC Leung, GJD Smith, D Vijaykrishna, TM Ellis, KC Dyrting, GSM Luk, JSM Peiris, Y Guan (2009). Characterization of viruses isolated from wild birds in Hong Kong. NIAID Centers of Excellence for influenza Research and Surveillance, 3rd Annual CEIRS Network Meeting Minneapolis, USA [Invited Speaker]
8. **J Bahl**, R Jeewon, & KD Hyde (2005). Intergeneric relationships of *Linocarpon* and *Neolinocarpon*: does phylogenetic analysis support the generic delineation? Annual MSA-MSJ Meeting, Hilo, Hawaii, USA. [Oral presentation]
9. **J Bahl**, R Jeewon, & KD Hyde (2004). *Apiosporaceae*, *Clypeosphaeriaceae*, *Hyponectriaceae*, *Myelospermataceae*: Molecular and morphological assessment of taxonomic hypotheses. The IV Asia-Pacific Mycological Congress & The IX International Marine and Freshwater Mycology Symposium, 2004, Chiang Mai, Thailand. [Oral presentation]
10. **J Bahl** & KD Hyde, (2003). Studies of *hyponectriaceous* fungi. Fifth Annual Scientific Meeting of the Mycological Association of Hong Kong. [Oral presentation]
11. **J Bahl**, R Jeewon, GJD Smith, & KD Hyde, (2002). *Linocarpon* vs *Neolinocarpon* - Does phylogenetic analysis support the generic delineation? The Third Asian Mycological Congress, Kunming China. [Oral presentation]

Annex F**Current Collaborative Projects*****Comparative genomics and hypothesis testing***

In collaboration with St Jude Children's Research Hospital and the Centers for Disease Control and Protection we are developing a population genetic framework for statistical assessment of amino acid marker fixation for pathogenicity, host adaptation anti-viral resistance and risk assessment. Other projects include molecular epidemiology and evolutionary dynamics of Dengue Virus, the global distribution and evolution of *Cyanobacteria* from environmental surveillance and metagenomics, and evaluating the diversity and transmission of *Astroviruses* isolated from non-human primates.

Population genetic framework for statistical assessment of genotype-phenotype correlations

H5N1 viruses continue to pose a pandemic threat. Recently a number of mutations have been identified that correlate with the aerosol transmission of this virus between mammalian models. By reconstructing the ancestral states of these mutations in a Bayesian phylogenetic framework we can assess the likelihood of mutation fixation and associated risk for H5N1 variant emergence (in collaboration with CDC). Extending this principle we have taken a modelled approach to assess the sequence of mutations associated with the emergence of antiviral resistance phenotypes (in collaboration with St Jude) in seasonal H3N2, H1N1 and H1N1/2009 influenza A viruses.

Ecological and evolutionary dynamics of influenza A virus in wild birds

The discontinuous distribution of susceptible hosts may produce long periods of co-circulation of competing virus strains before lineage extinction occurs. In this study we describe the complex migration dynamics underlying the persistence of viruses across North America. We show that North-South migration was rapid but viruses were not restricted to individual flyways. The viral gene pool mixed where east-west migration between discrete sampling sites may take as long as several years. Estimation of migration rates and patterns show that the long-term persistence and spatial transmission of influenza A virus in wild birds was independent of bird migratory flyways. This study highlights surveillance strategies, diversity in different locations and intra-continental transmission patterns necessary for prediction of disease diffusion through wild bird populations for both conservation and pandemic disease control and preparedness.