

## **Curriculum Vitae of Dr Justin Bahl**

Center for the Ecology of Infectious Diseases  
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### **Career synopsis**

My research is focused on the molecular epidemiology, ecology and genetic evolution of RNA viruses, particularly those that pose a risk to animal and human health. This work is directed towards uncovering how population structure, host immune pressure, geographic spread and transmission bottlenecks shape viral genetic diversity. My goal is to develop a molecular epidemiology program that can bridge the gap between academic research and applied public health. This program supports methodological advances, genomic data generation, management and integration with traditional epidemiological data streams to advance and promote the use of pathogen sequence analysis to inform public health response to infectious disease. Towards this end I have established multiple ongoing contracts with the Georgia Department of Public Health (direct contract), Houston Health Department (CDC funded contract), Department of Health US Virgin Islands (direct contract, pending) and working agreements with state public health across the US southeast.

I have >60 peer-reviewed publications in leading journals such as Nature, PNAS, PLoS Pathogens, Journal of Virology, and Emerging Infectious Diseases with >7000 citations. My i10-index is 50 and h-index is 34.

I have successfully obtained funding from NIH, NSF and CDC. I have a diverse funding application portfolio that includes a mixture of programmatic grants, contracts, and partnerships with industry. Since joining the University of Georgia in 2018-19, I have won research awards >\$3million as PI, >\$2.5million as Co-I and an additional >\$200million as an investigator with the Center for Influenza Vaccine Research in High-Risk Populations and the Center for Influenza Disease and Emergence Research. The multidisciplinary research team is drawn from the Department of Infectious Diseases, Institute for Bioinformatics and Department of Epidemiology and Biostatistics and currently consists of 7 PhD candidates, and 2 post-doctoral fellows. Our expertise has been in high demand since the global SARS-CoV-2 pandemic. The team is now working on methods to rapidly identify growing transmission clusters using genomic data, assisting multiple institutions with processing newly sequenced CoVID-19 samples and investigating interspecies transmission of emergence of beta-coronaviruses with recently collected samples from bats, snakes and camels.

### **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:**

Aug 2018 – Present Associate Professor University of Georgia

**Past Employment:**

2013 – 2017 Associate Professor The University of Texas Health Science Center at Houston

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

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

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.

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

**Honorary Positions**

2007 – 2013 Member, NIAID/NIH Center of Excellence for Influenza Research and Surveillance, St Jude Children's Research Hospital, Memphis, TN, USA

2011 – 2013 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*); Pejman Rohani, Mark Tompkins, John Drake, Andreas Handel, Ye Shen, David Stallknecht, Ted Ross (*University of Georgia*).

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

Annex A – NIH Biosketch

Annex B – Publications

Annex C – Awards and Grants

Annex D – Service and Professional Affiliations.

Annex E – Teaching

Annex F – Invited Lectures and Conference Presentations

## Annex A: NIH Biosketch

NAME: Justin Bahl

POSITION TITLE AND INSTITUTION: Associate Professor, University of Georgia

### EDUCATION/TRAINING:

INSTITUTION AND LOCATION	DEGREE	Completion Date MM/YYYY	FIELD OF STUDY
The University of Toronto, Toronto, Canada	B.A.	08/2001	Botany
The University of Hong Kong, Hong Kong	Ph.D.	01/2007	Systematics and Evolution
The University of Hong Kong, Hong Kong	Postdoc	02/2010	Influenza Systematics
Duke-NUS Graduate Medical School, Singapore	Postdoc	03/2011	Evolution and Epidemiology of RNA viruses

### A. Personal Statement

I direct an applied ecology, epidemiology, and evolutionary genetics research program to understand the underlying mechanisms of disease emergence, persistence, and spread in human and animal populations. Using genetic and phenotypic data I have developed phylodynamic models to test hypotheses and make statistical inferences on influenza virus evolution, including interspecies transmission, and transmission between ecosystems. My training makes me particularly well suited to mentor students and post-docs studying ecological and epidemiological processes that impact viral genetic diversity and evolvability. My current research program focuses on three areas of infectious disease dynamics: 1) Genomic Surveillance and phylodynamic modeling of influenza and other RNA viruses; 2) Impact and Risk Assessment of emerging influenza variants; 3) Forecasting of epidemic and pandemic influenza.

### B. Selected Positions and Honors

2007 – 2010 Post-Doctoral Fellow, Department of Microbiology, HKU, Hong Kong  
2010 – 2011 Research Fellow, Duke-NUS Graduate Medical School, Singapore  
2011 –2013 Assistant Professor, Duke-NUS Graduate Medical School, Singapore  
2013 – 2018 Associate Professor, The University of Texas Health Science Center, Houston, TX, USA  
2018 – Present Associate Professor, The University of Georgia, Athens, GA

### C. Selected Contributions to Science

**Seasonal and Pandemic influenza A Virus.** During the H1N1/2009 pandemic we described the origins and the early development of the epidemic. We showed that the H1N1/2009 virus was derived from several viruses circulating in swine, and that the initial transmission to humans occurred months before recognition of the outbreak (1). We later examined how the evolutionary dynamics of pandemic H1N1 virus changed from pandemic spread in a naive population to seasonal dynamics of a persistent human pathogen (2). We demonstrated how patterns of natural selection changed with pandemic and epidemic spread. Importantly, how these patterns of epidemic transmission may impact the evolution of antigenic sites and subsequently, control efforts.

1. Smith GJD, Vijaykrishna D, **Bahl J**, Lycett SJ, Worobey M, Pybus OG, Ma SK, Cheung CL, Raghwani 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  
doi:10.1038/nature08182 **PMID:19516283**

2. 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* 6:7952  
doi:10.1038/ncomms8952 **PMCID: PMC4918339**

**Avian influenza A Virus.** We have described the complex ecological and evolutionary dynamics underlying the persistence of viruses circulating in North America and Asia, including the competitive dynamics and extinction that resulted from introductions of Eurasian lineage AIV to North American waterfowl (1). In addition, we developed an influenza-specific method that utilized key features of gene exchange and reassortment to jointly estimate viral migration parameters from independent phylogenies (2). We later tested hypotheses of viral diffusion and to quantify viral spread by domestic trade or wild animal migration (3). Most recently we have shown that the structure of domestic production systems can predict the patterns of spread of a highly pathogenic virus introduced from a wild bird source (4). We showed viral flow the highest rates of viral movement among domestic populations, indicating that poultry trade or logistical networks may play a major role in spreading viral disease. Collectively, the influenza specific comparative genetic methods and models we have developed will provide critical information for virus characterization, epidemiology and risk assessment activities included in this proposal.

1. **Bahl J**, Vijaykrishna D, Holmes EC, Smith GJD, Guan Y (2009). Gene flow and competitive exclusion of avian influenza A virus in natural reservoir hosts. *Virology*, 390(2):289-97  
doi:10.1016/j.virol.2009.05.002. **PMCID: PMC2753668**
2. **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 **PMCID: PMC3757048**
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 MD, Smith GJD, Runstadler JA (2016) Ecosystem interaction underlie the spread of avian influenza A viruses with pandemic potential. *PLoS Pathog* 12(5):e1005620.  
doi:10.1371/journal.ppat.1005620. **PMID: 27166585**
4. Hicks JT, Lee D-H, Duvuuri VR, Kim Torchetti M, Swayne DE, **Bahl J** (2020) Agricultural and geographic factors shaped the North American 2015 highly pathogenic avian influenza H5N2 outbreak. *PLoS Pathog* 16(1): e1007857. doi.org/10.1371/journal.ppat.1007857 *in press*

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

CDC 75D30119C06826 Bahl (PI) 09/30/19 – 8/31/22

We are developing an integrated system that uses multiple data sources to accurately predict which seasonal influenza lineage will dominate in future epidemic seasons.

Role: Principal Investigator

NIAID HHSN272201400007C Rothman/Pekosz (PI) 4/1/14 – 3/31/21

I oversee the “Distributed Influenza Genomic Sequencing” project to increase the sequencing resources available to the CEIRS program.

Role: Subaward PI/Project Lead

NIAID HHSN272201400006C Webby (PI) 4/1/14 – 3/31/21

We develop statistical phylogenetic models and integrate novel data sources to enable inferences for avian, human, and swine influenza emergence, spread, and persistence. In 2015, my role expanded to include the “Distributed Influenza Genomic Sequencing” project to increase the sequencing resources available to the CEIRS program

Role: Subaward PI/Project Lead

## Annex B: Publications

### Peer Reviewed (‡Student/Mentored Post-Doc, \*corresponding author)

1. Kuhn, J.H., Adkins, S., Alioto, D. Alkhovsky SV, Amarasinghe GK, Anthony SJ, Avšič-Županc T, Ayllón MA, **Bahl J**, *et al.* (2020) 2020 taxonomic update for phylum *Negarnaviricota*(*Riboviria: Orthornavirae*), including the large orders *Bunyavirales* and *Mononegavirales*. **Arch Virol** **165**, 3023–3072 doi: 10.1007/s00705-020-04731-2
2. Zhang J, Yao J, Jiang J, Pan Z, Luo M, Xia Y, Fan Q, Ding X, Ruan J, Handel A, **Bahl J**, Chen W, Zha L, Fu T (2020) Migration interacts with the local transmission of HIV in developed trade areas: A molecular transmission network analysis in China, **Infection, Genetics and Evolution** Volume 84, doi: 10.1016/j.meegid.2020.104376
3. Kwon, J-H, **Bahl J**, Swayne DE, Lee Y-N, Lee Y-J, Song C-S, Lee D-H (2020) Domestic ducks play a major role in the maintenance and spread of H5N8 highly pathogenic avian influenza viruses in South Korea. **Transboundary and emerging diseases** doi: 10.1111/tbed.13406
4. Hicks JT‡, Lee D-H, Duvvuri‡ VR, Kim Torchetti M, Swayne DE, **Bahl J\*** (2020) Agricultural and geographic factors shaped the North American 2015 highly pathogenic avian influenza H5N2 outbreak. **PLoS Pathog** 16(1): e1007857. doi: 10.1371/journal.ppat.1007857
5. Piedra F-A, Qiu X‡, Teng MN, Avadhanula V, Machado AA, Kim D-K, Hixson J, **Bahl J**, Piedra PA (2020) Non-gradient and genotype-dependent patterns of RSV gene expression. **PLoS ONE** 15(1): e0227558. doi: 10.1371/journal.pone.0227558
6. Hicks JT‡, Dimitrov KM, Afonso C. Ramey AM, **Bahl J\*** (2019). Global phylodynamic analysis of avian paramyxovirus-1 provides evidence of inter-host transmission and intercontinental spatial diffusion. **BMC Evol Biol** **19**, 108 (2019). doi: 10.1186/s12862-019-1431-2
7. Kwon, J-H, **Bahl, J**, Swayne, DE, Lee Y-N, Lee Y-J, Song C-S, Lee D-H (2019). Domestic ducks play a major role in the maintenance and spread of H5N8 highly pathogenic avian influenza viruses in South Korea. **Transbound Emerg Dis**. 00: 1– 8. doi: 10.1111/tbed.13406
8. Dimitrov KM, Abolnik C, Afonso CL, Albina E, **Bahl J**, Berg M, Briand F-X, Brown IH, Choi K-S, Chvala I, Diel DG, Durr PA, Ferreira HL, Fusaro A, Gil P, Goujgoulova GV, Grund C, Hicks JT‡, Joannis TM, Torchetti MK, Kolosov S, Lambrecht B, Lewis NS, Liu H, Liu H, McCullough S, Miller PJ, Monne I, Muller CP, Munir M, Reischak D, Sabra M, Samal SK, Servan de Almeida R, Shittu I, Snoeck CJ, Suarez DL, Van Borm S, Wang Z, Wong FYK. (2019) Updated unified phylogenetic classification system and revised nomenclature for Newcastle disease virus. **Infection, Genetics and Evolution**, 74. doi: 10.1016/j.meegid.2019.103917
9. Qiu X‡, Duvvuri VR‡, **Bahl J\*** (2019). Computational Approaches and Challenges to Developing Universal Influenza Vaccines. **Vaccines**, 7, 45. doi: 10.3390/vaccines7020045
10. Kandeil A, Gomaa MR, Shehata MM, El Taweel AN, Mahmoud SH, Bagato O, Moatasim Y, Kutkat O, Kayed AS, Dawson P, Qiu X‡, **Bahl J**, Webby RJ, Karesh WB, Kayali G, Ali MA. 2019. Isolation and characterization of a distinct influenza A virus from Egyptian bats. **J Virol** 93:e01059-18. doi: 10.1128/JVI.01059-18.
11. Kandeil A, Hicks JT‡, Young SG, El Taweel AN, Kayed AS, Moatasim Y, Kutkat O, Bagato O, McKenzie PP, Cai Z, Badra R, Kutkat M, **Bahl J**, Webby RJ, Kayali G Ali MA (2019).

- Active surveillance and genetic evolution of avian influenza viruses in Egypt, 2016–2018, *Emerging Microbes & Infections*, 8:1, 1370-1382, doi: 10.1080/22221751.2019.1663712
12. Heri AR, **Bahl J**, Villa IM. (2019). Geochemical discrimination and petrogenetic affinities of dykes intruding the Ladakh batholith, NW India. *Geological Society, London, Special Publications*, 481, 231-250. doi: 10.1144/SP481-2017-150
  13. Lee D, Torchetti M, Hicks J, Killian M, **Bahl J**, Pantin-Jackwood M, Swayne DE. (2018). Transmission Dynamics of Highly Pathogenic Avian Influenza Virus A(H5Nx) Clade 2.3.4.4, North America, 2014–2015. *Emerging Infectious Diseases*, 24(10), 1840-1848. doi: 10.3201/eid2410.171891.
  14. Kirkpatrick E, Qiu X‡, Wilson PC, **Bahl J\***, Krammer F (2018). The influenza virus hemagglutinin head evolves faster than the stalk domain. *Scientific Reports* doi: 10.1038/s41598-018-28706-1
  15. Jimenez-Bluhm P‡, Di Pillo F, **Bahl J**, Osorio J, Schultz-Cherry S, Hamilton-West C (2018). Circulation of influenza in backyard productive systems in central Chile and evidence of spillover from wild birds. *Preventive Veterinary Medicine* doi: 10.1016/j.prevetmed.2018.02.018
  16. 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* doi: 10.1111/irv.12466
  17. 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
  18. 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
  19. 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
  20. **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
  21. 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
  22. 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
  23. 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

24. 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
25. 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.
26. Baranovich T‡, **Bahl J\***, (2016) Influenza A Virus diversity and transmission in exhibition swine. *J Infectious Diseases* doi: 10.1093/infdis/jiv400 (*Invited Editorial*)
27. 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
28. 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
29. 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
30. Zaraket H, Baranovich T, Kaplan B, Carter R, Song M-S, Paulson J, Rehg 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
31. 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.
32. 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
33. 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
34. 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

35. 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
36. 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
37. 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
38. **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
39. 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
40. 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
41. **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
42. Vijaykrishna D, Smith GJD, Pybus OG, Zhu H, Bhatt S, Poon LLM, Riley S, **Bahl J**, Ma SK, Cheung CL, Perera RAPM, Chen H, Shorridge 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
43. **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]
44. 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
45. 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
46. Guan Y, Vijaykrishna D, **Bahl J**, Huachen Z, Wang J, Smith GJD. (2010). The emergence of pandemic influenza viruses. *Protein & Cell* 1:9–13.
47. 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



48. 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]
49. 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]
50. **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.
51. 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.
52. 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.
53. 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.
54. 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
55. 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.
56. 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.
57. 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.
58. **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 C: Awards and Grants

### Awards

- 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
- 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)
- Sept 2011 European Scientific Working group on Influenza, "Young Scientist Award" (\$1,500 USD)
- 2010 NIAID/NIH Selected Science Advances 2009 for "Rapid Characterization of the 2009 H1N1 Influenza Virus"
- Sept 2010 Options for the Control of Influenza. Promising Young Investigator Award. "Source-sink dynamics of H3N2 seasonal influenza" (Approximately US\$8,000)

### Funded Grants

All amounts are total dollars awarded.

- 2021-2027 Co- Investigator "Center for Influenza Disease and Emergence Research (CIDER)" PI - Mark Tompkins NIH NIAID Centers of Excellence for Influenza Research and Response (75N93021C00018) \$65,813,901  
Comparative genomic analysis and statistical phylodynamic modeling of influenza B virus and avian influenza A virus to understand the processes of viral transmission and persistence in human and animal populations
- 2021-2023 Co-Principal Investigator "COVID-19: Community scaled viral sequence analysis and phylodynamics for SARS CoV2 using wastewater-based informatics" PI - Erin Lipp Center for Disease Control (CDC 75D30121C11163) \$949,898  
1) Develop and optimize a scalable target enrichment and sequencing strategy for SARS-CoV-2 from wastewater, 2) implement a wastewater-based testing approach for longitudinal and targeted analysis of SARS-CoV-2 variants, and 3) conduct community-scaled comparative sequence analysis and molecular epidemiology using wastewater and clinical surveillance data.
- 2021-2023 Principal Investigator "Molecular epidemiology and transmission dynamics of COVID-19 in Houston, Texas" Center for Disease Control (CDC 75D30121C10133) \$1,116,539  
Combine epidemiological surveillance with comparative genomic analysis of viral sequence data in a statistical phylodynamic framework to understand the characteristics of SARS-CoV-2 transmission dynamics. The rapid spread of SARS-CoV-2 complicates control efforts. This project aims to address the need for robust and rapid computational methods to understand how population characteristics determine the rate and patterns of community transmission to enhance control efforts.
- 2021-2023 Principal Investigator "A genomics-based system to predict the seasonal influenza virus evolution and epidemic dominance" Center for Disease Control (CDC 75D30121C11990) \$732,271

The main goal is to predict which influenza virus lineage will dominate in future epidemic seasons and early identification of vaccine escape variants, key predictions to effectively control, limit and eventually, eliminate influenza disease burden from human populations.

2020-2021 Co-Principal Investigator “RAPID: finding virulence genes as therapeutic targets in Covid-19” National Science Foundation, USA. PI – Jonathan Arnold (NSF AWD00011959), \$200,000 (\$71,000 to the Bahl Lab):

Oversees full genome sequencing of betacoronavirus samples collected from animals. Develop phylodynamic model of viral host switch and emergence

2019-2021 Principal Investigator “Integrated System to forecast dominant influenza virus in seasonal epidemics” Center for Disease Control (CDC 75D30119C06826), \$659,708 (\$305,192 to the Bahl Lab)

Oversees project development, prepares reports to CDC, supervises phylodynamic. modeling

2019-2026 Co-Investigator “The Center for Influenza Vaccine Research for High-Risk Populations (CIVR-HRP)” Research Area 003. PI - Ted Ross. (NIAID-NIH: HHS-NIH-NIAID-BAA2018) \$130,177,556 (\$398,436 to the Bahl Lab)

Coordinates statistical modeling research group for the contract. Serves on the scientific leadership committee. Oversees phylogenetic modeling of seasonal influenza viruses, with focus on mapping epitope drift and replacement, computational design of ancestral sequence for vaccine testing

2019-2021 Sub-contract Principal Investigator “NIAID Centers of Excellence for Influenza Research and Surveillance” National Institutes of Health USA. PI – Richard Rothman/Andrew Pekosz Johns Hopkins University. (NIAID-NIH CEIRS: HHSN272201400007C), \$186,238

Oversees full genome sequencing of Influenza viruses, MERS, and SARS-CoV2 Phylogenetic systematics and molecular ecology and epidemiology of avian, swine and human influenza A viruses

2019-2023 Principal Investigator “HEC Fellowship Subhan Ullah” Higher Education Commission of Pakistan, \$16,280

Supervise PhD candidate Subhan Ullah

2019 Co-Principal Investigator/Instructor “NIAID Centers of Excellence for Influenza Research and Surveillance Training Grant – Taiwan Workshop on comparative genomics” Research Center for Emerging Viral Infections, Chang Gung University, TaiWan. Co-PI Kuan Fu Chen (\$7000 USD – direct cost for travel accommodation and training materials. No Indirect)

2019 Mentor “NIAID Centers of Excellence for Influenza Research and Surveillance Training Grant” Erasmus University, Netherlands . PI Marjolein Poen (\$7000 USD – direct cost for travel accommodation and training materials. No Indirect)

2014-2021 Sub-contract Principal Investigator “NIAID Centers of Excellence for Influenza Research and Surveillance” National Institutes of Health USA. PI – Richard Webby, St Jude Children’s Research Hospital. (NIAID-NIH CEIRS: HHSN272201400006C) (\$876,387 to Bahl Lab)

Oversees full genome sequencing of Influenza viruses, MERS, and SARS-CoV2  
Phylogenetic systematics and molecular ecology and epidemiology of avian,  
swine and human influenza A viruses

Subaward PI/Project Lead. Distributed Influenza Genomic Sequencing.  
NIAID-NIH CEIRS, \$426,386.88, 04/01/2014 - 03/31/2016

Subaward PI/Project Lead. Distributed Influenza Genomic Sequencing.  
NIAID-NIH CEIRS, \$200,000.00, 04/01/2016 - 09/31/2018

Subaward PI/Project Lead. Distributed Influenza Genomic Sequencing.  
NIAID-NIH CEIRS, \$50,000.00, 04/01/2017 - 09/31/2017

Subaward PI/Project Lead. Distributed Influenza Genomic Sequencing.  
NIAID-NIH CEIRS, \$200,000.00, 10/01/2017 - 09/31/2020

- 2015 Mentor “NIAID Centers of Excellence for Influenza Research and Surveillance Training Grant” St Jude Children’s Research Hospital Memphis Tennessee, USA. PI Pedro Jimenez-Bluhm (\$7000 USD – direct cost for travel accommodation and training materials. No Indirect)
- 2015 – 2016 Principal Investigator. MERS-CoV & Influenza genome sequencing (FFSA) NIH, \$27,500.00  
Oversees full genome sequencing of Highly Pathogenic Avian Influenza A viruses and MERS-CoV
- 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 (\$183,000.00 to Bahl Lab)  
Subaward PI/Project Lead. 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  
Oversees full phylogenetic systematics and molecular ecology and epidemiology of avian, swine and human influenza A viruses
- 2013 Mentor “NIAID Centers of Excellence for Influenza Research and Surveillance Training Grant” Massachusetts Institute of Technology, Boston MA. USA. PI Islam Hussein (\$7000 USD – direct cost for travel accommodation and training materials. No Indirect)
- 2013 Mentor “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 – direct cost for travel accommodation and training materials. No Indirect)
- 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)
- 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)
- 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)

2002-2006 The University Grants Council Post-graduate Research Scholarship The University of Hong, Hong Kong SAR, China (\$85,000 USD)

## **Annex D: Professional Membership and Service**

2012-present	Member, Influenza Research Database ( <a href="http://www.fludb.org">www.fludb.org</a> ) Scientific Working Group
2010–2014	<i>Member</i> , CEIRS Influenza Research Database Scientific Working Group, DMID/NIAID/NIH Centers of Excellence for Influenza Research and Surveillance
2010 - 2011	<i>Member</i> , 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	<i>Member</i> , International Society for Influenza and other Respiratory Virus Diseases
2011-present	<i>Member</i> , WHO/OIE/FAO Working Group on Evolution and Nomenclature of Influenza A (H5N1) Virus
2009	<i>Member</i> , World Health Organization Working Group on Evolution and Nomenclature of Pandemic Influenza A (H1N1) Virus

### **Editorial Board Member:**

2012-2013	<i>Infection Genetics and Evolution</i>
2022-2025	<i>Proceedings of the Royal Society B</i>

### **Journal Reviewer – ad hoc:**

*Nature, Nature Communications, Nature Climate Change, Scientific Reports, Proceedings of the National Academy of Sciences, Molecular Biology and Evolution, The ISME Journal, 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 – ad hoc:**

*The Thiel Foundation, Auckland University of Science and Technology, Research Foundation - Flanders (Fonds Wetenschappelijk Onderzoek - Vlaanderen, FWO), Swiss National Fund – CoVID-19 Rapid response reviewer*

## Annex E: Teaching

### Courses Instructed

Fall 2019-2021	“EPID7500 Intro Coding in R for Public Health” University of Georgia
Sept 2019	“Introduction to phylogenetic analysis for Molecular Epidemiology - Workshop” Research Center for Emerging Viral Infections, Chang Gung University, TaiWan 16-20 Sept 2019.
August 2019	“Introduction to Molecular Epidemiology” Zhejiang Center for Disease Control, China, 8-11 July, 2019.
Spring 2019	“EPID4070 Fundamentals of Epidemiology” University of Georgia. (NOTE – Instructor of record – but did not teach full course)
Spring 2018	“PH2730: Epidemiology and Control of Infectious Disease” University of Texas School of Public Health. Co-taught with Lu-Yu Hwang
Summer 2017	“PHM2610 Fundamentals of Epidemiology” Core course University of Texas School of Public Health.
Spring 2017	“PH2730: Epidemiology and Control of Infectious Disease” University of Texas School of Public Health. Co-taught with Lu-Yu Hwang
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. Co-taught with Lu-Yu Hwang
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)

### **Students Mentored**

Garick Stott	PhD Candidate, Bioinformatics, University of Georgia
Gabriella Veytsel	PhD Candidate, Bioinformatics, University of Georgia
Subhan Ullah	PhD Candidate, Infectious Diseases, University of Georgia
Swan Tan	PhD Candidate, Infectious Diseases, University of Georgia
Leke Lyu	PhD Candidate, Bioinformatics, University of Georgia
Zachary Petty	PhD Candidate, Bioinformatics, University of Georgia
Jiani Chen	PhD Candidate, Bioinformatics, University of Georgia
Lambodhar Damodaran	PhD Candidate, Bioinformatics, University of Georgia
Cody Daily	PhD Candidate, Epidemiology, University of Georgia
Nichelle Jasper	MPH candidate, Epidemiology, University of Georgia
Xueting Qiu	PhD Infectious Diseases, University of Georgia, Graduated 2019
Joseph Hicks	PhD Infectious Diseases, University of Georgia, Graduated 2019
Rebecca Fisk	MS Epidemiology, The University of Texas School of Public Health at Houston. Graduated 2018
Chloe Ng	MS Epidemiology, The University of Texas School of Public Health at Houston. Graduated 2018
Xueting Qiu	MS Epidemiology, The University of Texas School of Public Health at Houston. Graduated 2015
Varuna Manthena	MS Epidemiology, The University of Texas School of Public Health at Houston. Graduated 2015
Antonio Leonardi-Cattolica	MPH, Epidemiology, The University of Texas School of Public Health at Houston. Graduated 2015

## **Annex F**

### **Invited Lectures and Conference Presentations**

1. **J Bahl** (2022). ASV Satellite Symposium “Shaking the trees: sequence based inference in viral ecology and evolution.” [Invited Speaker]
2. **J Bahl** (2019). “Ecology, Epidemiology and Evolution of Influenza A virus” Research Center for Emerging Viral Infections, Chang Gung University, TaiWan [Invited Speaker]
3. **J Bahl** (2019). “Ecology, Epidemiology and Evolution of Influenza A virus” Zhejiang Center for Disease Control, China [Invited Speaker]
4. **J Bahl** (2019). “The role of human mediated animal movement in the spread and emergence of epizootic outbreaks” NIAID Centers of Excellence for influenza Research and Surveillance, Annual CEIRS Surveillance Meeting. Columbus Ohio, USA [Invited Speaker]
5. **J Bahl** (2018) “Molecular Epidemiology Influenza A viruses” University of Georgia [Invited Speaker – Department of Epidemiology and Biostatistics]
6. **J Bahl** (2018) “Ecology and Evolution of RNA viruses in Animals and Humans” University of Georgia [Invited Speaker – Department of Infectious Diseases]
7. **J Bahl** (2016) “Ecology and Evolution of Influenza A virus” The University of Toronto [Invited Speaker]
8. **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]
9. **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]
10. **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]
11. **J Bahl** (2013) “What is a phylogenetic tree?” Massachusetts Institute of Technology, Boston, Massachusetts, USA [Invited Speaker]
12. **J Bahl** (2013) “Ecological and epidemiological inference from evolutionary trees.” Massachusetts Institute of Technology, Boston, Massachusetts, USA [Invited Speaker]
13. **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]
14. **J Bahl** (2013) Ecology, Evolution and Epidemiology of influenza A virus. The Department of Ecology and Evolutionary Biology. Rice University, Houston Texas. [Invited Speaker]
15. **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]
16. **J Bahl** (2012). Long-term evolutionary consequences of viral migration between wild bird populations. NIAID Centers of Excellence for influenza Research and Surveillance, 6<sup>th</sup> Annual CEIRS Network Meeting. New York, USA [Invited Speaker]

17. **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]
18. **J Bahl** (2011) Source-sink dynamics of H3N2 seasonal influenza. Centers for Disease Control and Prevention, Atlanta Georgia, USA [Invited Speaker]
19. **J Bahl** (2009). Evolutionary genomics and genesis of pandemic influenza. British Columbia Centres for Disease Control. British Columbia, Canada. [Invited Speaker]
20. **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]
21. **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, 3<sup>rd</sup> Annual CEIRS Network Meeting Minneapolis, USA [Invited Speaker]