

Curriculum Vitae of Dr Justin Bahl

Center for Infectious Diseases

The University of Texas School of Public Health

Email: justin.bahl@uth.tmc.edu

Career synopsis

My research is focused on the molecular epidemiology, ecology, genetic evolution, population dynamics, and interspecies transmission dynamics of emerging infectious diseases, particularly influenza. This work 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 and am a Co-Investigator with the NIAID/NIH St Jude Center of Excellence in Influenza Research and Surveillance.

Publications

I have >40 peer-reviewed publications in leading journals such as Nature, PNAS, PLoS Pathogens, Journal of Virology, and Emerging Infectious Diseases with >4000 citations. My i10-index is 32 and h-index is 22.

[Google Scholar Profile](#)

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)

Current Positions:

Mar 2013 – Present Associate Professor (Tenure Track) The University of Texas Health Science Center at Houston

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

Past Employment:

- 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.
- Jan 2007 – 2012 Member, Institute of Infection and Immunity, Shantou University, Guangdong, China

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
- April 2011-present Visiting Scientist, Influenza Division, Centers for Disease Control and Prevention, Georgia, USA

Collaborators

Richard Webby, Robert Webster, Stacey Shultz-Cherry (*St Jude Children’s Research Hospital*); Ruben Donis, Todd Davis, Rebecca Garten, Sam Sheppard, David Wentworth, Vivien Dugan (*CDC*); Gavin Smith, Ian Mendenhall, Eng Eong Ooi (*Duke-NUS*), Vijaykrishna Dhanasekaran (*Monash University*), Mathieu Fourment (*University of Technology Sydney*); Edward C Holmes (*The University of Sydney*); Steven Riley (*Imperial College*); Andrew Rambaut (*University of Edinburgh*); Oliver Pybus (*Oxford*); Alexei Drummond (*The University of Auckland*); Denise Kühnert (*ETHZ*); Martha Nelson (*FIC*); Ron Fouchier, Miranda de Graaf (*Erasmus Medical University*); Nicola Lewis (*Cambridge University*); Andy Ramey (*USGS*); David Stallknecht (*UGA*).

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

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Annex A: Publications**Peer Reviewed**

Ecology and Evolution of Animal Influenza

1. Qiu X*, Duvvuri VR, Gubbay JB, Webby R, Kayali G, **Bahl J** (2017). Lineage Specific Epitope Profiles for HPAI H5 Pre-Pandemic Vaccine Selection and Evaluation *Influenza and Other Respiratory Viruses*. *In press* [*Student Author]
2. Hussein ITM, Ma, EJ, Hill NJ, Meixell BW, Lindberg M, Albrecht RA, **Bahl J**, Runstadler JA. (2016). A point mutation in the polymerase protein PB2 allows a reassortant H9N2 influenza isolate of wild-bird origin to replicate in human cells. *Infection, Genetics and Evolution* doi: 10.1016/j.meegid.2016.04.011
3. **Bahl J**, Pham TT*, Hill NJ, Hussein ITM, Ma EJ, Easterday BC, Halpin RA, Stockwell TB, Wentworth DE, Kayali G, Krauss S, Schultz-Cherry S, Webster RG, Webby RJ, Swartz M, Smith GJD, Runstadler JA (2016) Ecosystem interactions and reassortment dynamics underlie the emergence of influenza A viruses with pandemic potential. *PLoS Pathogens* 12(5): e1005620. doi: 10.1371/journal.ppat.1005620 [*Student Author]
4. Lee D-H, **Bahl J**, Torchetti MK, Killian ML, Ip HS, Swayne DE (2016) Evolution and spread of H5 clade 2.3.4.4 highly pathogenic avian influenza virus subgroups and generation of novel reassortant viruses in the United States *Emerging Infectious Diseases* doi: 10.3201/eid2207.160048
5. Ramey AM, Reeves AB, TeSlaa JL, Mashold S, Donnelly T, **Bahl J**, Hall JS (2016) Evidence for Beringian origins of highly pathogenic intercontinental reassortant H5N1 and H5N2 influenza A viruses. *Infection, Genetics and Evolution* 40:176-85. doi: 10.1016/j.meegid.2016.02.035
6. Baranovich T, **Bahl J**, (2016) Influenza A Virus diversity and transmission in exhibition swine. *J Infectious Diseases* doi: 10.1093/infdis/jiv400 (Invited Editorial)
7. Baranovich T, **Bahl J**, Marathe BM, Culhane M, Stigger-Rosser E, Darnell D, Kaplan BS, Lowe JF, Webby RJ, Govorkova EA (2015) Influenza A viruses of swine circulating in the United States during 2009–2014 are susceptible to neuraminidase inhibitors but show lineage-dependent resistance to adamantanes. *Antiviral Research* doi:10.1016/j.antiviral.2015.02.004.
8. Lewis NS, Verhagen JH, Javakhishvili Z, Russell CA, Lexmond P, Westgeest KB, Bestebroer TM, Halpin RA, Lin X, Ransier A, Fedorova NB, Stockwell TB, Latorre-Margalef N, Olsen B, Smith GJD, **Bahl J**, Wentworth DE, Waldenström J, Fouchier RAM, de Graaf M (2015) Influenza A virus evolution and spatio-temporal dynamics in Eurasian Wild Birds: A phylogenetic and phylogeographic study of whole-genome sequence data. *J Gen Virol* doi:10.1099/vir.0.000155
9. WHO/ OIE /FAO H5N1 Evolution Working Group (2014) Revised and updated nomenclature for highly pathogenic avian influenza A (H5N1) viruses. *Influenza and Other Respiratory Viruses* doi:10.1111/irv.12230

10. **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) Influenza A virus migration and persistence in North American wild birds. *PLoS Pathogens* 9(8): e1003570. doi:10.1371/journal.ppat.1003570
11. 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
12. 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
13. 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]
14. **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.
15. 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.
16. 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.
17. 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.
18. 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
19. 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.
20. 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.

21. 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.

Human Infection with Seasonal, Zoonotic and Pandemic Influenza

22. Tan GS, Leon PE, Albrecht RA, Margine I, Wang TT, Hirsh A, Ravetch JV, Palese P, **Bahl J**, Krammer F (2016) Broadly-reactive neutralizing and non-neutralizing antibodies directed against the H7 influenza virus hemagglutinin reveal divergent mechanisms of protection. *PLoS Pathogens* doi: 10.1371/journal.ppat.1005578
23. Su YCF, **Bahl J**, Joseph U, Barr I, Koay ESC, Oon LLE, Vijaykrishna D, Smith GJD (2015) Evolutionary dynamics of H1N1/2009 influenza: The transition from host adaptation to immune driven directional selection *Nature Communications* doi: 10.1038/ncomms8952
24. Zaraket H, Baranovich T, Kaplan B, Carter R, Song M-S, Paulson J, Reh J, **Bahl J**, Crumpton J, Seiler P, Edmonson M, Wu G, Karlsson E, Fabrizio II T, Zhu H, Yi G, Schultz-Cherry S, Krauss S, McBride R, Webster RG, Govorkova E, Zhang H, Russell C, Webby R (2015) Mammalian adaptation of influenza A(H7N9) virus is limited by a narrow genetic bottleneck. *Nature Communications* doi: 10.1038/ncomms7553
25. Joseph U, Linster M, Suzuki Y, Krauss S, Halpin RA, Vijaykrishna D, Fabrizio T, Bestebroer TM, Maurer-Stroh S, Webby RJ, Wentworth DE, Fouchier RAM, **Bahl J***, Smith GJD* (2015) Adaptation of Pandemic H2N2 Influenza A Viruses in Humans. *Journal of Virology* doi:10.1128/JVI.02590-14 [*corresponding author]
26. Duan S, Govorkova EA, **Bahl J**, Zaraket H, Baranovich T, Seiler P, Prevost K, Webster RG, Webby RJ (2014) Multi-step acquisition of neuraminidase molecular determinants explains the spread of oseltamivir-resistant H1N1 influenza viruses during 2008-2009. *Nature Communications* doi:10.1038/ncomms6029
27. Westgeest K, Russell C, Lin X, Spronken M, Bestebroer T, **Bahl J**, van Beek R, Skepner E, Halpin R, de Jong J, Rimmelzwaan G, Osterhaus A, Smith D, Wentworth D, Fouchier R, De Graaf M. (2013) Genome-wide Analysis of Reassortment and Evolution of Human Influenza A(H3N2) Viruses Circulating between 1968 and 2011. *Journal of Virology* doi:10.1128/JVI.02163-13
28. **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]
29. 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

30. Guan Y, Vijaykrishna D, **Bahl J**, Huachen Z, Wang J, Smith GJD. (2010). The emergence of pandemic influenza viruses. *Protein & Cell* 1:9–13.
31. 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]
32. 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]

Applications to other model systems

33. Ramey AM, Goraichuk IV, Hicks JT*, Dimitrov KM, Poulson RL, Stallknecht DE, **Bahl J**, Afonso CL (2017). Assessment of contemporary genetic diversity and inter-taxa/inter-region exchange of avian paramyxovirus serotype 1 in wild birds sampled in North America. *Virology Journal* doi: 10.1186/s12985-017-0714-8 [*Student Author]
34. Pham TT*, Meng S, Sun Y, Lv W, **Bahl J** (2016). Ecological and Evolutionary Dynamics of Japanese Encephalitis Virus (JEV) Genotypes I and II. *Virus Evolution* doi: 10.1093/ve/vew009 [*Student Author]
35. Dimitrov KM, Ramey AM, Qiu X, **Bahl J**, Afonso CL (2016) Temporal, geographic, and host distribution of avian paramyxovirus 1 (Newcastle disease virus). *Infection, Genetics and Evolution* 39:22-34 doi: 10.1016/j.meegid.2016.01.008.
36. Duvvuri VR, Granados A, Rosenfeld P, **Bahl J**, Eshaghi A, Gubbay JB (2015) Genetic diversity and evolutionary insights of respiratory syncytial virus A ON1 genotype: global and local transmission dynamics. *Scientific Reports* doi: 10.1038/srep14268
37. Manokaran G, Finol E, Wang C, Gunaratne J, **Bahl J**, Ong EZ, Tan HC, Sessions OM, Ward AM, Gubler DJ, Harris E, Garcia-Blanco MA, Ooi EE (2015). Subgenomic RNA of dengue-2 virus binds tripartite motif 25 protein to inhibit interferon expression providing a mechanism for epidemiological fitness. *Science* doi: 10.1126/science.aab3369
38. 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
39. **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]
40. 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 *Helicobacter* in non-domestic animals. *Helicobacter* 15:126-42

41. **Bahl J**, Jeewon R, & Hyde KD (2005). Phylogeny of *Rosellinia capetribulensis* sp. nov. and its allies (Xylariaceae). *Mycologia* 97: 1102-1110.

Computational Methods

42. Shepard SS, Meno S, **Bahl J**, Wilson MM, Barnes J, Neuhaus (2016) Viral deep sequencing needs an adaptive approach: IRMA, the iterative refinement meta-assembler. *BMC Genomics*. 17:708. doi: 10.1186/s12864-016-3030-6
43. Shepard SS, Davis CT, **Bahl J**, Rivaller P, York IA, Donis R (2014) LABEL: fast and accurate lineage assignment with assessment of H5N1 and H9N2 influenza A hemagglutinins. *PLoS One* doi:10.1371/journal.pone.0086921

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: Awards and Grants

- July 2017 Charles C Shepard Science Award for Data Methods and Study Design, CDC. For Scientific Excellence demonstrated by the publication of “Viral deep sequencing needs an adaptive approach: IRMA, the iterative refinement meta-assembler.” *BMC Genomics*. 17:708. doi: 10.1186/s12864-016-3030-6
- 2017 – 2019 Principal Investigator. **Integrating genomic sequencing into active surveillance of avian influenza A viruses circulating in Egyptian poultry production systems.** USAID \$200,000.00. *Pending*

- 2015 – 2016 Principal Investigator. **MERS-CoV & Influenza genome sequencing (FFSA)** NIH, \$27,500.00
- 2014-2021 Co-investigator **“NIAID Centers of Excellence for Influenza Research and Surveillance”** National Institutes of Health USA. PI – Richard Webby, St Jude Children’s Research Hospital (UTHealth Subcontract). Centers of Excellence for Influenza Research and Surveillance (NIAID-NIH CEIRS)
- Principal Investigator. Distributed Influenza Genomic Sequencing. NIAID-NIH CEIRS, \$426,386.88, 04/01/2014 - 03/31/2016
- Principal Investigator. Distributed Influenza Genomic Sequencing. NIAID-NIH CEIRS, \$200,000.00, 04/01/2016 - 03/31/2017
- Principal Investigator. Distributed Influenza Genomic Sequencing. NIAID-NIH CEIRS, \$50,000.00, 04/01/2017 - 03/31/2018
- 2013 Instructor **“NIAID Centers of Excellence for Influenza Research and Surveillance Training Grant”** Massachusetts Institute of Technology, Boston MA. USA. PI Islam Hussein (\$7000 USD)
- 2013 Host **“NIAID Centers of Excellence for Influenza Research and Surveillance Training Grant”** St Jude Children’s Research Hospital Memphis Tennessee, USA. PI Tatianna Baronovich (\$7000 USD)
- 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”** (\$1,500 USD)
- 2011-2012 Principal Investigator. **“Adaptation and divergence of H1N1/2009 influenza A virus under controlled experimental conditions”** National Medical Research Council – New Investigator Grant. (\$140,000 USD)
- 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. (\$10,000 USD)
- 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 (\$85,000 USD)
- 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 (\$850,000 USD)

2007-2014 Co-Investigator **“NIAID Centers of Excellence for Influenza Research and Surveillance”** National Institutes of Health USA. PI – Robert Webster, St Jude Children’s Research Hospital (\$57,420,278 USD)

Unifying molecular evolution, spatial epidemiology and host adaptation of emerging influenza A viruses. Pilot Project Grant. NIAID-NIH CEIRS, \$183,000.00, 04/01/2013 - 03/31/2014

Annex C: Professional Membership and Service

2012 - Present Member, Influenza Research Database (www.fludb.org) Scientific Working Group

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:

2012-2013 *Infection Genetics and Evolution*

Journal Reviewer:

Nature, Nature Communications, Scientific Reports, Proceedings of the National Academy of Sciences, Molecular Biology and Evolution, Journal of Clinical Microbiology, Clinical Infectious Diseases, Journal of Infectious Diseases, PLoS Computational Biology, PLoS Pathogens, PLoS One, Journal of Virology, Virology, Journal of General Virology, Archives of Virology, Virus Genes,

Grant Reviewer

The Thiel Foundation, Auckland University of Science and Technology, Research Foundation - Flanders (Fonds Wetenschappelijk Onderzoek - Vlaanderen, FWO)

Annex D: Courses Instructed

- Fall 2016 “PH 1982L; GS11-1103 Evolution of DNA and Protein Sequence” University of Texas School of Public Health & Graduate School of Biomedical Sciences. Co-taught with Yun-Xin Fu, Xiaoming Liu
- Sept 2016 “Introduction to phylogenetic analysis for Avian Influenza A virus surveillance - Workshop” Animal Health Research Institute, Taiwan 17-24 Sept 2016
- Summer 2016 “PHM2610 Fundamentals of Epidemiology” Core course University of Texas School of Public Health.
- Spring 2016 “PH2730: Epidemiology and Control of Infectious Disease” University of Texas School of Public Health.
- Spring 2016 “PHD2998: Modeling infectious disease dynamics” University of Texas School of Public Health.
- Summer 2014 “PHM2610 Fundamentals of Epidemiology” Core course University of Texas School of Public Health.
- Oct 2013 “Phylogeography of Avian Influenza Workshop” Massachusetts Institute of Technology, Boston, USA, 7-11 Oct 2013
- 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)

Annex E**Invited Lectures and Conference Presentations**

1. **J Bahl** (2016) “Ecosystem interactions and the spread of emerging avian influenza A virus. Animal Health Research Institute, Taiwan 17-24 Sept 2016 [Invited Speaker and Workshop Instructor]
2. **J Bahl** (2013) “Ecological and epidemiological inference of influenza A virus from

- sequence data.” Infectious Diseases Microbiology Rounds – University of Toronto Health Network, Sunnybrook Hospital, Toronto Ontario [Invited Speaker]
3. **J Bahl** (2013) “Inference of epidemiological and ecological dynamics from sequence data.” Icahn School of Medicine, Mount Sinai Hospital, Manhattan New York, USA [Invited Speaker]
 4. **J Bahl** (2013) “What is a phylogenetic tree?” Massachusetts Institute of Technology, Boston, Massachusetts, USA [Invited Speaker]
 5. **J Bahl** (2013) “Ecological and epidemiological inference from evolutionary trees.” Massachusetts Institute of Technology, Boston, Massachusetts, USA [Invited Speaker]
 6. **J Bahl** (2013) Influenza A virus migration and persistence in North American wild birds. College of Veterinary Medicine at Kansas State University, Manhattan Kansas [Invited Speaker]
 7. **J Bahl** (2013) Ecology, Evolution and Epidemiology of influenza A virus. The Department of Ecology and Evolutionary Biology. Rice University, Houston Texas. [Invited Speaker]
 8. **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]
 9. **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]
 10. **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]
 11. **J Bahl** (2011) Source-sink dynamics of H3N2 seasonal influenza. Centers for Disease Control and Prevention, Atlanta Georgia, USA [Invited Speaker]
 12. **J Bahl** (2009). Evolutionary genomics and genesis of pandemic influenza. British Columbia Centres for Disease Control. British Columbia, Canada. [Invited Speaker]
 13. **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]
 14. **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]