

# RESUME

## PERSONAL INFORMATION:

Full Name: Mang Shi  
Date of Birth: 27th December 1985  
Nationality: P. R. China  
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## ACADEMIC EXPERIENCE:

2012-2015 PhD (Virus Evolution), The University of Sydney, Australia  
2011-2012 PhD (Virus Evolution), The Pennsylvania State University, USA  
2009-2011 Mphil (Virus Evolution), The University of Hong Kong, Hong Kong S.A.R.  
2007-2008 BSc-exchange (Microbiology), The University of British Columbia, Canada  
2005-2008 BSc (Biology), The University of Hong Kong, Hong Kong S.A.R.  
2004-2005 Pre-undergraduate, Zhejiang University, P.R.China

## CAREER EXPERIENCE:

2018-present Lecturer, The University of Sydney, Australia  
2015-2017 Associated Lecturer, The University of Sydney, Australia  
2013-present Guest Researcher, Chinese Centers for Disease Control and Prevention, China  
2011 ORISE Fellow, The Centers for Disease Control and Prevention, USA  
2009-2010 Guest Researcher, The Centers for Disease Control and Prevention, USA  
2008 Research Assistant, School of Biological Science, The University of Hong Kong

## CURRENT RESEARCH PROJECTS:

- Meta-transcriptomics based virus discovery in lower vertebrates, invertebrates, and environmental samples.
- Application of Next Generation Sequencing (NGS) approach on clinical pathogen discovery
- Macro-evolution of RNA viruses.
- Influence of wolbachia infection on virus diversity in fruit flies.
- Virome study of Australian arthropods.

## RESEARCH GRANTS:

1. Centre for Pathogen Discovery; DVC Research/Sydney Research Excellence Initiative 2020 (SREI). [Chief Investigator]
2. Revealing the Australian virome, HPC Grand Challenge award. [Chief Investigator]

## PEER REVIEWED JOURNAL ARTICLES:

Total publication: 54. Google scholar citations: 3569, h-index: 23, i10-index: 42

1. **Shi M**, White VL, Schlub T, Eden JS, Hoffmann AA, Holmes EC (2018). No detectable effect of Wolbachia wMel on the prevalence and abundance of the RNA virome of *Drosophila melanogaster*. *Proc Biol Sci.* 285. (IF = 4.85)
2. Russo AG, Eden JS, Enosi Tuipulotu D, **Shi M**, Selechnik D, Shine R, Rollins LA, Holmes EC, White PA (2018). Viral discovery in the invasive Australian cane toad (*Rhinella marina*) using metatranscriptomic and genomic approaches. *J. Virol.* 00768-18. (IF = 4.66)
3. Aghazadeh M#, **Shi M# (Co-first author)**, Barrs VR, McLuckie AJ, Lindsay SA, Jameson B, Hampson B, Holmes EC, Beatty JA. A Novel Hepadnavirus Identified in an Immunocompromised Domestic Cat in Australia. *Viruses* 10:269. (IF = 3.76)
4. Complete genome of *Aedes aegypti* anphevirus in the Aag2 mosquito cell line F Di Giallonardo, MD Audsley, M Shi, PR Young, EA McGraw, EC Holmes *Journal of General Virology*
5. **Shi M**, Lin XD, Chen X, Tian JH, Chen LJ, Li K, Wang W, Eden JS, Shen JJ, Liu L, Holmes EC, Zhang YZ (2018). The evolutionary history of vertebrate RNA viruses. *Nature* 556:197. (IF = 40.14, C = 14)
6. Zhang YZ, **Shi M**, Holmes EC (2018). Using metagenomics to characterize an expanding virosphere. *Cell* 172:1168-1172. (IF = 30.41, C = 4)
7. **Shi M**, Holmes EC, Zhang YZ. Meta-transcriptomics and the evolutionary biology of RNA viruses (2018). *Virus Res.* 243:83-90. (IF = 2.63, C = 7)
8. Paden CR, Yusof MFBM, Al Hammadi ZM, Queen K., Tao Y, Eltahir YM, Elsayed EA, Marzoug BA, Bensalah OKA, Khalafalla AI, Al Mulla M, Khudhair A, Elkheir KA, Issa ZB, Pradeep K, Elsaleh FN, Imambaccus H, Sasse J, Weber S, **Shi M**, Zhang J, Li Y, Pham H, Kim L, Hall AJ, Gerber SI, Al Hosani FI, Tong S, Al Muhairi SSM (2017). Zoonotic origin and transmission of Middle East respiratory syndrome coronavirus in the UAE. *Zoonoses Public Health.* Epub ahead of print. (IF = 2.32, C = 2)
9. Yusof MF, Queen K, Eltahir YM, Paden CR, Al Hammadi ZMAH, Tao Y, Li Y, Khalafalla AI, **Shi M**, Zhang J, Mohamed MSAE, Ahmed MHAE, Azeez IA, Bensalah OK, Eldahab ZS, Al Hosani FI, Gerber SI, Hall AJ, Tong S, Al Muhairi SS (2017). Diversity of Middle East respiratory syndrome coronaviruses in 109 dromedary camels based on full genome sequencing, Abu Dhabi, United Arab Emirates. *Emerg. Microbes. Infect.* 6:e101. (IF = 5.61, C=2)
10. Pettersson JH, **Shi M**, Bohlin J, Eldholm V, Brynildsrud OB, Paulsen KM, Andreassen A, Holmes EC (2017). Characterizing the virome of *Ixodes ricinus* ticks from northern Europe. *Sci. Rep.* 7:10870. (IF = 4.26, C = 3)
11. **Shi M**, Neville P, Nicholson J, Eden J-S, Imrie A, Holmes EC (2017). High resolution metatranscriptomics reveals the ecological dynamics of mosquito-associated RNA viruses in Western Australia. *J. Virol.* 91:e00680-17. (IF = 4.66, C = 10)
12. Eden J-S, Rose K, Ng J, **Shi M**, Wang Q, Sintchenko V, Holmes EC (2017). *Francisella tularensis* ssp *holarctica* in Ringtail Possums, Australia. *Emerg. Infect. Diseases.* 23:1198–1201. (IF = 8.22, C = 6)

13. Remnant EJ, **Shi M**, Buchmann G, Blacquièrre T, Holmes EC, Beekman M, Ashe A (2017). A diverse range of novel RNA viruses in geographically distinct honey bee populations. *J. Virol.* 91:e00158-17. (IF = 4.66, C = 16)
14. Velasco-Villa A, Mauldin MR, **Shi M**, Escobar LE, Gallardo-Romero NF, Damon I, Olson VA, Streicker DG, Emerson G (2017). The history of rabies in the Western Hemisphere. *Antiviral Res.* 146:221-232. (IF = 4.27, C = 14)
15. Velasco-Villa A, Escobar LE, Sanchez A, **Shi M**, Streicker DG, Gallardo-Romero NF, Vargas-Pino F, Gutierrez-Cedillo V, Damon I, Emerson G (2017). Successful strategies implemented towards the elimination of canine rabies in the Western Hemisphere. *Antiviral Res.* 143:1-12. (IF = 4.27, C = 10)
16. Di Giallonardo F, Schlub TE, **Shi M**, Holmes EC (2017). Dinucleotide composition in animal RNA viruses is shaped more by virus family than by host species. *J. Virol.* 91:e02381-16. (IF = 4.66, C = 5)
17. Chen LJ, Lin XD, Tian JH, Liao Y, Ying XH, Shao JW, Yu B, Guo JJ, Wang MR, Peng Y, **Shi M**, Holmes EC, Yang ZQ, Zhang YZ (2017). Diversity, evolution and population dynamics of avian influenza viruses circulating in the live poultry markets in China. *Virology.* 505:33-41. (IF = 3.35, C = 6)
18. Tao Y#, **Shi M# (Co-first author)**, Chommanard C, Queen K, Zhang J, Markotter W, Kuzmin IV, Holmes EC, Tong S (2017). Surveillance of bat coronaviruses in Kenya identifies relatives of human coronaviruses NL63 and 229E and their recombination history. *J. Virol.* 91:e01953-16. (IF = 4.66, C = 13)
19. **Shi M**, Lin XD, Tian JH, Chen LJ, Chen X, Li CX, Qin XC, Li J, Cao JP, Eden JS, Buchmann J, Wang W, Xu J, Holmes EC, Zhang YZ (2016). Redefining the invertebrate RNA virosphere. *Nature.* 540:539-543. (IF = 40.14, C = 163)
20. Li K, Lin XD, Huang KY, Zhang B, **Shi M**, Guo WP, Wang MR, Wang W, Xing JG, Li MH, Hong WS, Holmes EC, Zhang YZ (2016). Identification of novel and diverse rotaviruses in rodents and insectivores, and evidence of cross-species transmission into humans. *Virology.* 494:168-77. (IF = 3.35, C = 18)
21. Afonso CL, Amarasinghe GK, Bányai K, Bào Y, Basler CF, ..., **Shi M**, Smither SJ, Stenglein MD, Stone DM, Takada A, Terregino C, Tesh RB, Tian JH, Tomonaga K, Tordo N, Towner JS, Vasilakis N, Verbeek M, Volchkov VE, Wahl-Jensen V, Walsh JA, Walker PJ, Wang D, Wang LF, Wetzel T, Whitfield AE, Xiè JT, Yuen KY, Zhang YZ, Kuhn JH. Taxonomy of the order Mononegavirales: update 2016 (2016). *Arch. Virol.* 161:2351-60. (IF = 2.06, C = 136)
22. Chen LJ, Lin XD, Guo WP, Tian JH, Wang W, Ying XH, Wang MR, Yu B, Yang ZQ, **Shi M**, Holmes EC, Zhang YZ (2016). Diversity and evolution of avian influenza viruses in live poultry markets, free range poultry and wild wetland birds in China. *J. Gen. Virol.* 97:844-54. (IF = 2.84, C = 15)
23. **Shi M**, Lin XD, Vasilakis N, Tian JH, Li CX, Chen LJ, Eastwood G, Diao XN, Chen MH, Chen X, Qin XC, Widen SG, Wood TG, Tesh RB, Xu J, Holmes EC, Zhang YZ (2015). Divergent viruses discovered in arthropods and vertebrates revise the evolutionary history of the *Flaviviridae* and related viruses. *J. Virol.* 90:659-669. (IF = 4.66, C = 46)
24. Zhao K, Ye C, Chang XB, Jiang CG, Wang SJ, Cai XH, Tong GZ, Tian ZJ, **Shi M#(Co-corresponding author)**, An TQ# (2015). Importation and recombination are responsible for

the latest emergence of highly pathogenic Porcine Reproductive and Respiratory Syndrome virus in China. *J. Virol.* 89:10712-10716. (IF = 4.66, C = 51)

25. Guo WP, Lin XD, Chen YP, Liu Q, Wang W, Wang CQ, Li MH, Sun XY, **Shi M**, Holmes EC, Zhang YZ (2015). Fourteen types of co-circulating recombinant enterovirus were associated with hand, foot, and mouth disease in children from Wenzhou, China. *J. Clin. Virol.* 70:29-38. (IF = 3.05, C = 18)
26. Ye C, Zhang QZ, Tian ZJ, Zheng H, Zhao K, Liu F, Guo JC, Tong W, Jiang CG, Wang SJ, **Shi M**, Chang XB, Jiang YF, Peng JM, Zhou YJ, Tang YD, Sun MX, Cai XH, An TQ, Tong GZ (2015). Genomic characterization of emergent pseudorabies virus in China reveals marked sequence divergence: Evidence for the existence of two major genotypes. *Virology* 483:32-43. (IF = 3.35, C = 38)
27. Li K, Lin XD, Wang W, **Shi M**, Guo WP, Zhang XH, Xing JG, He JR, Wang K, Li MH, Cao JH, Jiang ML, Holmes EC, Zhang YZ (2015). Isolation and characterization of a novel arenavirus harbored by Rodents and Shrews in Zhejiang province, China. *Virology* 476:37-42. (IF = 3.35, C = 15)
28. Brar MS, **Shi M**, Murtaugh MP, Leung FC (2015). Evolutionary diversification of type 2 porcine reproductive and respiratory syndrome virus. *J. Gen. Virol.* 96:1570-1580. (IF = 2.84, C = 24)
29. Li CX#, **Shi M# (Co-first author)**, Tian JH, Lin XD, Kang YJ, Chen LJ, Qin XC, Xu J, Holmes EC, Zhang YZ (2015). Unprecedented genomic diversity of RNA viruses in arthropods reveals the ancestry of negative sense RNA viruses. *eLife* 4:e05378. (IF = 7.73, C = 140)
30. Wang W, Lin XD, Guo WP, Zhou RH, Wang MR, Wang CQ, Ge S, Mei SH, Li MH, **Shi M**, Holmes EC, Zhang YZ (2015). Discovery, diversity and evolution of novel coronaviruses sampled from rodents in China. *Virology* 474:19-27. (IF = 3.35, C = 17)
31. Kang YJ, Diao XN, Zhao GY, Chen MH, Xiong Y, **Shi M**, Fu WM, Guo YJ, Pan B, Chen XP, Holmes EC, Gillespie JJ, Dumler SJ, Zhang YZ (2014). Extensive diversity of Rickettsiales bacteria in two species of ticks from China and the evolution of the Rickettsiales. *BMC. Evol. Biol.* 14:167. (IF = 3.22, C = 30)
32. Qin XC#, **Shi M# (Co-first author)**, Tian JH, Lin XD, Gao DY, He JR, Wang JB, Li CX, Kang YJ, Yu B, Zhou DJ, Xu J, Plyusnin A, Holmes EC, Zhang YZ (2014). A tick-borne segmented RNA virus contains genome segments derived from unsegmented viral ancestors. *Proc. Natl. Acad. Sci. USA.* 111:6744-6749. (IF = 9.66, C = 27)
33. Brar MS, **Shi M**, Hui RK, Leung FC. Genomic evolution of porcine reproductive and respiratory syndrome virus (PRRSV) isolates revealed by deep sequencing (2014). *PLoS One* 9:e88807. (IF = 2.81, C = 22)
34. Devault AM, Golding GB, Waglechner N, Enk JM, Kuch M, Tien JH, **Shi M**, Fisman DN, Dhody AN, Forrest S, Bos KI, Earn DJ, Holmes EC, Poinar HN (2014). Second-pandemic strain of *Vibrio cholerae* from the Philadelphia cholera outbreak of 1849. *N. Engl. J. Med.* 370:334-340. (IF = 72.41, C = 69)

35. **Shi M**, Lemey P, Singh Brar M, Suchard MA, Murtaugh MP, Carman S, D'Allaire S, Delisle B, Lambert MÈ, Gagnon CA, Ge L, Qu Y, Yoo D, Holmes EC, Leung FC (2013). The spread of type 2 Porcine Reproductive and Respiratory Syndrome Virus (PRRSV) in North America: a phylogeographic approach. *Virology*. 447:146-154. (IF = 3.35, C = 19)
36. Tong S, Zhu X, Li Y, **Shi M**, Zhang J, Bourgeois M, Yang H, Chen X, Recuenco S, Gomez J, Chen LM, Johnson A, Tao Y, Dreyfus C, Yu W, McBride R, Carney PJ, Gilbert AT, Chang J, Guo Z, Davis CT, Paulson JC, Stevens J, Rupprecht CE, Holmes EC, Wilson IA, Donis RO (2013). New world bats harbor diverse influenza A viruses. *PLoS Pathog*. 9:e1003657. (IF = 6.61, C = 741)
37. **Shi M**, Holmes EC, Brar MS, Leung FC (2013). Recombination is associated with an outbreak of novel highly pathogenic porcine reproductive and respiratory syndrome viruses in China. *J. Virol*. 87:10904-10907. (IF = 4.66, C = 50)
38. Lam TT, Chong YL, **Shi M**, Hon CC, Li J, Martin DP, Tang JW, Mok CK, Shih SR, Yip CW, Jiang J, Hui RK, Pybus OG, Holmes EC, Leung FC (2013). Systematic phylogenetic analysis of influenza A virus reveals many novel mosaic genome segments. *Infect. Genet. Evol*. 18:367-378. (IF = 2.89, C = 22)
39. Seetahal JF, Velasco-Villa A, Allicock OM, Adesiyun AA, Bissessar J, Amour K, Phillip-Hosein A, Marston DA, McElhinney LM, **Shi M**, Wharwood CA, Fooks AR, Carrington CV (2013). Evolutionary history and phylogeography of rabies viruses associated with outbreaks in Trinidad. *PLoS Negl. Trop. Dis*. 7:e2365. (IF = 3.83, C = 15)
40. Tao Y#, **Shi M# (Co-first author)**, Conrardy C, Kuzmin IV, Recuenco S, Agwanda B, Alvarez DA, Ellison JA, Gilbert AT, Moran D, Niezgodna M, Lindblade KA, Holmes EC, Breiman RF, Rupprecht CE, Tong S (2013). Discovery of diverse polyomaviruses in bats and the evolutionary history of the Polyomaviridae. *J. Gen. Virol*. 94:738-748. (IF = 2.84, C = 38)
41. **Shi M**, Jagger BW, Wise HM, Digard P, Holmes EC, Taubenberger JK (2012). Evolutionary conservation of the PA-X open reading frame in segment 3 of influenza A virus. *J. Virol*. 86:12411-12413. (IF = 4.66, C = 57)
42. Tao Y, Tang K, **Shi M**, Conrardy C, Li KS, Lau SK, Anderson LJ, Tong S (2012). Genomic characterization of seven distinct bat coronaviruses in Kenya. *Virus Res*. 167:67-73. (IF = 2.63, C = 16)
43. Kuzmin IV, **Shi M**, Orciari LA, Yager PA, Velasco-Villa A, Kuzmina NA, Streicker DG, Bergman DL, Rupprecht CE (2012). Molecular inferences suggest multiple host shifts of rabies viruses from bats to mesocarnivores in Arizona during 2001-2009. *PLoS Pathog*. 8:e1002786. (IF = 6.61, C = 82)
44. Lam TT, Hon CC, Lemey P, Pybus OG, **Shi M**, Tun HM, Li J, Jiang J, Holmes EC, Leung FC (2012). Phylodynamics of H5N1 avian influenza virus in Indonesia. *Mol. Ecol*. 2:3062-3077. (IF = 6.09, C = 26)
45. Tong S, Li Y, Rivaille P, Conrardy C, Castillo DA, Chen LM, Recuenco S, Ellison JA, Davis CT, York IA, Turmelle AS, Moran D, Rogers S, **Shi M**, Tao Y, Weil MR, Tang K, Rowe LA,

- Sammons S, Xu X, Frace M, Lindblade KA, Cox NJ, Anderson LJ, Rupprecht CE, Donis RO (2012). A distinct lineage of influenza A virus from bats. *Proc. Natl. Acad. Sci. USA* 109:4269-4274. (IF = 9.66, C = 842)
46. Van Doorselaere J, Brar MS, **Shi M**, Karniychuk U, Leung FC, Nauwynck HJ (2012). Complete genome characterization of a East European Type 1 subtype 3 porcine reproductive and respiratory syndrome virus. *Virus Genes* 44:51-54. (IF = 1.43, C = 15)
  47. Cai S, Li J, Wong MT, Jiao P, Fan H, Liu D, Liao M, Jiang J, **Shi M**, Lam TT, Ren T, Leung FC (2011). Genetic characterization and evolutionary analysis of 4 Newcastle disease virus isolate full genomes from waterbirds in South China during 2003-2007. *Vet. Microbiol.* 152:46-54. (IF = 2.63, C = 23)
  48. Brar MS, **Shi M**, Ge L, Carman S, Murtaugh MP, Leung FC (2011). Porcine reproductive and respiratory syndrome virus in Ontario, Canada 1999 to 2010: genetic diversity and restriction fragment length polymorphisms. *J. Gen. Virol.* 92:1391-1397. (IF = 2.84, C = 22)
  49. Tun HM, **Shi M**, Wong CL, Ayudhya SN, Amonsin A, Thanawonguwech R, Leung FC (2011). Genetic diversity and multiple introductions of porcine reproductive and respiratory syndrome viruses in Thailand. *Virol. J.* 8:164. (IF = 2.14, C = 19)
  50. **Shi M**, Lam TT, Hon CC, Hui RK, Faaberg KS, Wennblom T, Murtaugh MP, Stadejek T, Leung FC (2010). Molecular epidemiology of PRRSV: a phylogenetic perspective. *Virus Res.* 154:7-17. (IF = 2.63, C = 187)
  51. **Shi M**, Lam TT, Hon CC, Murtaugh MP, Davies PR, Hui RK, Li J, Wong LT, Yip CW, Jiang JW, Leung FC (2010). Phylogeny-based evolutionary, demographical, and geographical dissection of North American type 2 porcine reproductive and respiratory syndrome viruses. *J. Virol.* 84:8700-11. (IF = 4.66, C = 166)
  52. Aréchiga-Ceballos N, Velasco-Villa A, **Shi M**, Flores-Chávez S, Barrón B, Cuevas-Domínguez E, González-Origel A, Aguilar-Setién A (2010). New rabies virus variant found during an epizootic in white-nosed coatis from the Yucatan Peninsula. *Epidemiol. Infect.* 15:1-4. (IF = 2.08, C = 21)
  53. Yip CW, Hon CC, **Shi M**, Lam TT, Chow KY, Zeng F, Leung FC (2009). Phylogenetic perspectives on the epidemiology and origins of SARS and SARS-like coronaviruses. *Infect. Genet. Evol.* 9:1185-1196. (IF = 2.89, C = 23)
  54. Hon CC, Lam TT, Yip CW, Wong RT, **Shi M**, Jiang J, Zeng F, Leung FC (2008). Phylogenetic evidence for homologous recombination within the family *Birnaviridae*. *J. Gen. Virol.* 89:3156-64. (IF = 2.84, C = 31)

#### BOOK CHAPTERS:

1. K Queen, **M Shi**, LJ Anderson, S Tong. Other Bat-Borne Viruses. In *Bats and Viruses: A New Frontier of Emerging Infectious Diseases*. (Ed. L-F Wang & C Cowled). pp. 217-247. John Wiley & Sons, Inc.

#### CONFERENCE AND SEMINAR:

- [Invited speaker] **Infection and Immunity Seminar Series (2018)**. Sydney, Australia.
- [Oral presenter] **Society of Molecular Biology and Evolution Meetings (2018)**. Yokohama, Japan
- [Oral presenter] **International Society of Microbiology Meetings (2016)**. Montreal, Canada
- [Oral presenter] **The Australian Society for Microbiology Meetings (2016)**. Perth, Australia
- [Oral presenter] **The Australian Society for Virology Meetings (2015)**. Hunter Valley, Australia
- [Oral presenter] **Carles Perkins Center EMCR Symposium (2015)**. Sydney, Australia
- [Attendee] **ISIRV Workshop on Next Generation Sequencing of Viruses (2015)**. Institut Pasteur, Paris, France.
- [Attendee] **7th European Meeting on Viral Zoonoses (2014)**. Saint-Raphaël, France.
- [Oral presenter] **International PRRS Symposium (2011)**. Chicargo, USA.
- [Attendee with travel grant] **The 8th Annual Workshop and Conference of EEID (ecology and evolution of infectious diseases) (2010)**. Cornell University, USA.
- [Oral presenter] **The 90<sup>th</sup> Annual Meeting of the CRWAD (conference of research workers in animal diseases) (2009)**. Chicargo, USA.
- [Oral presenter] **2009 International PRRS Symposium (2009)**. Chicargo, USA.
- [Attendee with travel grant] **The 15<sup>th</sup> International Bioinformatics Workshop on Virus Evolution and Molecular Epidemiology: Advanced Courses (2009)**. Rotterdam, The Netherlands.
- [Oral presenter] **XIX International Conference on Rabies in the Americas (RITA) (2008)**. CDC; Atlanta, USA.
- [Poster presenter] **The 5<sup>th</sup> Aquatic Virus Workshop (5<sup>th</sup> AVW) (2008)**. UBC; Vancouver, Canada.
- [Poster presenter] **Keystone symposium: Molecular Evolution as a Driving Force in Infectious Diseases (Keystone D4) (2008)**. Breckenridge, USA.

## **HONORS AND AWARDS**

- Postgraduate Research Prize for Outstanding Academic Achievement (2015)
- Australian Postgraduate Awards (APA) (2012-2015)
- International Postgraduate Research Scholarships (IPRS) (2012-2015)
- Postgraduate studentship (Hong Kong, 2012)
- Dr. Lo Kwee Seong Education Foundation Travel and Conference Grants (2008-09)
- Postgraduate studentship (2009-2011)
- Chan Tat Chee Memorial Education Abroad Scholarship (2007-08).
- Incentive Program for Undergraduate Research Excellence in Science (I-PURES) (2007)