
From: 胡犇[huben@wh.iov.cn]
Sent: Fri 7/8/2016 10:08:26 AM (UTC-04:00)
To: Baric, Ralph S[rbaric@email.unc.edu]; Gralinski, Lisa E[lgralins@email.unc.edu]
Cc: 石正丽[zhishi@wh.iov.cn]
Subject: Re: RE: RE: Invitation letter of the 7th International Symposium on Emerging Viral Diseases
Attachment: Invitation letter Lisa Gralinski.doc

Dear Prof Baric and Dr. Gralinski:

We are very glad that our symposium still have change to include a talk about the work of your lab, which is one of the leading research groups on coronavirus pathogenesis.

Please find the invitation letter to Dr. Gralinski which will help her for visa application.

Best regards

Ben

-----原始邮件-----

发件人: "Baric, Ralph S" <rbaric@email.unc.edu>

发送时间: 2016年7月8日 星期五

收件人: "石正丽" <zhishi@wh.iov.cn>

抄送: "胡犇" <huben@wh.iov.cn>, "Gralinski, Lisa E" <lgralins@email.unc.edu>

主题: RE: RE: Invitation letter of the 7th International Symposium on Emerging Viral Diseases

Hi Zhengli, Thanks for understanding, I am so sorry that I can't make the meeting. However on a brighter note, Lisa Gralinski can attend, she has been studying SARS-CoV and Bat-SARS like virus pathogenesis in the Collaborative Cross Mouse Resource, including mapping susceptibility alleles that regulate disease severity and outcomes. I think the resource and her talk will be of broad interest to the meeting participants. I have cc'd her on the email. Hope you are doing well. Ralph

From: 石正丽 [mailto:zhishi@wh.iov.cn]

Sent: Thursday, July 07, 2016 8:59 PM

To: Baric, Ralph S

Cc: 胡犇

Subject: Re: RE: Invitation letter of the 7th International Symposium on Emerging Viral Diseases

Dear Ralph,

Thank you for your reply. It's pity that you will not be able to come. It'll be great if someone from your lab can make it. Can you please ask this person to contact us and we will send him/her an invitation letter for Visa application.

Best regards,

Zhengli,

-----原始邮件-----

发件人: "Baric, Ralph S" <rbaric@email.unc.edu>

发送时间: 2016年7月8日 星期五

收件人: "胡犇" <huben@wh.iov.cn>

抄送: "石正丽" <zlshi@wh.iov.cn>

主题: RE: Invitation letter of the 7th International Symposium on Emerging Viral Diseases

Hi Ben, Thanks for your email. Unfortunately, I will not be able to attend this meeting. For whatever reason, I had it booked on my calendar for the week after and now have commitments that I cannot escape. Please pass on my sincere regrets to Zhengli as I was very interested in visiting and talking science. If you all are willing, I could have a representative from my lab attend, recognizing that this isn't what you were hoping for. My sincerest apologies again. Ralph

From: 胡犇 [<mailto:huben@wh.iov.cn>]

Sent: Wednesday, July 06, 2016 5:43 AM

To: Baric, Ralph S

Cc: 石正丽

Subject: Re: Invitation letter of the 7th International Symposium on Emerging Viral Diseases

Dear Prof. Baric:

How are you?

I wonder whether you have received the invitation letter of the 7th International symposium on Emerging Viral Diseases which I sent in late April.

Emerging coronavirus is a special session in the symposium this year. It will be great if you are able to attend the meeting and give a talk. If you plan to come, please let me know and submit your abstract before 31th July. We sincerely hope that you can attend the meeting. As the chairman of the conference, Prof. Zhengli Shi is looking forward to seeing you in Wuhan.

Best regards

Ben Hu Ph.D

Secretary of the 7th International Symposium on Emerging Viral Diseases

Wuhan Institute of Virology

Chinese Academy of Sciences

Wuhan 430071, P.R. China

Tel: 86-27-87197311

E-mail: huben@wh.iov.cn

-----原始邮件-----

发件人: "胡犇" <huben@wh.iov.cn>

发送时间: 2016年4月29日 星期五

收件人: rbaric@email.unc.edu

抄送:

主题: Invitation letter of the 7th International Symposium on Emerging Viral Diseases

Dear Prof. Baric:

The 7th International Symposium on Emerging Viral Diseases will be held in October 19-21, 2016, in Wuhan, China. The biennial symposium, which covers various topics of emerging viruses including epidemiology, evolution, molecular biology, pathogenesis and immunology, has become an important event for leading Chinese and international virologists to discuss cutting-edge science as well as to foster global collaborations.

You are highly reputable in coronavirus researches and we sincerely hope that you can attend the symposium. Please find the invitation letter by the chairmen of the symposium, Dr. Zhengli Shi from Wuhan Institute of Virology, Chinese Academy of Sciences, and Dr. Linfa Wang from the Programme in Emerging Infectious Diseases, Duke-NUS Medical School, Singapore.

If you have any question regarding the conference, please contact me.

Thank you!

Best regards

Ben Hu Ph.D

Secretary of the 7th International Symposium on Emerging Viral Diseases

Wuhan Institute of Virology

Chinese Academy of Sciences

Wuhan 430071, P.R. China

Tel: 86-27-87197311

E-mail: huben@wh.iov.cn



The 7th International Symposium on Emerging Viral Diseases

Address: Xiaohongshan 44, Wuchang, Wuhan 430071, Hubei, P.R. China

Tel: +86-27-87197311 Fax: +86-27-87197240 <http://www.whiov.ac.cn>

July 07, 2016

Dr. Lisa Gralinski

Department of Epidemiology

Gillings School of Global Public Health

University of North Carolina

Dear Dr. Lisa Gralinski:

The 7th International Symposium on Emerging Viral Diseases will be held in October 19-21, 2016 in Wuhan, China. The symposium will be organized by the Wuhan Institute of Virology, Chinese Academy of Sciences, and will cover various topics of emerging viruses, including epidemiology, molecular biology, evolution, immunology, and pathogenesis. This biennial symposium has become an important event for leading Chinese and international virologists to discuss cutting-edge science as well as to foster global collaborations.

It is our great pleasure to invite you as a plenary speaker to present your work at this symposium. Your accommodation and expenses in Wuhan will be covered by the conference. However, due to budget constrain, we are regretfully unable to cover your travel expenses.

If you are able to attend the symposium, please register and submit the abstract of your presentation online (<http://isevd2016.csp.escience.cn>) by July 31, 2016. As an invited speaker, your registration fee will be waived.

We look forward to seeing you in Wuhan.

Sincerely Yours,

Zhengli SHI Ph.D

Wuhan Institute of Virology
Chinese Academy of Sciences
zlshi@wh.iov.cn

Linfa WANG Ph.D

Programme in Emerging Infectious Diseases
Duke-NUS Medical School
linfa.wang@duke-nus.edu.sg

Abstract template

Difference in receptor usage between SARS coronavirus and SARS-like coronavirus of bat origin

Wuze Ren¹, Xiuxia Qu², Wendong Li¹, Zhenggang Han¹, Meng Yu, Peng Zhou, Shuyi Zhang, Lin-Fa Wang³, Hongkui Deng², Zhengli Shi¹

¹State key Laboratory of Virology, Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan, China; ²Key Laboratory of Cell Proliferation and Differentiation of the Ministry of Education, College of Life Sciences, Peking University, Beijing, China; ³CSIRO Livestock Industries, Australian Animal Health Laboratory and Australian Biosecurity Cooperative Research Center for Emerging Infectious Diseases, Geelong, Australia; and School of Life Science, ⁴East China Normal University, Shanghai, China

Severe acute respiratory syndrome (SARS) was caused by the SARS-associated coronavirus (SARS-CoV), which uses the angiotensin converting enzyme 2 (ACE2) as its receptor for cell entry. A group of SARS-like coronaviruses (SL-CoVs) has been identified in horseshoe bats. SL-CoVs and SARS-CoVs share an identical genome organization and high sequence identities with the main exception of the N-terminus of the spike protein (S), known to be responsible for receptor binding in coronaviruses. In this study, we investigated the receptor usage of the SL-CoV S by combining an HIV-based pseudovirus system with cell lines expressing the ACE2 molecules of human, civet or horseshoe bat. In addition to full-length S of SL-CoV and SARS-CoV, a series of S chimeras was constructed by inserting different sequences of the SARS-CoV S into the SL-CoV S backbone. Several important observations were made from this study. First, the SL-CoV S was unable to use any of the three ACE2 molecules as its receptor. Second, the SARS-CoV S failed to enter cells expressing the bat ACE2. Third, the chimeric S covering the previously defined receptor-binding domain gained their ability to enter cells via human ACE2, albeit with different efficiency for different constructs. Fourth, a minimal insert region (aa 310-518) was found to be sufficient to convert the SL-CoV S from ACE2-non-binding to human ACE2-binding, indicating that the SL-CoV S is largely compatible to SARS-CoV S protein both in structure and function.

From: zhanghan@wh.iov.cn[zhanghan@wh.iov.cn]
Sent: Wed 7/27/2016 12:52:32 PM (UTC-04:00)
To: Gralinski, Lisa E[lgralins@email.unc.edu]
Subject: Registration confirmation for Nature Conference on Viral Infection and Immune response

Dear Dr. Lisa Gralinski:

Thank you for registering Nature Conference on Viral Infection and Immune response.

Your registration application has been accepted.

Your registration details are:

Serial Number:102

Registration Date:2016-07-28 00:52:28

First Name: Lisa

Last Name:Gralinski

Chinese Name :

Birth Date :

National Identification Number :

Passport Number :

Institute/Company : University of North Carolina

Fax :

Province :

City :

Postal Address : 2107 McGavran-Greenberg Hall

CB 7435

Chapel Hill, NC 27599-7435

Notes :

Phone Number : 9199663890

Zip Code : 27599-7435

Gender :

Title : Dr.

Country/Region : United States

register fee :

price : CNY 1800.0, title : Regular Booking (Academic)

Total Amount:CNY 1800.0

If you want to cancel registration, please click

http://viir2016.csp.escience.cn:80/dct/page/65574/___rpcsp0x2MySpace!65574%7C0_action/cancelRegistion/___rpcsp0x2MySpace!65574%7C0_info/ec7494c84e75ca0ef61214f6b9fa7629/___rpcsp0x2MySpace!65574%7C0_id/106657? .

Note: Please pay your registration fee before the deadline of regular registration. If you choose the "Students" or "Academic" to register, you will need to enter an invitation code to pay your fees. Please send the scanning copies of relevant certificates (i.e. students' identity cards, academic employment certificates and etc.) to zhanghan@wh.iov.cn to request for the invitation code before paying your fees.

Please contact me directly if you have any questions or concerns. I will be glad to help you.

Thank you again and we look forward to seeing you in Wuhan!

Best regards,

Han Zhang
VIIR Conference Secretariat
Wuhan Institute of Virology, CAS
No. 44, Xiao Hong Shan, Wuhan, Hubei, China, 430071
Tel: 0086-27-87198593
Fax: 0086-27-87198921
Email: zhanghan@wh.iov.cn

From: Gralinski, Lisa E[lgralins@email.unc.edu]
Sent: Tue 8/9/2016 10:59:56 AM (UTC-04:00)
To: 张晗[zhanghan@wh.iov.cn]
Subject: Re: invitation letter for Nature Conference on Viral Infection and Immune Response
Attachment: Gralinski passport.pdf
Attachment: Gralinski CV.doc
Attachment: InvitationApplication - Gralinski.docx

Dear Ms. Han,

Thank you so much for your prompt response. I have submitted my abstract to the conference but need an invitation code in order to pay as an academic. Can you assist with this code?

This is indeed my first trip to China. Attached you will find a scan of my passport and a copy of my CV. Please let me know if you need any further information and I will send it to you asap!

thank you again,

Lisa Gralinski

From: 张晗 <zhanghan@wh.iov.cn>
Sent: Tuesday, August 9, 2016 3:03 AM
To: Gralinski, Lisa E
Subject: Re: invitation letter for Nature Conference on Viral Infection and Immune Response

Dear Dr. Gralinski,

Thank you for registering our conference. For your information, please pay your registration fee first and submit your abstract. Then we will arrange the invitation letter for you.

To ensure the success of visa application, I will help you apply the letter from the duly authorized unit, i.e. the Chinese Academy of Sciences (CAS). Please download **the attached form** and fill in the information we need, and then send the completed form to me.

In addition, **the scanning picture of your passport** and **your Cv** is needed.

Note: In order to obtain the visa, I have some other questions: 1) Is it your first time to come to China?
2) Have you ever obtained the Business Visiting Visa (F) issued by China?

If you have ever come to China and had been obtained the visa, please send me the scanning picture of China's visa page on your passport.

Thank you for your cooperation! To finalize the official letter issued by CAS will take 3-4 weeks, so you are strongly recommended to send me the documents above we need asap.

The invitation letter issued by CAS will focus strictly to the duration of the two meeting that you are going to attend, which means Oct. 18/19- Oct. 24/25 (only one entry).

If you have any questions or concerns, please feel free to contact.

Zhang Han

-----原始邮件-----

发件人: "Gralinski, Lisa E" <lgralins@email.unc.edu>

发送时间: 2016年8月9日 星期二

收件人: "zhanghan@wh.iov.cn" <zhanghan@wh.iov.cn>

抄送:

主题: invitation letter for Nature Conference on Viral Infection and Immune Response

Dear Ms. Han,

I have registered for the Nature Conference on Viral Infection and Immune Response happening October 21-23 and am very excited about the scientific program. I am coming from the United States and will need a letter of invitation for my Visa application. Attached please find my invitation application form with the relevant information.

Also, I do not know if this impacts my Visa application but I will also be attending the 7th International Symposium on Emerging Viral Diseases in Wuhan immediately prior to the start of this meeting.

thank you very much for your assistance,

Lisa Gralinski

Lisa Gralinski

Research Associate

Baric Laboratory

University of North Carolina at Chapel Hill

919-966-3890

Lisa E. Gralinski

Curriculum Vitae

Personal Information

Department of Epidemiology
2107 McGavran-Greenberg Hall
CB 7435
University of North Carolina
Chapel Hill, NC 27599-7435
919-966-7430

919-966-3890 (w)
lgralins@email.unc.edu

Education

- | | |
|-----------|---|
| 2002-2008 | Ph.D. University of Michigan, Ann Arbor, MI (Microbiology and Immunology) |
| 1998-2002 | B.A. Haverford College, Haverford, PA (Biology major, Chemistry minor) |

Research Experience

- | | |
|--------------|---|
| 2013-present | Research associate and project manager with Dr. Ralph Baric, University of North Carolina. Systems Immunogenetics of SARS-Coronavirus and Influenza pathogenesis. |
| 2008-2013 | Postdoctoral research associate with Dr. Ralph Baric, University of North Carolina. Host gene contribution to SARS-Coronavirus pathogenesis with an emphasis on systems genetics |
| 2002-2008 | Graduate student with Dr. Katherine Spindler, University of Michigan. Thesis: Pathogenesis of mouse adenovirus type 1 infection. Identified alteration of tight junction formation as responsible for MAV-1 induced breakdown of the blood brain barrier. |
| 2001-2002 | Internship and undergraduate research student with Dr. Stephan McMahon, Wistar Institute, Philadelphia, PA. Undergraduate Thesis: Interaction of the adenoviral protein E1A with human histone acetyltransferase complexes |

Honors and Awards

- | | |
|------------|---|
| 2014 | Keystone Symposia scholarship |
| 2013 | 27 th International Mammalian Genome Conference - Outstanding Presentation |
| 2013 | 27th International Mammalian Genome Conference Travel Award |
| 2011 | UNC Microbiology and Immunology Postdoc Symposium Award Winner |
| 2008-2010 | American Society of Virology Travel Award |
| 2006, 2007 | Horace H. Rackham School of Graduate Studies Travel Award |

2006	DNA Tumor Virus Meeting travel award
2004-2005	Molecular Mechanisms of Microbial Pathogenesis Training Grant, U of M
1998-2002	Magill-Rhoads Scholar, Haverford College

Publications

Menachery VD, Yount BL Jr, Sims AC, Debbink K, Agnihothram SS, Gralinski LE, Graham RL, Scobey T, Plante JA, Royal SR, Swanstrom J, Sheahan TP, Pickles RJ, Corti D, Randell SH, Lanzavecchia A, Marasco WA, Baric RS. SARS-like WIV1-CoV poised for human emergence. *PNAS*. 2016 113(11) 3048-3053.

Morgan AP, Fu CP, Kao CY, Welsh CE, Didion JP, Yadgary L, Hyacinth L, Ferris MT, Bell TA, Miller DR, Giusti-Rodriguez P, Nonneman RJ, Cook KD, Whitmire JK, Gralinski LE, Keller M, Attie AD, Churchill GA, Petkov P, Sullivan PF, Brennan JR, McMillan L, Pardo-Manuel de Villena F. The Mouse Universal Genotyping Array: From Substrains to Subspecies. *G3*. 2015 Dec 18;6(2):263-79. doi: 10.1534/g3.115.022087.

Menachery VD, Yount BL Jr, Debbink K, Agnihothram S, Gralinski LE, Plante JA, Graham RL, Scobey T, Ge XY, Donaldson EF, Randell SH, Lanzavecchia A, Marasco WA, Shi ZL, Baric RS. SARS-like cluster of circulating bat coronaviruses pose threat for human emergence. *Nature Medicine*. 2015 Dec;21(12):1508-13. doi: 10.1038/nm.3985

Gralinski et al. Identification and confirmation of Trim55 contribution to SARS-CoV-induced vascular cuffing. *PloS Genetics*. 2015 Oct 9;11(10):e1005504.

Menachery VD*, Gralinski LE*, Baric RS, Ferris MT. New Metrics for Evaluating Respiratory Pathogenesis. *PLoS One*. 2015 Jun 26;10(6):e0131451.

* Authors contributed equally to this work

Gralinski LE, Baric RS. Molecular Pathology of Emerging Coronavirus Infections. *J Pathol*. 2015 Jan;235(2):185-95.

Josset L, Tchitchek N, Gralinski LE, Ferris MT, Einfeld AJ, Green RR, Thomas MJ, Tisoncik-Go J, Schroth GP, Kawaoka Y, Manuel de Villena FP, Baric RS, Heise MT, Peng X, Katze MG. Annotation of long non-coding RNAs expressed in Collaborative Cross founder mice in response to respiratory virus infection reveals a new class of interferon-stimulated transcripts. *RNA Biol*. 2014 Jul 1;11(7):875-90. doi: 10.4161/rna.29442. Epub 2014 Jun 12.

Xiong H, Morrison J, Ferris MT, Gralinski LE, Whitmore AC, Green R, Thomas MJ, Tisoncik-Go J, Schroth GP, Pardo-Manuel de Villena F, Baric RS, Heise MT, Peng X, Katze MG. Genomic profiling of collaborative cross founder mice infected with respiratory viruses reveals novel transcripts and infection-related strain-specific gene and isoform expression. *G3 (Bethesda)*. 2014 Jun 5;4(8):1429-44. doi: 10.1534/g3.114.011759.

Menachery VD, Einfeld AJ, Schäfer A, Josset L, Sims AC, Proll S, Fan S, Li C, Neumann G, Tilton SC, Chang J, Gralinski LE, Long C, Green R, Williams CM, Weiss J, Matzke MM,

Webb-Robertson BJ, Schepmoes AA, Shukla AK, Metz TO, Smith RD, Waters KM, Katze MG, Kawaoka Y, Baric RS. Pathogenic influenza viruses and coronaviruses utilize similar and contrasting approaches to control interferon-stimulated gene responses. *MBio*. 2014 May 20;5(3):e01174-14. doi: 10.1128/mBio.01174-14.

Agnihothram S, Yount BL Jr, Donaldson EF, Huynh J, Menachery VD, Gralinski LE, Graham RL, Becker MM, Tomar S, Scobey TD, Osswald HL, Whitmore A, Gopal R, Ghosh AK, Mesecar A, Zambon M, Heise M, Denison MR, Baric RS. A mouse model for Betacoronavirus subgroup 2c using a bat coronavirus strain HKU5 variant. *MBio*. 2014 Mar 25;5(2):e00047-14. doi: 10.1128/mBio.00047-14.

Menachery VD, Yount BL Jr, Josset L, Gralinski LE, Scobey T, Agnihothram S, Katze MG, Baric RS. Attenuation and restoration of severe acute respiratory syndrome coronavirus mutant lacking 2'-O-methyltransferase activity. *J Virol*. 2014 Apr;88(8):4251-64. doi: 10.1128/JVI.03571-13. Epub 2014 Jan 29.

Gibbs DL, Gralinski L, Baric RS, McWeeney SK. Multi-omic network signatures of disease. *Front Genet*. 2014 Jan 7;4:309. doi: 10.3389/fgene.2013.00309. eCollection 2014 Jan 7.

Agnihothram S, Gopal R, Yount BL Jr, Donaldson EF, Menachery VD, Graham RL, Scobey TD, Gralinski LE, Denison MR, Zambon M, Baric RS. Evaluation of serologic and antigenic relationships between middle eastern respiratory syndrome coronavirus and other coronaviruses to develop vaccine platforms for the rapid response to emerging coronaviruses. *J Infect Dis*. 2014 Apr 1;209(7):995-1006. doi: 10.1093/infdis/jit609.

Gralinski et al. Mechanisms of SARS-CoV Induced Acute Lung Injury. *mBio* 2013. doi:10.1128/mBio.00271-13.

Tchitchek N, Einfeld AJ, Tisoncik-Go J, Josset L, Gralinski LE, Bécavin C, Tilton SC, Webb-Robertson BJ et al. *BMC Systems Biology* 2013 doi:10.1186/1752-0509-7-69.

Josset L, Menachery VD, Gralinski LE, Agnihothram S, Sova P, Carter VS, Yount BL, Graham RL, Baric RS, Katze MG. Cell host response to infection with novel human coronavirus EMC predicts potential antivirals and important differences with SARS coronavirus. *MBio*. 2013 Apr 30;4(3):e00165-13. doi: 10.1128/mBio.00165-13.

Ferris et al. Modeling Host Genetic Regulation of Influenza Pathogenesis in the Collaborative Cross. *PLoS Pathogens*, 2013. 2013 Feb;9(2):e1003196. doi:10.1371/journal.ppat.1003196

Sims AC, Tilton SC, Menachery VD, Gralinski LE, Schäfer A, Matzke MM, Webb-Robertson BJ, Chang J, Luna ML, Long CE, Shukla AK, Bankhead AR 3rd, Burkett SE, Zornetzer G, Tseng CT, Metz TO, Pickles R, McWeeney S, Smith RD, Katze MG, Waters KM, Baric RS. Release of SARS-CoV Nuclear Import Block Enhances Host Transcription in Human Lung Cells. *J Virol*. 2013 Jan 30. [Epub ahead of print]

Bottomly et al. Expression Quantitative Trait Loci for Extreme Host Response to Influenza A in pre-Collaborative Cross mice. *G3* 2012, vol. 2 no. 2 213-221

Collaborative Cross Consortium. The Genome Architecture of the Collaborative Cross Mouse Genetic Reference Population. *GENETICS* 2012, vol. 190 no. 2 389-402

Peng X, Gralinski L, Ferris MT, Frieman MB, Thomas MJ, Proll S, Korth MJ, Tisoncik JR, Heise M, Luo S, Schroth GP, Tumpey TM, Li C, Kawaoka Y, Baric RS, Katze MG. Integrative deep sequencing of the mouse lung transcriptome reveals differential expression of diverse classes of small RNAs in response to respiratory virus infection. *MBio*. 2011 Nov 15;2(6). pii: e00198-11. doi: 10.1128/mBio.00198-11.

Bolles, M, Deming, D, Long, K, Whitmore, A, Ferris, F, Funkhouser, W, Gralinski, L, Totura, A, Heise, M, Baric, RS. 2011. A Double-Inactivated SARS-CoV Vaccine Provides Incomplete Protection In Mice And Induces Increased Eosinophilic Pro-Inflammatory Pulmonary Response Upon Challenge. *J Virol*. 2011 Dec;85(23):12201-15.

Aylor et al. 2011. Genetic Analysis of Complex Traits in the Emerging Collaborative Cross. *Genome Research*. *Genome Res*. 2011. 21: 1213-1222.

Sheahan, T, Whitmore, A, Long, K, Ferris, M, Rockx, B, Funkhouser, W, Donaldson, E, Gralinski, L, Collier, M, Heise, M, Davis, N, Johnston, R and Baric, R. Successful Vaccination Strategies that Protect Aged Mice from Lethal Influenza and Lethal Heterologous SARS-CoV Challenge. *J Virol*. 2011. Jan;85(1):217-30

Peng X, Gralinski L, Armour CD, Ferris MT, Thomas MJ, Proll S, Bradel-Tretheway BG, Korth MJ, Castle JC, Biery MC, Bouzek HK, Haynor DR, Frieman MB, Heise M, Raymond CK, Baric RS, Katze MG. Unique signatures of long non-coding RNA expression in response to virus infection and altered innate immune signaling. *MBio*. 2010 Oct 26;1(5). pii: e00206-10.

Gralinski LE, Ashley SL, Dixon SD, and Spindler KR. 2009. Mouse adenovirus type 1-induced breakdown of the blood brain barrier. *J Virol*. 83:9398-410.

*Welton AR, *Gralinski LE, Spindler KR. 2008. Mouse adenovirus type 1 infection of natural killer cell-deficient mice. *Virology*. 373:163-70.

* Authors contributed equally to this work

Weinberg JB, Jensen DR, Gralinski LE, Lake AR, Stempfle GS, Spindler KR. 2007 Contributions of E1A to mouse adenovirus type 1 pathogenesis following intranasal inoculation. *Virology*. 357:54-67.

Ard PG, Chatterjee C, Kunjibettu S, Adside LR, Gralinski LE, McMahon SB. 2002 Transcriptional regulation of the mdm2 oncogene by p53 requires TRRAP acetyltransferase complexes. *Mol. Cell. Biol*. 22:5650-5661.

Oral Presentations

2015 American Society of Virology - Diverse Immune Response to SARS-CoV Infection in the Collaborative Cross

2014 American Society of Virology - New Metrics for Measuring Respiratory Disease Following Viral Infection

13th International Nidovirus Symposium - Mechanisms of SARS-CoV-Induced Acute Lung Injury and Respiratory Disease

27th International Mammalian Genome Conference - QTL identification and confirmation of Trim55 contribution to SARS-CoV-induced vascular cuffing using the Collaborative Cross

2013 American Society of Virology - A pathologic and protective role for the host complement system following respiratory virus infection

4th Annual Systems Biology Programmatic Meeting Agenda- Understanding Viral Pathogenesis Through The Use of Systems Biology (2012)

UNC Microbiology Department 2011 Postdoc Symposium - Importance of wound healing and extra-cellular matrix remodeling genes in SARS coronavirus infection – a systems virology approach

2011 American Society of Virology - Understanding SARS-CoV Pathogenesis: Genome Wide Identification of Susceptibility Loci using the Collaborative Cross

12th International Nidovirus Symposium - Importance of wound healing and extra-cellular matrix remodeling genes in SARS coronavirus infection – a systems virology approach (2011)

2nd Annual Systems Biology Programmatic and SBWG Meeting - Comparative Analysis of Gene Expression in SARS-Coronavirus- or H5N1 Influenza-Infected Mice (2010)

2010 American Society of Virology - Genome wide identification of susceptibility loci to SARS Coronavirus using the collaborative cross

9th Annual Meeting of the Complex Trait Community - Genome wide identification of susceptibility loci to SARS Coronavirus using the Collaborative Cross (2010)

UNC Microbiology Department 2009 Postdoc Symposium - Understanding SARS-CoV Pathogenesis: Genome Wide Identification of Susceptibility Loci using the Collaborative Cross

2009 American Society of Virology - SARS-CoV and the Collaborative Cross: Genome Wide Identification of Susceptibility Loci for an Emerging Highly Pathogenic Respiratory Virus

2008 American Society of Virology - Mouse Adenovirus Type 1-Induced Breakdown of the Blood Brain Barrier

2007 American Society of Virology - Mouse Adenovirus Type 1 Infection Causes Breakdown of the Blood Brain Barrier and Recruitment of Inflammatory Cells to the Brain

2006 DNA Tumor Virus Meeting - Infection with Mouse Adenovirus Type 1 Causes Breakdown of the Blood Brain Barrier and Recruitment of Inflammatory Cells to the Brain

Poster Presentations

2014 Respiratory Virus Keystone Symposia – Pathophysiology of SARS-CoV-Induced Acute Lung Injury

2011 American Society of Virology - Identification and Validation of Urokinase Pathway Members in SARS-CoV Pathogenesis

The Ninth International Symposium on Positive-Strand RNA Viruses - Systems biology of SARS Coronavirus pathogenesis (2010)

Training and Teaching Experience

2012 - present – Trained and directed undergraduate students, junior lab technician

2010 – Trained and directed graduate rotation student

2004-2005 – Teaching Assistant for Dental School Microbiology Laboratory

2007-2008 – Supervised and trained undergraduate researcher in the lab

Service

Ad hoc reviewer for Scientific Reports and Case Reports in Neurological Medicine - 2016

Poster Judge – 27th International Mammalian Genome Conference

Graduate Studies Committee – 2005-2006

Rackham Student Council – 2004-2005

Memberships

American Society of Virology – 2005 - present

Information Form to Apply for the Invitation Letter of Duly Authorized Unit

Name of Duly Authorized Unit		Bureau of International Cooperation, Chinese Academy of Sciences	
Information of the Invited			
Full Name	Lisa Elizabeth Gralinski	Sex	
Date of Birth		Nationality	
Affiliation	University of North Carolina	Title	Research Associate
Passport No.		Validity of Visa Intended to Apply	Dual Entry F Visa, 30 days
Number of Entries	2	Longest Stay	16 days
Date of First Entry	October 5, 2016	Date of Departure	October 25, 2016
The Country you apply for visa	Embassy (Consulate General/ Consulate/ Office) of the P.R China in <u>United States of America</u>		

From: zhanghan@wh.iov.cn[zhanghan@wh.iov.cn]
Sent: Wed 8/10/2016 11:30:08 AM (UTC-04:00)
To: Gralinski, Lisa E[lgralins@email.unc.edu]
Subject: Registration payment confirmation

Dear Lisa Gralinski:

You have paid for Nature Conference on Viral Infection and Immune response registration successfully.

Payment status: SUCCESS

Payment details:

[REGISTRATION EXPENSES]:

register fee :

price : CNY 1800.0,title : Regular Booking (Academic) ,quantity : 1

[EXPECTED TOTAL PAID]: CNY 1800.0

[ACTUALLY TOTAL PAID]: CNY 1800.0

Nature Conference on Viral Infection and Immune response.

Please visit http://viir2016.csp.escience.cn:80/dct/page/65574/___rpcsp0x2MySpace!65574%7C0_action/downloadView? to download your participant files.

Please contact me directly if you have any questions or concerns. I will be glad to help you.

Thank you again and we look forward to seeing you in Wuhan!

Best regards,

Han Zhang
VIIR Conference Secretariat
Wuhan Institute of Virology, CAS
No. 44, Xiao Hong Shan, Wuhan, Hubei, China, 430071
Tel: 0086-27-87198593
Fax: 0086-27-87198921
Email: zhanghan@wh.iov.cn

From: Gralinski, Lisa E[lgralins@email.unc.edu]
Sent: Wed 8/10/2016 11:30:19 AM (UTC-04:00)
To: 张哈[zhanghan@wh.iov.cn]
Subject: Re: Re: invitation letter for Nature Conference on Viral Infection and Immune Response

From: 张哈 <zhanghan@wh.iov.cn>
Sent: Tuesday, August 9, 2016 10:07 PM
To: Gralinski, Lisa E
Subject: Re: Re: invitation letter for Nature Conference on Viral Infection and Immune Response

Dear Dr. Gralinski,

Thank you very much. The documents have been well received.

For your information, the invitation code is '.

We will arrange the invitation letter to you asap.

Best regards,

Zhang Han

-----原始邮件-----

发件人: "Gralinski, Lisa E" <lgralins@email.unc.edu>

发送时间: 2016年8月9日 星期二

收件人: "张哈" <zhanghan@wh.iov.cn>

抄送:

主题: Re: invitation letter for Nature Conference on Viral Infection and Immune Response

Dear Ms. Han,

Thank you so much for your prompt response. I have submitted my abstract to the conference but need an invitation code in order to pay as an academic. Can you assist with this code?

This is indeed my first trip to China. Attached you will find a scan of my passport and a copy of my CV. Please let me know if you need any further information and I will send it to you asap!

thank you again,

Lisa Gralinski

From: 张晗 <zhanghan@wh.iov.cn>

Sent: Tuesday, August 9, 2016 3:03 AM

To: Gralinski, Lisa E

Subject: Re: invitation letter for Nature Conference on Viral Infection and Immune Response

Dear Dr. Gralinski,

Thank you for registering our conference. For your information, please pay your registration fee first and submit your abstract. Then we will arrange the invitation letter for you.

To ensure the success of visa application, I will help you apply the letter from the duly authorized unit, i.e. the Chinese Academy of Sciences (CAS). Please download **the attached form** and fill in the information we need, and then send the completed form to me.

In addition, **the scanning picture of your passport and your Cv** is needed.

Note: In order to obtain the visa, I have some other questions: 1) Is it your first time to come to China?
2) Have you ever obtained the Business Visiting Visa (F) issued by China?

If you have ever come to China and had been obtained the visa, please send me the scanning picture of China's visa page on your passport.

Thank you for your cooperation! To finalize the official letter issued by CAS will take 3-4 weeks, so you are strongly recommended to send me the documents above we need asap.

The invitation letter issued by CAS will focus strictly to the duration of the two meeting that you are going to attend, which means Oct. 18/19- Oct. 24/25 (only one entry).

If you have any questions or concerns, please feel free to contact.

Zhang Han

-----原始邮件-----

发件人: "Gralinski, Lisa E" <lgralins@email.unc.edu>

发送时间: 2016年8月9日 星期二

收件人: "zhanghan@wh.iov.cn" <zhanghan@wh.iov.cn>

抄送:

主题: invitation letter for Nature Conference on Viral Infection and Immune Response

Dear Ms. Han,

I have registered for the Nature Conference on Viral Infection and Immune Response happening October 21-23 and am very excited about the scientific program. I am coming from the United States and will need a letter of invitation for my Visa application. Attached please find my invitation application form with the relevant information.

Also, I do not know if this impacts my Visa application but I will also be attending the 7th International Symposium on Emerging Viral Diseases in Wuhan immediately prior to the start of this meeting.

thank you very much for your assistance,

Lisa Gralinski

Lisa Gralinski

Research Associate

Baric Laboratory

University of North Carolina at Chapel Hill

919-966-3890

From: 张晗 [zhanghan@wh.iov.cn]
Sent: Wed 8/10/2016 9:26:24 PM (UTC-04:00)
To: Gralinski, Lisa E [lgralins@email.unc.edu]
Subject: Re: Re: Re: invitation letter for Nature Conference on Viral Infection and Immune Response

Dear Dr. Gralinski,

Thank you very much.

We will send the invitation letter to you as soon as it is finalized.

Best regards,

Zhang Han

-----原始邮件-----

发件人: "Gralinski, Lisa E" <lgralins@email.unc.edu>

发送时间: 2016年8月10日 星期三

收件人: "张晗" <zhanghan@wh.iov.cn>

抄送:

主题: Re: Re: invitation letter for Nature Conference on Viral Infection and Immune Response

Dear Ms Han,

Thank you for the invitation code, I have now successfully paid for my registration fee. Please let me know if any further information is needed.

thanks again,

Lisa Gralinski

From: 张晗 <zhanghan@wh.iov.cn>
Sent: Tuesday, August 9, 2016 10:07 PM
To: Gralinski, Lisa E
Subject: Re: Re: invitation letter for Nature Conference on Viral Infection and Immune Response

Dear Dr. Gralinski,

Thank you very much. The documents have been well received.

For your information, the invitation code is .

We will arrange the invitation letter to you asap.

Best regards,

Zhang Han

-----原始邮件-----

发件人: "Gralinski, Lisa E" <lgralins@email.unc.edu>

发送时间: 2016年8月9日 星期二

收件人: "张晗" <zhanghan@wh.iov.cn>

抄送:

主题: Re: invitation letter for Nature Conference on Viral Infection and Immune Response

Dear Ms. Han,

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thank you again,

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From: 张晗 <zhanghan@wh.iov.cn>

Sent: Tuesday, August 9, 2016 3:03 AM

To: Gralinski, Lisa E

Subject: Re: invitation letter for Nature Conference on Viral Infection and Immune Response

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Zhang Han

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发件人: "Gralinski, Lisa E" <lgralins@email.unc.edu>

发送时间: 2016年8月9日 星期二

收件人: "zhanghan@wh.iov.cn" <zhanghan@wh.iov.cn>

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thank you very much for your assistance,

Lisa Gralinski

Lisa Gralinski

Research Associate

Baric Laboratory

University of North Carolina at Chapel Hill

919-966-3890

From: 张晗 [zhanghan@wh.iov.cn]
Sent: Sun 8/21/2016 11:21:31 PM (UTC-04:00)
To: Gralinski, Lisa E [lgralins@email.unc.edu]
Subject: Re: Re: Re: invitation letter for Nature Conference on Viral Infection and Immune Response
Attachment: Lisa Elizabeth Gralinski-invitation letter.pdf

Dear Lisa Gralinski,

Please see attached the invitation letter issued by CAS for Prof. Klenerman.

FYI, please print it in color and submit it with other documents to the embassy and please apply for the "F" visa.

If you have any questions during this process, please feel free to contact.

With best wishes,

Zhang Han

-----原始邮件-----

发件人: "Gralinski, Lisa E" <lgralins@email.unc.edu>

发送时间: 2016年8月10日 星期三

收件人: "张晗" <zhanghan@wh.iov.cn>

抄送:

主题: Re: Re: invitation letter for Nature Conference on Viral Infection and Immune Response

Dear Ms Han,

Thank you for the invitation code, I have now successfully paid for my registration fee. Please let me know if any further information is needed.

thanks again,

Lisa Gralinski

From: 张晗 <zhanghan@wh.iov.cn>

Sent: Tuesday, August 9, 2016 10:07 PM

To: Gralinski, Lisa E

Subject: Re: Re: invitation letter for Nature Conference on Viral Infection and Immune Response

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We will arrange the invitation letter to you asap.

Best regards,

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发件人: "Gralinski, Lisa E" <lgralins@email.unc.edu>

发送时间: 2016年8月9日 星期二

收件人: "张晗" <zhanghan@wh.iov.cn>

抄送:

主题: Re: invitation letter for Nature Conference on Viral Infection and Immune Response

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thank you again,

Lisa Gralinski

From: 张晗 <zhanghan@wh.iov.cn>

Sent: Tuesday, August 9, 2016 3:03 AM

To: Gralinski, Lisa E

Subject: Re: invitation letter for Nature Conference on Viral Infection and Immune Response

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If you have any questions or concerns, please feel free to contact.

Zhang Han

-----原始邮件-----

发件人: "Gralinski, Lisa E" <lgralins@email.unc.edu>

发送时间: 2016年8月9日 星期二

收件人: "zhanghan@wh.iov.cn" <zhanghan@wh.iov.cn>

抄送:

主题: invitation letter for Nature Conference on Viral Infection and Immune Response

Dear Ms. Han,

I have registered for the Nature Conference on Viral Infection and Immune Response happening October 21-23 and am very excited about the scientific program. I am coming from the United States and will need a letter of invitation for my Visa application. Attached please find my invitation application form with the relevant information.

Also, I do not know if this impacts my Visa application but I will also be attending the 7th International Symposium on Emerging Viral Diseases in Wuhan immediately prior to the start of this meeting.

thank you very much for your assistance,

Lisa Gralinski

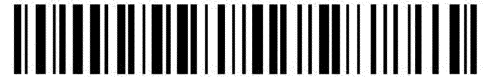
Lisa Gralinski

Research Associate

Baric Laboratory

University of North Carolina at Chapel Hill

919-966-3890



125520160817112708

被授权单位邀请函

Invitation Letter of Duly Authorized Unit

编号/No. : 125520160817112708

此函仅限申请人前往中华人民共和国驻美国大使馆申请签证时使用。

please apply forthwith for visa at the Embassy of P.R.China in the United States of America with this letter.

被授权单位名称 Name of Duly Authorized Unit		中国科学院			
被邀请人(共1人) Information of the Invited(1 people in total)					
	外文姓名 Full Name	性别 Sex	出生日期 Date of Birth	国籍 Nationality	护照号码 Passport No.
1	Lisa Elizabeth Gralinski				
申请签证有效期 1 个月 Validity of Visa Intended to Apply		拟入境次数 1 次 Number of Entries		最长停留天数 8 Longest Stay	
拟入境日期 2016-10-18 Date of First Entry		访问地点 武汉病毒所 小洪山 Places to Visit		事由 国际会议 Purpose of Visit	
联系人 张晗 Contact Person		被授权单位盖章及负责人签署 Seal and Signature  2016年 08月 17日 Year Month Day			
电话 027-87198593 Tel					
传真 010-68511095 Fax					
邮箱 ffzhao@cashq.ac.cn E-mail					

注:1. 本邀请函有效期三个月。

Notes: 1.This letter is valid for three months.

From: 胡犇[huben@wh.iov.cn]
Sent: Fri 9/9/2016 1:10:42 AM (UTC-04:00)
To: Gralinski, Lisa E[lgralins@email.unc.edu]
Subject: Re: Re: RE: RE: Invitation letter of the 7th International Symposium on Emerging Viral Diseases

Oh, that sounds an exciting trip.

See you soon.

Ben

-----原始邮件-----

发件人: "Gralinski, Lisa E" <lgralins@email.unc.edu>

发送时间: 2016年9月9日 星期五

收件人: "胡犇" <huben@wh.iov.cn>

抄送:

主题: Re: Re: RE: RE: Invitation letter of the 7th International Symposium on Emerging Viral Diseases

Hi Ben,

I'm very much looking forward to the meeting! My visa application is in progress right now and I will let you know as soon as I receive the final paperwork. I will arrive in Wuhun during the night of October 18/19 on the sleeper train from Zhangjiajie.

I had gone ahead and booked us a room at the Wanda Realm, slightly further away but closer to tourist locations. It will probably be better for us to stay there, but I appreciate the offer to book us at the Hong Shan Hotel.

I look forward to the conference and meeting you next month!

Lisa

From: 胡犇 <huben@wh.iov.cn>

Sent: Wednesday, September 7, 2016 9:49 AM

To: Gralinski, Lisa E

Subject: Re: Re: RE: RE: Invitation letter of the 7th International Symposium on Emerging Viral Diseases

Hello Lisa:

There is one month left before the meeting in Wuhan.

May I know how is the status of your visa application? When your visa is ready, please update me. Have you fixed the date of arrival in Wuhan? I will reserve a room for you at Hong Shan Hotel (the hotel for invited speakers, superior to Marshal Palace Hotel indicated in the meeting website)

Once you have purchased your air tickets, please provide me with the flight detail.

See you soon!

Best regards

Ben

-----原始邮件-----

发件人: "Gralinski, Lisa E" <lgralins@email.unc.edu>

发送时间: 2016年7月10日 星期日

收件人: "胡犇" <huben@wh.iov.cn>, "Baric, Ralph S" <rbaric@email.unc.edu>

抄送: "石正丽" <zlshi@wh.iov.cn>

主题: Re: RE: RE: Invitation letter of the 7th International Symposium on Emerging Viral Diseases

Dear Dr. Hu,

Thank you very much for the invitation to speak at the Symposium. I look forward to presenting our work from the Baric lab and interacting with the other attendees. In particular the session on emerging Coronaviruses will be extremely interesting.

thank you again,

Lisa Gralinski

From: 胡犇 <huben@wh.iov.cn>

Sent: Friday, July 8, 2016 10:08 AM

To: Baric, Ralph S; Gralinski, Lisa E

Cc: 石正丽

Subject: Re: RE: RE: Invitation letter of the 7th International Symposium on Emerging Viral Diseases

Dear Prof Baric and Dr. Gralinski:

We are very glad that our symposium still have change to include a talk about the work of your lab, which is

one of the leading research groups on coronavirus pathogenesis.

Please find the invitation letter to Dr. Gralinski which will help her for visa application.

Best regards

Ben

-----原始邮件-----

发件人: "Baric, Ralph S" <rbaric@email.unc.edu>

发送时间: 2016年7月8日 星期五

收件人: "石正丽" <zlshi@wh.iov.cn>

抄送: "胡犇" <huben@wh.iov.cn>, "Gralinski, Lisa E" <lgralins@email.unc.edu>

主题: RE: RE: Invitation letter of the 7th International Symposium on Emerging Viral Diseases

Hi Zhengli, Thanks for understanding, I am so sorry that I can't make the meeting. However on a brighter note, Lisa Gralinski can attend, she has been studying SARS-CoV and Bat-SARS like virus pathogenesis in the Collaborative Cross Mouse Resource, including mapping susceptibility alleles that regulate disease severity and outcomes. I think the resource and her talk will be of broad interest to the meeting participants. I have cc'd her on the email. Hope you are doing well. Ralph

From: 石正丽 [<mailto:zlshi@wh.iov.cn>]

Sent: Thursday, July 07, 2016 8:59 PM

To: Baric, Ralph S

Cc: 胡犇

Subject: Re: RE: Invitation letter of the 7th International Symposium on Emerging Viral Diseases

Dear Ralph,

Thank you for your reply. It's pity that you will not be able to come. It'll be great if someone from your lab can make it. Can you please ask this person to contact us and we will send him/her an invitation letter for Visa application.

Best regards,

Zhengli,

-----原始邮件-----

发件人: "Baric, Ralph S" <rbaric@email.unc.edu>

发送时间: 2016年7月8日 星期五

收件人: "胡犇" <huben@wh.iov.cn>

抄送: "石正丽" <zlshi@wh.iov.cn>

主题: RE: Invitation letter of the 7th International Symposium on Emerging Viral Diseases

Hi Ben, Thanks for your email. Unfortunately, I will not be able to attend this meeting. For whatever reason, I had it booked on my calendar for the week after and now have commitments that I cannot escape. Please pass on my sincere regrets to Zhengli as I was very interested in visiting and talking science. If you all are willing, I could have

a representative from my lab attend, recognizing that this isn't what you were hoping for. My sincerest apologies again. Ralph

From: 胡犇 [mailto:huben@wh.iov.cn]

Sent: Wednesday, July 06, 2016 5:43 AM

To: Baric, Ralph S

Cc: 石正丽

Subject: Re: Invitation letter of the 7th International Symposium on Emerging Viral Diseases

Dear Prof. Baric:

How are you?

I wonder whether you have received the invitation letter of the 7th International symposium on Emerging Viral Diseases which I sent in late April.

Emerging coronavirus is a special session in the symposium this year. It will be great if you are able to attend the meeting and give a talk. If you plan to come, please let me know and submit your abstract before 31th July. We sincerely hope that you can attend the meeting. As the chairman of the conference, Prof. Zhengli Shi is looking forward to seeing you in Wuhan.

Best regards

Ben Hu Ph.D

Secretary of the 7th International Symposium on Emerging Viral Diseases

Wuhan Institute of Virology

Chinese Academy of Sciences

Wuhan 430071, P.R. China

Tel: 86-27-87197311

E-mail: huben@wh.iov.cn

-----原始邮件-----

发件人: "胡犇" <huben@wh.iov.cn>

发送时间: 2016年4月29日 星期五

收件人: rbaric@email.unc.edu

抄送:

主题: Invitation letter of the 7th International Symposium on Emerging Viral Diseases

Dear Prof. Baric:

The 7th International Symposium on Emerging Viral Diseases will be held in October 19-21, 2016, in Wuhan, China. The biennial symposium, which covers various topics of emerging viruses including epidemiology, evolution, molecular biology, pathogenesis and immunology, has become an important event for leading Chinese and international virologists to discuss cutting-edge science as well as to foster global collaborations.

You are highly reputable in coronavirus researches and we sincerely hope that you can attend the symposium. Please find the invitation letter by the chairmen of the symposium, Dr. Zhengli Shi from Wuhan Institute of Virology, Chinese Academy of Sciences, and Dr. Linfa Wang from the Programme in Emerging Infectious Diseases, Duke-NUS Medical School, Singapore.

If you have any question regarding the conference, please contact me.

Thank you!

Best regards

Ben Hu Ph.D

Secretary of the 7th International Symposium on Emerging Viral Diseases

Wuhan Institute of Virology

Chinese Academy of Sciences

Wuhan 430071, P.R. China

Tel: 86-27-87197311

E-mail: huben@wh.iov.cn

From: Gralinski, Lisa E[lgralins@email.unc.edu]
Sent: Mon 9/12/2016 10:53:10 AM (UTC-04:00)
To: 胡犇[huben@wh.iov.cn]
Subject: Re: Re: Re: RE: RE: Invitation letter of the 7th International Symposium on Emerging Viral Diseases

Hi Ben,

The morning of the 21st would work well for me as I'm not leaving Wuhan until the 23rd.

thanks very much,

Lisa

From: 胡犇 <huben@wh.iov.cn>
Sent: Saturday, September 10, 2016 2:25 AM
To: Gralinski, Lisa E
Subject: Re: Re: Re: RE: RE: Invitation letter of the 7th International Symposium on Emerging Viral Diseases

Hello Lisa:

We are now making the final program of the conference, there would be a session with topic on emerging coronaviruses, which is scheduled in the morning of 21st.

Is this time OK for you? Do you plan to leave Wuhan at what time?

Thank you!

Kind regards

Ben

-----原始邮件-----

发件人: "Gralinski, Lisa E" <lgralins@email.unc.edu>
发送时间: 2016年9月9日 星期五
收件人: "胡犇" <huben@wh.iov.cn>
抄送:

主题: Re: Re: RE: RE: Invitation letter of the 7th International Symposium on Emerging Viral Diseases

Hi Ben,

I'm very much looking forward to the meeting! My visa application is in progress right now and I will let you know as soon as I receive the final paperwork. I will arrive in Wuhun during the night of October 18/19 on the sleeper train from Zhangjiajie.

I had gone ahead and booked us a room at the Wanda Realm, slightly further away but closer to tourist locations. It will probably be better for us to stay there, but I appreciate the offer to book us at the Hong Shan Hotel.

I look forward to the conference and meeting you next month!

Lisa

From: 胡犇 <huben@wh.iov.cn>

Sent: Wednesday, September 7, 2016 9:49 AM

To: Gralinski, Lisa E

Subject: Re: Re: RE: RE: Invitation letter of the 7th International Symposium on Emerging Viral Diseases

Hello Lisa:

There is one month left before the meeting in Wuhan.

May I know how is the status of your visa application? When your visa is ready, please update me. Have you fixed the date of arrival in Wuhan? I will reserve a room for you at Hong Shan Hotel (the hotel for invited speakers, superior to Marshal Palace Hotel indicated in the meeting website)

Once you have purchased your air tickets, please provide me with the flight detail.

See you soon!

Best regards

Ben

-----原始邮件-----

发件人: "Gralinski, Lisa E" <lgralins@email.unc.edu>

发送时间: 2016年7月10日 星期日

收件人: "胡犇" <huben@wh.iov.cn>, "Baric, Ralph S" <rbaric@email.unc.edu>

抄送: "石正丽" <zlishi@wh.iov.cn>

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Dear Dr. Hu,

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thank you again,

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Cc: 石正丽

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Dear Prof Baric and Dr. Gralinski:

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To: Baric, Ralph S
Cc: 胡犇
Subject: Re: RE: Invitation letter of the 7th International Symposium on Emerging Viral Diseases

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Zhengli,

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发件人: "Baric, Ralph S" <rbaric@email.unc.edu>
发送时间: 2016年7月8日 星期五
收件人: "胡犇" <huben@wh.iov.cn>
抄送: "石正丽" <zlshi@wh.iov.cn>
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Sent: Wednesday, July 06, 2016 5:43 AM
To: Baric, Ralph S
Cc: 石正丽
Subject: Re: Invitation letter of the 7th International Symposium on Emerging Viral Diseases

Dear Prof. Baric:

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Best regards

Ben Hu Ph.D

Secretary of the 7th International Symposium on Emerging Viral Diseases

Wuhan Institute of Virology

Chinese Academy of Sciences

Wuhan 430071, P.R. China

Tel: 86-27-87197311

E-mail: huben@wh.iov.cn

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发件人: "胡犇" <huben@wh.iov.cn>

发送时间: 2016年4月29日 星期五

收件人: rbaric@email.unc.edu

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Tel: 86-27-87197311

E-mail: huben@wh.iov.cn

From: 胡犇[huben@wh.iov.cn]
Sent: Thur 9/15/2016 10:48:18 PM (UTC-04:00)
To: Gralinski, Lisa E[lgralins@email.unc.edu]
Subject: Re: Re: Re: RE: RE: Invitation letter of the 7th International Symposium on Emerging Viral Diseases

Dear Lisa:

Glad to hear that your visa is ready.

The time duration for each speaker is 15-20 min (it is suggested to finish the talk within 15min) plus 5 min of questions and answers.

Best regards

Ben

-----原始邮件-----

发件人: "Gralinski, Lisa E" <lgralins@email.unc.edu>

发送时间: 2016年9月15日 星期四

收件人: "胡犇" <huben@wh.iov.cn>

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发送时间: 2016年9月9日 星期五

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I had gone ahead and booked us a room at the Wanda Realm, slightly further away but closer to tourist locations. It will probably be better for us to stay there, but I appreciate the offer to book us at the Hong Shan Hotel.

I look forward to the conference and meeting you next month!

Lisa

From: 胡犇 <huben@wh.iov.cn>

Sent: Wednesday, September 7, 2016 9:49 AM

To: Gralinski, Lisa E

Subject: Re: Re: RE: RE: Invitation letter of the 7th International Symposium on Emerging Viral Diseases

Hello Lisa:

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May I know how is the status of your visa application? When your visa is ready, please update me. Have you fixed the date of arrival in Wuhan? I will reserve a room for you at Hong Shan Hotel (the hotel for invited speakers, superior to Marshal Palace Hotel indicated in the meeting website)

Once you have purchased your air tickets, please provide me with the flight detail.

See you soon!

Best regards

Ben

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发件人: "Gralinski, Lisa E" <lgralins@email.unc.edu>

发送时间: 2016年7月10日 星期日

收件人: "胡犇" <huben@wh.iov.cn>, "Baric, Ralph S" <rbaric@email.unc.edu>

抄送: "石正丽" <zlishi@wh.iov.cn>

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From: 胡犇 <huben@wh.iov.cn>

Sent: Friday, July 8, 2016 10:08 AM

To: Baric, Ralph S; Gralinski, Lisa E

Cc: 石正丽

Subject: Re: RE: RE: Invitation letter of the 7th International Symposium on Emerging Viral Diseases

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E-mail: huben@wh.iov.cn

From: zhanghan@wh.iov.cn[zhanghan@wh.iov.cn]
Sent: Mon 9/26/2016 4:43:53 AM (UTC-04:00)
To: Gralinski, Lisa E[lgralins@email.unc.edu]
Subject: Final Programme for Nature Conference on Viral Infection and Immune Response

Dear Colleague,

Together with the rest of the organizing committee, I am looking forward to hosting you in Wuhan next month for the Nature Conference on Viral Infection and Immune Response.

Please find the final programme for the meeting, which is uploaded onto the website recently (<http://www.nature.com/natureconferences/viir2016/program.html>).

If you have any questions regarding registration or accommodation, please feel free to contact.

See you in Wuhan next month.

Best regards,

Zhang Han

From: zhanghan@wh.iov.cn[zhanghan@wh.iov.cn]
Sent: Mon 9/26/2016 4:54:55 AM (UTC-04:00)
To: Gralinski, Lisa E[lgralins@email.unc.edu]
Subject: Nature Conference on Viral Infection and Immune Response

Nature Conference on Viral Infection and Immune Response

October 21-23, 2016

Shangri-La Hotel, Wuhan

Dear all,

As the Nature Conference on Viral Infection and Immune Response is coming, please pay your registration fee online before October 21 as the fees for onsite registration is much higher.

FYI, we have reserved some rooms in Shangri-La Hotel. The single room is RMB 600 per night (with breakfasts) and the twin room is RMB 700 per night (with breakfasts).

If you would like to stay in this hotel during the conference, please send me your name, passport number, hotel arrival and departure dates, room type and number of rooms needed, so as to enable us to reserve your room in advance.

If possible, please send us your itinerary details.

If you are a foreign attendee, please apply the visa in advance.

You can get further information about the conference in the attached program. If you have any questions, please feel free to contact me at zhanghan@wh.iov.cn.

Regards,

Zhang Han

Sent on behalf of the organizers

From: zhanghan@wh.iov.cn[zhanghan@wh.iov.cn]
Sent: Mon 9/26/2016 4:59:55 AM (UTC-04:00)
To: Gralinski, Lisa E[lgralins@email.unc.edu]
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Sent on behalf of the organizers

From: Gralinski, Lisa E[lgralins@email.unc.edu]
Sent: Mon 10/3/2016 11:51:08 AM (UTC-04:00)
To: 胡犇[huben@wh.iov.cn]
Subject: Re: RE: Invitation letter of the 7th International Symposium on Emerging Viral Diseases
Attachment: Gralinski CV.doc

Hi Ben,

Thank you very much for the invitation to dinner, I will be delighted to attend. Please find a copy of my CV attached. I am greatly looking forward to this meeting, I will see you in just a few weeks!

thanks,

Lisa

From: 胡犇 <huben@wh.iov.cn>
Sent: Friday, September 30, 2016 10:22 AM
To: Gralinski, Lisa E
Subject: RE: RE: Invitation letter of the 7th International Symposium on Emerging Viral Diseases

Hello Lisa :

The program of our meeting has been made. Your talk entitled "Investigating emerging coronavirus susceptibility using the Collaborative Cross" is scheduled from 10:50 to 11:15 in the morning of 21st October, in the session of "Emerging Coronavirus".

As an invited speaker, could you please send me a copy of your CV or biosketch?

Please note that Prof. Zhengli Shi's lab will treat all speakers on coronaviruses for dinner after the end of the meeting on 21st.

Best regards

Ben

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发件人: "Gralinski, Lisa E" <lgralins@email.unc.edu>

发送时间: 2016年9月15日 星期四

收件人: "胡犇" <huben@wh.iov.cn>

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抄送: "石正丽" <zlshi@wh.iov.cn>

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Lisa E. Gralinski
Curriculum Vitae

Personal Information

Department of Epidemiology
2107 McGavran-Greenberg Hall
CB 7435
University of North Carolina
Chapel Hill, NC 27599-7435
919-966-7430

919-966-3890 (w)
lgralins@email.unc.edu

Education

2002-2008	Ph.D. University of Michigan, Ann Arbor, MI (Microbiology and Immunology)
1998-2002	B.A. Haverford College, Haverford, PA (Biology major, Chemistry minor)

Research Experience

2013-present	Research associate and project manager with Dr. Ralph Baric, University of North Carolina. Systems Immunogenetics of SARS-Coronavirus and Influenza pathogenesis.
2008-2013	Postdoctoral research associate with Dr. Ralph Baric, University of North Carolina. Host gene contribution to SARS-Coronavirus pathogenesis with an emphasis on systems genetics
2002-2008	Graduate student with Dr. Katherine Spindler, University of Michigan. Thesis: Pathogenesis of mouse adenovirus type 1 infection. Identified alteration of tight junction formation as responsible for MAV-1 induced breakdown of the blood brain barrier.
2001-2002	Internship and undergraduate research student with Dr. Stephan McMahon, Wistar Institute, Philadelphia, PA. Undergraduate Thesis: Interaction of the adenoviral protein E1A with human histone acetyltransferase complexes

Honors and Awards

2014	Keystone Symposia scholarship
2013	27 th International Mammalian Genome Conference - Outstanding Presentation
2013	27th International Mammalian Genome Conference Travel Award
2011	UNC Microbiology and Immunology Postdoc Symposium Award Winner
2008-2010	American Society of Virology Travel Award
2006, 2007	Horace H. Rackham School of Graduate Studies Travel Award
2006	DNA Tumor Virus Meeting travel award

2004-2005 Molecular Mechanisms of Microbial Pathogenesis Training Grant, U of M
1998-2002 Magill-Rhoads Scholar, Haverford College

Publications

Menachery VD, Yount BL Jr, Sims AC, Debbink K, Agnihothram SS, Gralinski LE, Graham RL, Scobey T, Plante JA, Royal SR, Swanstrom J, Sheahan TP, Pickles RJ, Corti D, Randell SH, Lanzavecchia A, Marasco WA, Baric RS. SARS-like WIV1-CoV poised for human emergence. *PNAS*. 2016 113(11) 3048-3053.

Morgan AP, Fu CP, Kao CY, Welsh CE, Didion JP, Yadgary L, Hyacinth L, Ferris MT, Bell TA, Miller DR, Giusti-Rodriguez P, Nonneman RJ, Cook KD, Whitmire JK, Gralinski LE, Keller M, Attie AD, Churchill GA, Petkov P, Sullivan PF, Brennan JR, McMillan L, Pardo-Manuel de Villena F. The Mouse Universal Genotyping Array: From Substrains to Subspecies. *G3*. 2015 Dec 18;6(2):263-79. doi: 10.1534/g3.115.022087.

Menachery VD, Yount BL Jr, Debbink K, Agnihothram S, Gralinski LE, Plante JA, Graham RL, Scobey T, Ge XY, Donaldson EF, Randell SH, Lanzavecchia A, Marasco WA, Shi ZL, Baric RS. SARS-like cluster of circulating bat coronaviruses pose threat for human emergence. *Nature Medicine*. 2015 Dec;21(12):1508-13. doi: 10.1038/nm.3985

Gralinski et al. Identification and confirmation of Trim55 contribution to SARS-CoV-induced vascular cuffing. *PloS Genetics*. 2015 Oct 9;11(10):e1005504.

Menachery VD*, Gralinski LE*, Baric RS, Ferris MT. New Metrics for Evaluating Respiratory Pathogenesis. *PLoS One*. 2015 Jun 26;10(6):e0131451.

* Authors contributed equally to this work

Gralinski LE, Baric RS. Molecular Pathology of Emerging Coronavirus Infections. *J Pathol*. 2015 Jan;235(2):185-95.

Josset L, Tchitchek N, Gralinski LE, Ferris MT, Einfeld AJ, Green RR, Thomas MJ, Tisoncik-Go J, Schroth GP, Kawaoka Y, Manuel de Villena FP, Baric RS, Heise MT, Peng X, Katze MG. Annotation of long non-coding RNAs expressed in Collaborative Cross founder mice in response to respiratory virus infection reveals a new class of interferon-stimulated transcripts. *RNA Biol*. 2014 Jul 1;11(7):875-90. doi: 10.4161/rna.29442. Epub 2014 Jun 12.

Xiong H, Morrison J, Ferris MT, Gralinski LE, Whitmore AC, Green R, Thomas MJ, Tisoncik-Go J, Schroth GP, Pardo-Manuel de Villena F, Baric RS, Heise MT, Peng X, Katze MG. Genomic profiling of collaborative cross founder mice infected with respiratory viruses reveals novel transcripts and infection-related strain-specific gene and isoform expression. *G3 (Bethesda)*. 2014 Jun 5;4(8):1429-44. doi: 10.1534/g3.114.011759.

Menachery VD, Einfeld AJ, Schäfer A, Josset L, Sims AC, Proll S, Fan S, Li C, Neumann G, Tilton SC, Chang J, Gralinski LE, Long C, Green R, Williams CM, Weiss J, Matzke MM, Webb-Robertson BJ, Schepmoes AA, Shukla AK, Metz TO, Smith RD, Waters KM, Katze MG, Kawaoka Y, Baric RS. Pathogenic influenza viruses and coronaviruses

utilize similar and contrasting approaches to control interferon-stimulated gene responses. *MBio*. 2014 May 20;5(3):e01174-14. doi: 10.1128/mBio.01174-14.

Agnihothram S, Yount BL Jr, Donaldson EF, Huynh J, Menachery VD, Gralinski LE, Graham RL, Becker MM, Tomar S, Scobey TD, Osswald HL, Whitmore A, Gopal R, Ghosh AK, Mesecar A, Zambon M, Heise M, Denison MR, Baric RS. A mouse model for Betacoronavirus subgroup 2c using a bat coronavirus strain HKU5 variant. *MBio*. 2014 Mar 25;5(2):e00047-14. doi: 10.1128/mBio.00047-14.

Menachery VD, Yount BL Jr, Josset L, Gralinski LE, Scobey T, Agnihothram S, Katze MG, Baric RS. Attenuation and restoration of severe acute respiratory syndrome coronavirus mutant lacking 2'-O-methyltransferase activity. *J Virol*. 2014 Apr;88(8):4251-64. doi: 10.1128/JVI.03571-13. Epub 2014 Jan 29.

Gibbs DL, Gralinski L, Baric RS, McWeeney SK. Multi-omic network signatures of disease. *Front Genet*. 2014 Jan 7;4:309. doi: 10.3389/fgene.2013.00309. eCollection 2014 Jan 7.

Agnihothram S, Gopal R, Yount BL Jr, Donaldson EF, Menachery VD, Graham RL, Scobey TD, Gralinski LE, Denison MR, Zambon M, Baric RS. Evaluation of serologic and antigenic relationships between middle eastern respiratory syndrome coronavirus and other coronaviruses to develop vaccine platforms for the rapid response to emerging coronaviruses. *J Infect Dis*. 2014 Apr 1;209(7):995-1006. doi: 10.1093/infdis/jit609.

Gralinski et al. Mechanisms of SARS-CoV Induced Acute Lung Injury. *mBio* 2013. doi:10.1128/mBio.00271-13.

Tchitchek N, Einfeld AJ, Tisoncik-Go J, Josset L, Gralinski LE, Bécavin C, Tilton SC, Webb-Robertson BJ et al. *BMC Systems Biology* 2013 doi:10.1186/1752-0509-7-69.

Josset L, Menachery VD, Gralinski LE, Agnihothram S, Sova P, Carter VS, Yount BL, Graham RL, Baric RS, Katze MG. Cell host response to infection with novel human coronavirus EMC predicts potential antivirals and important differences with SARS coronavirus. *MBio*. 2013 Apr 30;4(3):e00165-13. doi: 10.1128/mBio.00165-13.

Ferris et al. Modeling Host Genetic Regulation of Influenza Pathogenesis in the Collaborative Cross. *PLoS Pathogens*, 2013. 2013 Feb;9(2):e1003196. doi:10.1371/journal.ppat.1003196

Sims AC, Tilton SC, Menachery VD, Gralinski LE, Schäfer A, Matzke MM, Webb-Robertson BJ, Chang J, Luna ML, Long CE, Shukla AK, Bankhead AR 3rd, Burkett SE, Zornetzer G, Tseng CT, Metz TO, Pickles R, McWeeney S, Smith RD, Katze MG, Waters KM, Baric RS. Release of SARS-CoV Nuclear Import Block Enhances Host Transcription in Human Lung Cells. *J Virol*. 2013 Jan 30. [Epub ahead of print]

Bottomly et al. Expression Quantitative Trait Loci for Extreme Host Response to Influenza A in pre-Collaborative Cross mice. *G3* 2012, vol. 2 no. 2 213-221

Collaborative Cross Consortium. The Genome Architecture of the Collaborative Cross Mouse Genetic Reference Population. *GENETICS* 2012, vol. 190 no. 2 389-402

Peng X, Gralinski L, Ferris MT, Frieman MB, Thomas MJ, Proll S, Korth MJ, Tisoncik JR, Heise M, Luo S, Schroth GP, Tumpey TM, Li C, Kawaoka Y, Baric RS, Katze MG. Integrative deep sequencing of the mouse lung transcriptome reveals differential expression of diverse classes of small RNAs in response to respiratory virus infection. *MBio*. 2011 Nov 15;2(6). pii: e00198-11. doi: 10.1128/mBio.00198-11.

Bolles, M, Deming, D, Long, K, Whitmore, A, Ferris, F, Funkhouser, W, Gralinski, L, Totura, A, Heise, M, Baric, RS. 2011. A Double-Inactivated SARS-CoV Vaccine Provides Incomplete Protection In Mice And Induces Increased Eosinophilic Pro-Inflammatory Pulmonary Response Upon Challenge. *J Virol*. 2011 Dec;85(23):12201-15.

Aylor et al. 2011. Genetic Analysis of Complex Traits in the Emerging Collaborative Cross. *Genome Research*. *Genome Res*. 2011. 21: 1213-1222.

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Peng X, Gralinski L, Armour CD, Ferris MT, Thomas MJ, Proll S, Bradel-Tretheway BG, Korth MJ, Castle JC, Biery MC, Bouzek HK, Haynor DR, Frieman MB, Heise M, Raymond CK, Baric RS, Katze MG. Unique signatures of long non-coding RNA expression in response to virus infection and altered innate immune signaling. *MBio*. 2010 Oct 26;1(5). pii: e00206-10.

Gralinski LE, Ashley SL, Dixon SD, and Spindler KR. 2009. Mouse adenovirus type 1-induced breakdown of the blood brain barrier. *J Virol*. 83:9398-410.

*Welton AR, *Gralinski LE, Spindler KR. 2008. Mouse adenovirus type 1 infection of natural killer cell-deficient mice. *Virology*. 373:163-70.

* Authors contributed equally to this work

Weinberg JB, Jensen DR, Gralinski LE, Lake AR, Stempfle GS, Spindler KR. 2007 Contributions of E1A to mouse adenovirus type 1 pathogenesis following intranasal inoculation. *Virology*. 357:54-67.

Ard PG, Chatterjee C, Kunjibettu S, Adside LR, Gralinski LE, McMahon SB. 2002 Transcriptional regulation of the mdm2 oncogene by p53 requires TRRAP acetyltransferase complexes. *Mol. Cell. Biol*. 22:5650-5661.

Oral Presentations

2016 American Society of Virology - Mapping SARS-Coronavirus susceptibility alleles using the Collaborative Cross

2015 American Society of Virology - Diverse Immune Response to SARS-CoV Infection in the Collaborative Cross

2014 American Society of Virology - New Metrics for Measuring Respiratory Disease Following Viral Infection

13th International Nidovirus Symposium - Mechanisms of SARS-CoV-Induced Acute Lung Injury and Respiratory Disease

27th International Mammalian Genome Conference - QTL identification and confirmation of Trim55 contribution to SARS-CoV-induced vascular cuffing using the Collaborative Cross

2013 American Society of Virology - A pathologic and protective role for the host complement system following respiratory virus infection

4th Annual Systems Biology Programmatic Meeting Agenda- Understanding Viral Pathogenesis Through The Use of Systems Biology (2012)

UNC Microbiology Department 2011 Postdoc Symposium - Importance of wound healing and extra-cellular matrix remodeling genes in SARS coronavirus infection – a systems virology approach

2011 American Society of Virology - Understanding SARS-CoV Pathogenesis: Genome Wide Identification of Susceptibility Loci using the Collaborative Cross

12th International Nidovirus Symposium - Importance of wound healing and extra-cellular matrix remodeling genes in SARS coronavirus infection – a systems virology approach (2011)

2nd Annual Systems Biology Programmatic and SBWG Meeting - Comparative Analysis of Gene Expression in SARS-Coronavirus- or H5N1 Influenza-Infected Mice (2010)

2010 American Society of Virology - Genome wide identification of susceptibility loci to SARS Coronavirus using the collaborative cross

9th Annual Meeting of the Complex Trait Community - Genome wide identification of susceptibility loci to SARS Coronavirus using the Collaborative Cross (2010)

UNC Microbiology Department 2009 Postdoc Symposium - Understanding SARS-CoV Pathogenesis: Genome Wide Identification of Susceptibility Loci using the Collaborative Cross

2009 American Society of Virology - SARS-CoV and the Collaborative Cross: Genome Wide Identification of Susceptibility Loci for an Emerging Highly Pathogenic Respiratory Virus

2008 American Society of Virology - Mouse Adenovirus Type 1-Induced Breakdown of the Blood Brain Barrier

2007 American Society of Virology - Mouse Adenovirus Type 1 Infection Causes Breakdown of the Blood Brain Barrier and Recruitment of Inflammatory Cells to the Brain

2006 DNA Tumor Virus Meeting - Infection with Mouse Adenovirus Type 1 Causes Breakdown of the Blood Brain Barrier and Recruitment of Inflammatory Cells to the Brain

Poster Presentations

2016 Nidovirus Symposium – Complement Regulation of SARS-CoV Pathogenesis

2014 Respiratory Virus Keystone Symposia – Pathophysiology of SARS-CoV-Induced Acute Lung Injury

2011 American Society of Virology - Identification and Validation of Urokinase Pathway Members in SARS-CoV Pathogenesis

The Ninth International Symposium on Positive-Strand RNA Viruses - Systems biology of SARS Coronavirus pathogenesis (2010)

Training and Teaching Experience

2012 - present – Trained and directed undergraduate students, junior lab technician

2010 – Trained and directed graduate rotation student

2004-2005 – Teaching Assistant for Dental School Microbiology Laboratory

2007-2008 – Supervised and trained undergraduate researcher in the lab

Service

Ad hoc reviewer for Scientific Reports and Case Reports in Neurological Medicine - 2016

Poster Judge – 27th International Mammalian Genome Conference

Graduate Studies Committee – 2005-2006

Rackham Student Council – 2004-2005

Memberships

American Society of Virology – 2005 - present

From: zhanghan@wh.iov.cn[zhanghan@wh.iov.cn]
Sent: Sat 10/8/2016 4:52:59 AM (UTC-04:00)
To: Gralinski, Lisa E[lgralins@email.unc.edu]
Subject: Nature Conference on Viral Infection and Immune Response (Hotel Reservation)

Nature Conference on Viral Infection and Immune Response

October 21-23, 2016

Shangri-La Hotel, Wuhan

Dear Dr.Wu,

As the Nature Conference on Viral Infection and Immune Response is coming, please allow me to remind you of paying the registration fee online before Oct. 21.

FYI, we have reserved some rooms in Shangri-La Hotel. The single room is RMB 600 per night (with breakfasts) and the twin room is RMB 700 per night (with breakfasts).

If you would like to stay in this hotel during the conference, please send me your name, passport number, hotel arrival and departure dates, room type and number of rooms needed, so as to enable us to reserve your room in advance.

The deadline is Oct. 09 (12:00 pm). We will not accept the hotel reservation after then.

You can get further information about the conference in the attached program. If you have any questions, please feel free to contact me at zhanghan@wh.iov.cn.

Regards,

Zhang Han

Sent on behalf of the organizers

From: zhanghan@wh.iov.cn[zhanghan@wh.iov.cn]
Sent: Sat 10/8/2016 9:03:06 PM (UTC-04:00)
To: Gralinski, Lisa E[lgralins@email.unc.edu]
Subject: Nature Conference on Viral Infection and Immune Response (Conference Venue and Program)

Nature Conference on Viral Infection and Immune Response

October 21-23, 2016

Shangri-La Hotel, Wuhan

Dear Colleague,

For your information, our conference will be held in the Wuhan Shangri-La Hotel. For the address and transportation, please see details at the website (<http://www.shangri-la.com/wuhan/shangrila/about/map-directions/>).

About the meeting program, you can get further information by visiting the website (<http://www.nature.com/natureconferences/viir2016/program.pdf>).

Besides, as the Nature Conference on Viral Infection and Immune Response is coming, please allow me to remind you of paying the registration fee online before Oct. 21. And we have reserved some rooms in Shangri-La Hotel. The single room is RMB 600 per night (with breakfasts) and the twin room is RMB 700 per night (with breakfasts).

If you would like to stay in this hotel during the conference, please send me your name, passport number, hotel arrival and departure dates, room type and number of rooms needed, so as to enable us to reserve your room in advance. The deadline is Oct. 09 (12:00 pm). We will not accept the hotel reservation after then.

If you have any questions, please feel free to contact me at zhanghan@wh.iov.cn.

Note: this is a mass email sending to all participants. If you have already paid your registration fee and reserved the hotel, you may not reply please. Thank you for your understanding.

Regards,

Zhang Han

Sent on behalf of the organizers

From: 张晗[zhanghan@wh.iov.cn]
Sent: Mon 10/10/2016 4:45:26 AM (UTC-04:00)
To: Gralinski, Lisa E[lgralins@email.unc.edu]
Subject: Nature Conference on Viral Infection and Immune Response (Poster Collection, Oct. 12)
Attachment: poster background.jpg

Dear Lisa,

In order to arrange the venue better, the conference committee decides to collect your poster and help to print and post directly. Please send us your poster no later than Oct. 12. Exceeding the sending time limit or print it by yourself will not be permitted in the conference. Thank you for your understanding and cooperation.

Requirement: please send us the original document and JPG with 200 DPI respectively. Please use the attachment as the background.

Poster: Complement regulation of SARS-Coronavirus pathogenesis

With many thanks,

Zhang Han



anatureconference

Viral Infection and Immune Response 2016

October 21–23, 2016 Shangri-la Hotel | Wuhan, China #VIIR2016



nature
microbiology



From: 张晗 [zhanghan@wh.iov.cn]
Sent: Mon 10/10/2016 8:59:12 PM (UTC-04:00)
To: Gralinski, Lisa E [lgralins@email.unc.edu]
Subject: Re: Re: Nature Conference on Viral Infection and Immune Response (Poster Collection, Oct. 12)

Dear Dr. Gralinski,

Please accept my apology to tell that we will print the posters on board directly. Therefore there are no blank boards for posting when we hold the conference.

Could you please use the computer in hotel or ask someone help to send the copy to us?

With many thanks,

Zhang Han

-----原始邮件-----

发件人: "Gralinski, Lisa E" <lgralins@email.unc.edu>

发送时间: 2016年10月11日 星期二

收件人: "张晗" <zhanghan@wh.iov.cn>

抄送:

主题: Re: Nature Conference on Viral Infection and Immune Response (Poster Collection, Oct. 12)

Hello,

Unfortunately I am already in China traveling and have my printed poster with me. I do not have a computer with me so I cannot send a copy of the document. Is there any way I can use the poster that I already printed? It is on the correct background and meets the size requirements.

Thank you very much,

Lisa Gralinski

From: 张晗 <zhanghan@wh.iov.cn>

Sent: Monday, October 10, 2016 4:45:26 AM

To: Gralinski, Lisa E

Subject: Nature Conference on Viral Infection and Immune Response (Poster Collection, Oct. 12)

Dear Lisa,

In order to arrange the venue better, the conference committee decides to collect your poster and help to print and post directly. Please send us your poster no later than Oct. 12. Exceeding the sending time limit or print it by yourself will not be permitted in the conference. Thank you for your understanding and cooperation.

Requirement: please send us the original document and JPG with 200 DPI respectively. Please use the attachment as the background.

Poster: Complement regulation of SARS-Coronavirus pathogenesis

With many thanks,

Zhang Han

From: Gralinski, Lisa E[lgralins@email.unc.edu]
Sent: Mon 10/17/2016 6:51:15 AM (UTC-04:00)
To: 胡犇[huben@wh.iov.cn]
Subject: Re: Re: RE: Invitation letter of the 7th International Symposium on Emerging Viral Diseases

Hi Ben,

I am happy to have the jet lag out of the way before needing to focus on the talks. We should arrive in Wuhan in plenty of time for me to make the registration at the Hong Shan Hotel, do you know what time it will open and close? I look forward to meeting you in just two days!

Thanks,
Lisa

From: 胡犇 <huben@wh.iov.cn>
Sent: Sunday, October 16, 2016 3:10:40 AM
To: Gralinski, Lisa E
Subject: Re: Re: RE: Invitation letter of the 7th International Symposium on Emerging Viral Diseases

Dear Lisa:

I hope you are enjoying your trip

Next Wednesday (19th), the registration of our meeting will take place in Hong Shan Hotel, which is 15 min by walking from your hotel (Wanda). If you arrive late and tired, you need not do the registration on that day. I will bring all the conference documents for you to the venue on 20th.

What you need to do is to get the direction from Wanda to our institute. If you come to our registration on 19th, I will show you.

See you soon!

Cheers

Ben

-----原始邮件-----

发件人: "Gralinski, Lisa E" <lgralins@email.unc.edu>

发送时间: 2016年10月3日 星期一

收件人: "胡犇" <huben@wh.iov.cn>

抄送:

主题: Re: RE: Invitation letter of the 7th International Symposium on Emerging Viral Diseases

Hi Ben,

Thank you very much for the invitation to dinner, I will be delighted to attend. Please find a copy of my CV attached. I am greatly looking forward to this meeting, I will see you in just a few weeks!

thanks,

Lisa

From: 胡犇 <huben@wh.iov.cn>

Sent: Friday, September 30, 2016 10:22 AM

To: Gralinski, Lisa E

Subject: RE: RE: Invitation letter of the 7th International Symposium on Emerging Viral Diseases

Hello Lisa :

The program of our meeting has been made. Your talk entitled "Investigating emerging coronavirus susceptibility using the Collaborative Cross" is scheduled from 10:50 to 11:15 in the morning of 21st October, in the session of "Emerging Coronavirus".

As an invited speaker, could you please send me a copy of your CV or biosketch?

Please note that Prof. Zhengli Shi's lab will treat all speakers on coronaviruses for dinner after the end of the meeting on 21st.

Best regards

Ben

-----原始邮件-----

发件人: "Gralinski, Lisa E" <lgralins@email.unc.edu>

发送时间: 2016年9月15日 星期四

收件人: "胡犇" <huben@wh.iov.cn>

抄送:

主题: Re: Re: Re: RE: RE: Invitation letter of the 7th International Symposium on Emerging Viral Diseases

Hi Ben,

I just received my visa for China so now I am ready to attend the meeting! I do have one question as I prepare for the conference; do you know how much time will be allotted for each talk?

thanks so much,

Lisa

From: 胡犇 <huben@wh.iov.cn>

Sent: Saturday, September 10, 2016 2:25 AM

To: Gralinski, Lisa E

Subject: Re: Re: Re: RE: RE: Invitation letter of the 7th International Symposium on Emerging Viral Diseases

Hello Lisa:

We are now making the final program of the conference, there would be a session with topic on emerging coronaviruses, which is scheduled in the morning of 21st.

Is this time OK for you? Do you plan to leave Wuhan at what time?

Thank you!

Kind regards

Ben

-----原始邮件-----

发件人: "Gralinski, Lisa E" <lgralins@email.unc.edu>

发送时间: 2016年9月9日 星期五

收件人: "胡犇" <huben@wh.iov.cn>

抄送:

主题: Re: Re: RE: RE: Invitation letter of the 7th International Symposium on Emerging Viral Diseases

Hi Ben,

I'm very much looking forward to the meeting! My visa application is in progress right now and I will let you know as soon as I receive the final paperwork. I will arrive in Wuhun during the night of October 18/19 on the sleeper train from Zhangjiajie.

I had gone ahead and booked us a room at the Wanda Realm, slightly further away but closer to tourist locations. It will probably be better for us to stay there, but I appreciate

the offer to book us at the Hong Shan Hotel.

I look forward to the conference and meeting you next month!

Lisa

From: 胡犇 <huben@wh.iov.cn>

Sent: Wednesday, September 7, 2016 9:49 AM

To: Gralinski, Lisa E

Subject: Re: Re: RE: RE: Invitation letter of the 7th International Symposium on Emerging Viral Diseases

Hello Lisa:

There is one month left before the meeting in Wuhan.

May I know how is the status of your visa application? When your visa is ready, please update me. Have you fixed the date of arrival in Wuhan? I will reserve a room for you at Hong Shan Hotel (the hotel for invited speakers, superior to Marshal Palace Hotel indicated in the meeting website)

Once you have purchased your air tickets, please provide me with the flight detail.

See you soon!

Best regards

Ben

-----原始邮件-----

发件人: "Gralinski, Lisa E" <lgralins@email.unc.edu>

发送时间: 2016年7月10日 星期日

收件人: "胡犇" <huben@wh.iov.cn>, "Baric, Ralph S" <rbaric@email.unc.edu>

抄送: "石正丽" <zlshi@wh.iov.cn>

主题: Re: RE: RE: Invitation letter of the 7th International Symposium on Emerging Viral Diseases

Dear Dr. Hu,

Thank you very much for the invitation to speak at the Symposium. I look forward to presenting our work from the Baric lab and interacting with the other attendees. In particular the session on emerging

Coronaviruses will be extremely interesting.

thank you again,

Lisa Gralinski

From: 胡犇 <huben@wh.iov.cn>
Sent: Friday, July 8, 2016 10:08 AM
To: Baric, Ralph S; Gralinski, Lisa E
Cc: 石正丽
Subject: Re: RE: RE: Invitation letter of the 7th International Symposium on Emerging Viral Diseases

Dear Prof Baric and Dr. Gralinski:

We are very glad that our symposium still have change to include a talk about the work of your lab, which is one of the leading research groups on coronavirus pathogenesis.

Please find the invitation letter to Dr. Gralinski which will help her for visa application.

Best regards

Ben

-----原始邮件-----

发件人: "Baric, Ralph S" <rbaric@email.unc.edu>
发送时间: 2016年7月8日 星期五
收件人: "石正丽" <zlshi@wh.iov.cn>
抄送: "胡犇" <huben@wh.iov.cn>, "Gralinski, Lisa E" <lgralins@email.unc.edu>
主题: RE: RE: Invitation letter of the 7th International Symposium on Emerging Viral Diseases

Hi Zhengli, Thanks for understanding, I am so sorry that I can't make the meeting. However on a brighter note, Lisa Gralinski can attend, she has been studying SARS-CoV and Bat-SARS like virus pathogenesis in the Collaborative Cross Mouse Resource, including mapping susceptibility alleles that regulate disease severity and outcomes. I think the resource and her talk will be of broad interest to the meeting participants. I have cc'd her on the email. Hope you are doing well. Ralph

From: 石正丽 [<mailto:zlshi@wh.iov.cn>]
Sent: Thursday, July 07, 2016 8:59 PM
To: Baric, Ralph S
Cc: 胡犇
Subject: Re: RE: Invitation letter of the 7th International Symposium on Emerging Viral Diseases

Dear Ralph,

Thank you for your reply. It's pity that you will not be able to come. It'll be great if someone from your lab can make it. Can you please ask this person to contact us and we will send him/her an invitation letter for Visa application.

Best regards,

Zhengli,

-----原始邮件-----

发件人: "Baric, Ralph S" <rbaric@email.unc.edu>

发送时间: 2016年7月8日 星期五

收件人: "胡犛" <huben@wh.iov.cn>

抄送: "石正丽" <zlishi@wh.iov.cn>

主题: RE: Invitation letter of the 7th International Symposium on Emerging Viral Diseases

Hi Ben, Thanks for your email. Unfortunately, I will not be able to attend this meeting. For whatever reason, I had it booked on my calendar for the week after and now have commitments that I cannot escape. Please pass on my sincere regrets to Zhengli as I was very interested in visiting and talking science. If you all are willing, I could have a representative from my lab attend, recognizing that this isn't what you were hoping for. My sincerest apologies again. Ralph

From: 胡犛 [mailto:huben@wh.iov.cn]

Sent: Wednesday, July 06, 2016 5:43 AM

To: Baric, Ralph S

Cc: 石正丽

Subject: Re: Invitation letter of the 7th International Symposium on Emerging Viral Diseases

Dear Prof. Baric:

How are you?

I wonder whether you have received the invitation letter of the 7th International symposium on Emerging Viral Diseases which I sent in late April.

Emerging coronavirus is a special session in the symposium this year. It will be great if you are able to attend the meeting and give a talk. If you plan to come, please let me know and submit your abstract before 31th July. We sincerely hope that you can attend the meeting. As the chairman of the conference, Prof. Zhengli Shi is looking forward to seeing you in Wuhan.

Best regards

Ben Hu Ph.D

Secretary of the 7th International Symposium on Emerging Viral Diseases

Wuhan Institute of Virology
Chinese Academy of Sciences
Wuhan 430071, P.R. China

Tel: 86-27-87197311

E-mail: huben@wh.iov.cn

-----原始邮件-----

发件人: "胡犇" <huben@wh.iov.cn>

发送时间: 2016年4月29日 星期五

收件人: rbaric@email.unc.edu

抄送:

主题: Invitation letter of the 7th International Symposium on Emerging Viral Diseases

Dear Prof. Baric:

The 7th International Symposium on Emerging Viral Diseases will be held in October 19-21, 2016, in Wuhan, China. The biennial symposium, which covers various topics of emerging viruses including epidemiology, evolution, molecular biology, pathogenesis and immunology, has become an important event for leading Chinese and international virologists to discuss cutting-edge science as well as to foster global collaborations.

You are highly reputable in coronavirus researches and we sincerely hope that you can attend the symposium. Please find the invitation letter by the chairmen of the symposium, Dr. Zhengli Shi from Wuhan Institute of Virology, Chinese Academy of Sciences, and Dr. Linfa Wang from the Programme in Emerging Infectious Diseases, Duke-NUS Medical School, Singapore.

If you have any question regarding the conference, please contact me.

Thank you!

Best regards

Ben Hu Ph.D

Secretary of the 7th International Symposium on Emerging Viral Diseases

Wuhan Institute of Virology

Chinese Academy of Sciences

Wuhan 430071, P.R. China

Tel: 86-27-87197311

E-mail: huben@wh.iov.cn

From: 周鹏 [peng.zhou@wh.iov.cn]
Sent: Sun 10/23/2016 2:06:26 AM (UTC-04:00)
To: Gralinski, Lisa E [lgralins@email.unc.edu]
Subject: Re: Good to meet you!

Nice to meet you Lisa! Happy to see you in Wuhan.
Keep in touch.

Cheers,
Peng

在 2016-10-23 11:17:47, "Gralinski, Lisa E" <lgralins@email.unc.edu> 写道 :

>
>Great to meet a fellow coronavirus scientist, I'm looking forward to seeing more great bat data!
>Lisa Gralinski
>Baric lab
>

From: zengleiping <zengleiping@163.com>
Sent: Wednesday, October 26, 2016 11:07 PM
To: Gralinski, Lisa E
Subject: Re: Re: Could you find Laurence Josset's email address for me?

Hi Lisa,

It's so nice to have your reply. Yes, I feel much easy now.
Thank you for your kind help. I will look forward to you reply again.
You must have a long and tired trip. I hope you have a good rest. :)

Lei-Ping

Zeng Leiping
Wuhan Institute of Virology, Chinese Academy of Science,
Xiao Hong Shan No.44,
430071, Wuhan
China
Tel:+86 27 87197311

From: [Gralinski, Lisa E](#)
Date: 2016-10-27 05:47
To: [zengleiping](#)
Subject: Re: Could you find Laurence Josset's email address for me?

Hi Lei-Ping,

Good to hear from you! Laurence was a postdoc in Seattle with Michael Katze when she did this work this us. She is now back in France and I've asked a fellow collaborator for her new contact information. I should be able to send her email address to you in a day or two.

I hope you are having a good week now that the conferences are done!

Lisa

From: zengleiping
Sent: Monday, October 24, 2016 8:39 AM
To: Gralinski, Lisa E
Subject: Could you find Laurence Josset's email address for me?
Hi Lisa,

Sorry to bother you! I am learning the analysis method of microarray data. I have some questions to ask him. Could you please find his email address for me?
His paper is attached.

Thank you!

Best,
Lei-Ping (Frank)

Zeng Leiping
Wuhan Institute of Virology, Chinese Academy of Science,
Xiao Hong Shan No.44,
430071, Wuhan
China
Tel:+86 27 87197311

From: Virologica[virosin@wh.iov.cn]
Sent: Tue 5/9/2023 7:52:10 PM (UTC-04:00)
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Subject: Explore our latest articles in issue 2 2023. Virologica Sinica

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Dear Dr. Lisa E Gralinski,

We would like to share with you the latest issue published in [Virologica Sinica](#). Here are the articles in this issue.

About the cover: The advent of metagenomics has revealed remarkable complexity of the human virome, and more and more evidence suggest that these viromes involve in human health and immune status. As an important but understudied component of the human microbes, the role of vaginal virome in local microenvironment and cervical disease is unclear. In this issue, Li et al. investigated the vaginal virome and linked specific viral compositions in local vaginal tract with women's genital health and disease status. Besides, as the 'commensal' but neglected part of our virome, the strong association of anelloviruses with specific disease status and their correlations with other viruses indicate that these viruses could be attractive targets to predict the risk of HPV persistent infection and/or cervical disease progression. The cover image describes that diverse viromes ("characters") are present in vaginal tract ("stage"), and more viruses will come into the spotlight and be noticed in the future (kindly designed and provided by Yanpeng Li, Shujun Gao and Chiyu Zhang).

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Review Article

Altered vaginal eukaryotic virome is associated with different cervical disease status

Yanpeng Li, Le Cao, Xiao Han, Yingying Ma, Yanmei Liu, Shujun Gao, Chiyu Zhang

Virol Sin. 2023 Apr.;38(2):184-197.

<https://doi.org/10.1016/j.virs.2022.12.004>

Research Articles

Discovery and characterization of novel paramyxoviruses from bat samples in China

Haoxiang Su, Yuyang Wang, Yelin Han, Qi Jin, Fan Yang, Zhiqiang Wu

Virol Sin. 2023 Apr.;38(2):198-207.

<https://doi.org/10.1016/j.virs.2023.01.002>

Identification of broad neutralizing antibodies against Omicron subvariants from COVID-19 convalescents and vaccine recipients

Jun Chen, Jing Yang, Fangfang Chang, Yabin Hu, Qian Wu, Shishan Teng, Yongchen Liu, Jian Zhang, Rongzhang He, Bo Liu, Xingyu Zheng, Ze Liu, Yanxi Peng, Zhenhua Xie, Yuanfang Zhang, Rui Lu, Dong Pan, You Wang, Liting Peng, Wenpei Liu, Yi-Ping Li, Xiaowang Qu

Virol Sin. 2023 Apr.;38(2):313-316.

<https://doi.org/10.1016/j.virs.2023.01.005>

Omicron variants breakthrough infection elicited higher specific memory immunity than third dose booster in healthy vaccinees

Pei Yu, Zijian Liu, Zhuoqi Zhu, Jiaqing Yang, Min Deng, Mingxiao Chen, Changchun Lai, Weiya Kong, Shilong Xiong, Li Wan, Weikang Mai, Lu Chen, Yu Lei, Shahzad Akbar Khan, Jianfeng Ruan, An Kang, Xuguang Guo, Qiang Zhou, Wenrui Li, Zheng Chen, Yuemei Liang, Pingchao Li, Lei Zhang, Tianxing Ji

Virol Sin. 2023 Apr.;38(2):233-243.

<https://doi.org/10.1016/j.virs.2022.12.008>

Diagnostic performance of different specimens in detecting enterovirus A71 in children with hand, foot and mouth disease

Yonghong Zhou, Chongchen Zhou, Kai Wang, Qi Qiu, Yibing Cheng, Yu Li, Peng Cui, Lu Liang, Peng Li, Xiaowei Deng, Lili Wang, Wen Zheng, Hui Gong, Fang Wang, Meng Xu, Justin Jang Hann Chu, Lance Turtle, Hongjie Yu

Virol Sin. 2023 Apr.;38(2):268-275.

<https://doi.org/10.1016/j.virs.2022.11.004>

Hybridoma-derived neutralizing monoclonal antibodies against Beta and Delta variants of SARS-CoV-2 *in vivo*

Qianran Wang, Lu Peng, Yanqiu Nie, Yanni Shu, Huajun Zhang, Zidan Song, Yufeng Li, Hengrui Hu, Liushuai Li, Xi Wang, Jia Liu, Jiang Li, Zhengli Shi, Fei Deng, Yu Guo, Yiwu Zhou, Bing Yan, Zhihong Hu, Manli Wang

Virol Sin. 2023 Apr.;38(2):257-267.

<https://doi.org/10.1016/j.virs.2022.12.007>

Identification of niclosamide as a novel antiviral agent against porcine epidemic diarrhea virus infection by targeting viral internalization

Yue Wang, Huimin Huang, Dongliang Li, Chenxu Zhao, Shuai Li, Panpan Qin, Yaqin Li, Xia Yang, Wenjuan Du, Wentao Li, Yongtao Li

Virol Sin. 2023 Apr.;38(2):296-308.

<https://doi.org/10.1016/j.virs.2023.01.008>

Splicing factor SF3B3, a NS5-binding protein, restricts ZIKV infection by targeting GCH1

Tanxiu Chen, Hao Yang, Penghui Liu, Moliduer Hamiti, Xintian Zhang, Yi Xu, Wenqi Quan, Yong Zhang, Wenhai Yu, Li Jiao,

Tingfu Du, Juemin Xi, Bin Yin, Wei Zhou, Shuaiyao Lu, Xiaozhong Peng

Virol Sin. 2023 Apr.;38(2):222-232.

<https://doi.org/10.1016/j.virs.2022.12.005>

Letters

Genome-wide characterization of alternative splicing in blood cells of COVID-19 and respiratory infections of relevance

Rui Huang, Wenbo Chen, Xueya Zhao, Yuefei Ma, Qiong Zhou, Junsen Chen, Muyi Zhang, Dingran Zhao, Yu Hou, Chunjiang He, Ying Wu

Virol Sin. 2023 Apr.;38(2):309-312.

<https://doi.org/10.1016/j.virs.2023.01.007>

PLX8394, a RAF inhibitor, inhibits enterovirus 71 replication by blocking RAF/MEK/ERK signaling

Chengyuan Wu, Guangyan Zhu, Fang Qiu, Fuli Ren, Binbin Lin, Dingyu Zhang, Qingyu Yang, Chaolin Huang

Virol Sin. 2023 Apr.;38(2):276-284.

<https://doi.org/10.1016/j.virs.2023.01.006>

Crimean-Congo hemorrhagic fever virus in Central, Eastern, and South-eastern Asia

Mohammad Fereidouni, Dmitry A. Apanaskevich, David B. Pecor, Natalia Yu. Pshenichnaya, Gulzhan N. Abuova, Farida H. Tishkova, Yekaterina Bumburidi, Xiankun Zeng, Jens H. Kuhn, Maryam Keshtkar-Jahromi

Virol Sin. 2023 Apr.;38(2):171-183.

<https://doi.org/10.1016/j.virs.2023.01.001>

An inactivated recombinant rabies virus chimerically expressed RBD induces humoral and cellular immunity against SARS CoV-2 and RABV

Haili Zhang, Hongli Jin, Feihu Yan, Yumeng Song, Jiaxin Dai, Cuicui Jiao, Yujie Bai, Jingxuan Sun, Di Liu, Shen Wang, Mengyao Zhang, Jilong Lu, Jingbo Huang, Pei Huang, Yuanyuan Li, Xianzhu Xia, Hualei Wang

Virol Sin. 2023 Apr.;38(2):244-256.

<https://doi.org/10.1016/j.virs.2022.12.006>

Allogeneic gene-edited HIV-specific CAR-T cells secreting PD-1 blocking scFv enhance specific cytotoxic activity against HIV Env+ cells *in vivo*

Hanyu Pan, Xinyi Yang, Jing Wang, Huitong Liang, Zhengtao Jiang, Lin Zhao, Yanan Wang, Zhiming Liang, Xiaoting Shen, Qinru Lin, Yue Liang, Jinglong Yang, Panpan Lu, Yuqi Zhu, Min Li, Pengfei Wang, Jianqing Xu, Hongzhou Lu, Huanzhang Zhu

Virol Sin. 2023 Apr.;38(2):285-295.

<https://doi.org/10.1016/j.virs.2023.01.003>

Perspective on the application of genome sequencing for monkeypox virus surveillance

Yuda Chen, Changcheng Wu, Ruhan A, Li Zhao, Zhongxian Zhang, Wenjie Tan

Virol Sin. 2023 Apr.;38(2):327-333.

<https://doi.org/10.1016/j.virs.2023.03.006>

Identification of bovine coronavirus in a Daurian ground squirrel expands the host range of *Betacoronavirus 1*

Lin Xu, Wei Liu, Mengyu Bie, Tao Hu, Dong Yan, Zhishu Xiao, Edward C. Holmes, Weifeng Shi

Virol Sin. 2023 Apr.;38(2):321-323.

<https://doi.org/10.1016/j.virs.2023.02.002>

Virome diversity of ticks feeding on domestic mammals in China

Zijun Yang, Hao Wang, Shixing Yang, Xiaochun Wang, Quan Shen, Likai Ji, Jian Zeng, Wen Zhang, Haiyan Gong, Tongling Shan

Virol Sin. 2023 Apr.;38(2):208-221.

<https://doi.org/10.1016/j.virs.2023.02.001>

Perspectives

Natural co-infection of fowl adenovirus type E-8b and avian hepatitis E virus in parental layer breeders in Hebei, China

Lidan Hou, Zengna Chi, Yawen Zhang, Qi Xue, Tianshu Zhai, Shuang Chang, Jia Wang, Peng Zhao

Virol Sin. 2023 Apr.;38(2):317-320.

<https://doi.org/10.1016/j.virs.2023.01.004>

Role of inactivated SARS-CoV-2 vaccine induced T cell responses in ameliorating COVID-19 severity

Hongming Huang, Jia Liu

Virol Sin. 2023 Apr.;38(2):324-326.

<https://doi.org/10.1016/j.virs.2023.02.003>

About Virologica Sinica

Virologica Sinica is an international journal which aims at presenting the cutting-edge research on viruses all over the world. The journal publishes peer-reviewed original research articles, reviews, and letters to the editor, to encompass the latest developments in all branches of virology, including research on animal, plant and microbe viruses. The journal welcomes articles on virus discovery and characterization, viral epidemiology, viral pathogenesis, virus-host interaction, vaccine development, antiviral agents and therapies, and virus related bio-techniques.

Virologica Sinica, the official journal of the Chinese Society for Microbiology, holds an editorial board of experts from a

broad range of research fields worldwide, and will serve as a platform for the communication and exchange of academic information and ideas in an international context.

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<https://www.ncbi.nlm.nih.gov/pmc/journals/3534/>

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From: Virologica[virosin@wh.iov.cn]
Sent: Sun 6/25/2023 10:14:38 PM (UTC-04:00)
To: Gralinski, Lisa E[lgralins@email.unc.edu]
Subject: Explore our latest articles in issue 3 2023. Virologica Sinica

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Dear Dr. Lisa E Gralinski,

We would like to share with you the latest issue published in [Virologica Sinica](#). Here are the articles in this issue.

About the cover: Commensal microbiota is closely related to hepatitis B virus (HBV) infection. However, existing studies have not elucidated the effect of gut bacteria on HBV immune tolerant phase yet. In this issue, Bu et al. altered gut bacteria richness and diversity using broad spectrum antibiotic mixtures and generated HBV immune tolerance mouse model via recombinant adeno-associated virus-HBV transduction to investigate the effects of gut bacteria on HBV replication. Their study provides new thoughts for elucidating the correlation between gut bacteria dysbiosis caused by antibiotic abuse and clinical chronic HBV infection. The cover image describes that antibiotic-induced gut bacteria depletion fails to affect HBV replication in HBV immune tolerance mouse model but contributes to increase HBV replication after immune activation (kindly designed and provided by Yuchen Xia). See page 335–343 for details.

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Research Article

Antibiotic-induced gut bacteria depletion has no effect on HBV replication in HBV immune tolerance mouse model

Yanan Bu, Kaitao Zhao, Zaichao Xu, Yingcheng Zheng, Rong Hua, Chuanjian Wu, Chengliang Zhu, Yuchen Xia, Xiaoming Cheng
Virol Sin. 2023 Jun.;38(3):335-343.

<https://doi.org/10.1016/j.virs.2023.04.010>

A novel bat coronavirus with a polybasic furin-like cleavage site

Wentao Zhu, Yuyuan Huang, Jian Gong, Lingzhi Dong, Xiaojie Yu, Haiyun Chen, Dandan Li, Libo Zhou, Jing Yang, Shan Lu
Virol Sin. 2023 Jun.;38(3):344-350.

<https://doi.org/10.1016/j.virs.2023.04.009>

Epidemiology and genetic diversity of norovirus GII genogroups among children in Hubei, China, 2017–2019

Jing Li, Lingyao Zhang, Wenjing Zou, Zhaohui Yang, Jianbo Zhan, Jing Cheng
Virol Sin. 2023 Jun.;38(3):351-362.

<https://doi.org/10.1016/j.virs.2023.04.002>

Prevalence, variation, and transmission patterns of human respiratory syncytial virus from pediatric patients in Hubei, China during 2020–2021

Yi Yan, Decheng Wang, Ying Li, Zhiyong Wu, Haizhou Liu, Yue Shi, Xiaoxia Lu, Di Liu

Virol Sin. 2023 Jun.;38(3):363-372.

<https://doi.org/10.1016/j.virs.2023.05.001>

Construction and characterization of a synthesized herpes simplex virus H129-Syn-G2

Han Xiao, Hengrui Hu, Yijia Guo, Jiang Li, Le Wen, Wen-Bo Zeng, Manli Wang, Min-Hua Luo, Zhihong Hu

Virol Sin. 2023 Jun.;38(3):373-379.

<https://doi.org/10.1016/j.virs.2023.03.005>

Deletion of the first glycosylation site promotes Lassa virus glycoprotein-mediated membrane fusion

Siqi Dong, Wenting Mao, Yang Liu, Xiaoying Jia, Yueli Zhang, Minmin Zhou, Yuxia Hou, Gengfu Xiao, Wei Wang

Virol Sin. 2023 Jun.;38(3):380-386.

<https://doi.org/10.1016/j.virs.2023.04.003>

3C^{pro} of FMDV inhibits type II interferon-stimulated JAK-STAT signaling pathway by blocking STAT1 nuclear translocation

Xiangju Wu, Lei Chen, Chao Sui, Yue Hu, Dandan Jiang, Fan Yang, Laura C. Miller, Juntong Li, Xiaoyan Cong, Nataliia Hrabchenko, Changhee Lee, Yijun Du, Jing Qi

Virol Sin. 2023 Jun.;38(3):387-397.

<https://doi.org/10.1016/j.virs.2023.03.003>

Transcriptome analysis of CD4⁺ T cells from HIV-infected individuals receiving ART with LLV revealed novel transcription factors regulating HIV-1 promoter activity

Jingliang Chen, Yaozu He, Huolin Zhong, Fengyu Hu, Yonghong Li, Yeyang Zhang, Xia Zhang, Weiyin Lin, Quanmin Li, Feilong Xu, Shaozhen Chen, Hui Zhang, Weiping Cai, Linghua Li

Virol Sin. 2023 Jun.;38(3):398-408.

<https://doi.org/10.1016/j.virs.2023.03.001>

FOLR1-induced folate deficiency reduces viral replication via modulating APOBEC3 family expression

Jing Wu, Yajing Han, Ruining Lyu, Fang Zhang, Na Jiang, Hongji Tao, Qiao You, Rui Zhang, Meng Yuan, Waqas Nawaz, Deyan Chen, Zhiwei Wu

Virol Sin. 2023 Jun.;38(3):409-418.

<https://doi.org/10.1016/j.virs.2023.04.001>

TRAF7 negatively regulates the RLR signaling pathway by facilitating the K48-linked ubiquitination of TBK1

Jing-Ping Huang, Ya-Xian Yang, Tian Chen, Dan-Dan Wang, Jing Li, Liang-Guo Xu

Virol Sin. 2023 Jun.;38(3):419-428.

<https://doi.org/10.1016/j.virs.2023.04.005>

Vagal-mAChR4 signaling promotes Friend virus complex (FV)-induced acute erythroleukemia

Shuting Song, Zhekai Lin, Caiqi Zhao, Jing Wen, Jie Chen, Shitao Xie, Huaxin Qi, Jianhua Wang, Xiao Su

Virol Sin. 2023 Jun.;38(3):429-439.

<https://doi.org/10.1016/j.virs.2023.05.005>

Temperature-regulated type II grass carp reovirus establishes latent infection in *Ctenopharyngodon idella* brain

Rui Jiang, Jie Zhang, Zhiwei Liao, Wentao Zhu, Hang Su, Yongan Zhang, Jianguo Su

Virol Sin. 2023 Jun.;38(3):440-447.

<https://doi.org/10.1016/j.virs.2023.04.006>

Spastin is required for human immunodeficiency virus-1 efficient replication through cooperation with the endosomal sorting complex required for transport (ESCRT) protein

Wenyuan Shen, Chang Liu, Yue Hu, Qian Ding, Jiabin Feng, Zhou Liu, Xiaohong Kong

Virol Sin. 2023 Jun.;38(3):448-458.

<https://doi.org/10.1016/j.virs.2023.05.006>

ASFV transcription reporter screening system identifies aianthone as a broad antiviral compound

Yuhang Zhang, Zhenjiang Zhang, Fan Zhang, Jiwen Zhang, Jun Jiao, Min Hou, Nianchao Qian, Dongming Zhao, Xiaofeng Zheng, Xu Tan

Virol Sin. 2023 Jun.;38(3):459-469.

<https://doi.org/10.1016/j.virs.2023.03.004>

Oridonin inhibits SARS-CoV-2 replication by targeting viral proteinase and polymerase

Zherui Zhang, Hongqing Zhang, Yanan Zhang, Qiuyan Zhang, Qiaojie Liu, Yanyan Hu, Xiaoling Chen, Jing Wang, Yujia Shi, Chenglin Deng, Peng Gong, Bo Zhang, Xiaodan Li, Bing Zhu, Hanqing Ye

Virol Sin. 2023 Jun.;38(3):470-479.

<https://doi.org/10.1016/j.virs.2023.04.008>

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Sent: Mon 8/28/2023 7:51:45 AM (UTC-04:00)
To: Gralinski, Lisa E[lgralins@email.unc.edu]
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We sincerely thank you for your continued support and look forward to your contribution!

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Review Article

Host cell restriction factors of equine infectious anemia virus

Xue-Feng Wang, Xiangmin Zhang, Weiwei Ma, Jiwei Li, Xiaojun Wang

Virol Sin. 2023 Aug.;38(4): 485-496.

<https://doi.org/10.1016/j.virs.2023.07.001>

Research Articles

Elucidating cellular interactome of chikungunya virus identifies host dependency factors

Peiqi Yin, Xia Jian, Yihan Liu, Yuwen Liu, Lu Lv, Haoran Cui, Leiliang Zhang

Virol Sin. 2023 Aug.;38(4): 497-507.

<https://doi.org/10.1016/j.virs.2023.05.007>

Integrated interactome and transcriptome analysis reveals key host factors critical for SARS-CoV-2 infection

Jie Sheng, Lili Li, Xueying Lv, Meiling Gao, Ziyi Chen, Zhuo Zhou, Jingfeng Wang, Aiping Wu, Taijiao Jiang

Virol Sin. 2023 Aug.;38(4): 508-519.

<https://doi.org/10.1016/j.virs.2023.05.004>

SARS-CoV-2 Nsp8 induces mitophagy by damaging mitochondria

Shan Zong, Yan Wu, Weiling Li, Qiang You, Qian Peng, Chenghai Wang, Pin Wan, Tao Bai, Yanling Ma, Binlian Sun, Jialu Qiao

Virol Sin. 2023 Aug.;38(4): 520-530.

<https://doi.org/10.1016/j.virs.2023.05.003>

Unusual substructure conformations observed in crystal structures of a dicistrovirus RNA-dependent RNA polymerase suggest contribution of the N-terminal extension in proper folding

Xiang Fang, Guoliang Lu, Yanchun Deng, Sa Yang, Chunsheng Hou, Peng Gong

Virol Sin. 2023 Aug.;38(4): 531-540.

<https://doi.org/10.1016/j.virs.2023.05.002>

Development of PREDAC-H1pdm to model the antigenic evolution of influenza A/(H1N1) pdm09 viruses

Mi Liu, Jingze Liu, Wenjun Song, Yousong Peng, Xiao Ding, Lizong Deng, Taijiao Jiang

Virol Sin. 2023 Aug.;38(4): 541-548.

<https://doi.org/10.1016/j.virs.2023.05.008>

Construction of coxsackievirus B5 viruses with luciferase reporters and their applications *in vitro* and *in vivo*

Shangrui Guo, Meng Xun, Tingting Fan, Xinyu Li, Haoyan Yao, Xiaozhen Li, Bo Wu, Hang Yang, Chaofeng Ma, Hongliang Wang

Virol Sin. 2023 Aug.;38(4): 549-558.

<https://doi.org/10.1016/j.virs.2023.05.010>

PA-E18G substitution in influenza A virus confers resistance to ZX-7101, a cap-dependent endonuclease inhibitor

Dan Luo, Qing Ye, Rui-Ting Li, Hang-Yu Zhou, Jing-Jing Guo, Suo-Qun Zhao, Sen Zhang, Tao Jiang, Yong-Qiang Deng, Cheng Feng Qin

Virol Sin. 2023 Aug.;38(4): 559-567.

<https://doi.org/10.1016/j.virs.2023.06.002>

STING strengthens host anti-hantaviral immunity through an interferon-independent pathway

Kerong Wang, Jian Zhang, Yongheng Yang, Yue Si, Ziqing Zhou, Xudong Zhu, Sushan Wu, He Liu, Hui Zhang, Liang Zhang, Linfeng Cheng, Wei Ye, Xin Lv, Yingfeng Lei, Xijing Zhang, Shilin Cheng, Lixin Shen, Fanglin Zhang, Hongwei Ma

Virol Sin. 2023 Aug.;38(4): 568-584.

<https://doi.org/10.1016/j.virs.2023.06.006>

A high throughput antiviral screening platform for alphaviruses based on Semliki Forest virus expressing eGFP reporter gene

Yu-Jia Shi, Jia-Qi Li, Hong-Qing Zhang, Cheng-Lin Deng, Qin-Xuan Zhu, Bo Zhang, Xiao-Dan Li

Virol Sin. 2023 Aug.;38(4): 585-594.

<https://doi.org/10.1016/j.virs.2023.06.007>

Altered hACE2 binding affinity and S1/S2 cleavage efficiency of SARS-CoV-2 spike protein mutants affect viral cell entry

Ke Wang, Yu Pan, Dianbing Wang, Ye Yuan, Min Li, Yuanyuan Chen, Lijun Bi, Xian-En Zhang

Virol Sin. 2023 Aug.;38(4): 595-605.

<https://doi.org/10.1016/j.virs.2023.06.005>

SARS-CoV-2-specific T cell responses wane profoundly in convalescent individuals 10 months after primary infection

Ziwei Li, Tiandan Xiang, Boyun Liang, Jing Liu, Hui Deng, Xuecheng Yang, Hua Wang, Xuemei Feng, Gennadiy Zelinskyy, Mirko Trilling, Kathrin Sutter, Mengji Lu, Ulf Dittmer, Baoju Wang, Dongliang Yang, Xin Zheng, Jia Liu

Virol Sin. 2023 Aug.;38(4): 606-619.

<https://doi.org/10.1016/j.virs.2023.06.011>

Multicenter evaluation of a simple and sensitive nucleic acid self-testing for SARS-CoV-2

Xin-Xin Shen, Feng-Yu Li, Meng Qin, Guo-Hao Zhang, Meng-Yi Zhang, Hong Liu, Xiu-Li Sun, Zhen-Jiang Xin, Xue-Jun Ma

Virol Sin. 2023 Aug.;38(4): 620-626.

<https://doi.org/10.1016/j.virs.2023.06.009>

Letters

Delta (B.1.617.2) inactivated vaccine candidate elicited neutralizing antibodies to SARS-CoV-2 and circulating variants in rhesus macaques

YanJun Zhang, Haiyan Mao, Ju Li, Jianhua Li, Chen Huang, Jiaxuan Li, Minglei Chu, Fengbo Xue, Linhui Wang, Zhongbiao Fang, Zhen Wang, Jinan Wu, Keda Chen

Virol Sin. 2023 Aug.;38(4): 627-630.

<https://doi.org/10.1016/j.virs.2023.05.009>

Optimization and applications of an *in vivo* bioluminescence imaging model of influenza A virus infections

Xiaojing Lin, Murong Zhu, Xiujuan Zhao, Longlong Si, Meiyue Dong, Varada Anirudhan, Qinghua Cui, Lijun Rong, Ruikun Du

Virol Sin. 2023 Aug.;38(4): 631-634.

<https://doi.org/10.1016/j.virs.2023.04.007>

A visual assay panel for the identification of monkeypox virus DNA belonging to the clades I and II

Pei Huang, Zanheng Huang, Meihui Liu, Yujie Bai, Hongli Jin, Jingbo Huang, Xingqi Liu, Zhenhong Guan, Ming Duan, Haili Zhang, Yuanyuan Li, Sandra Chiu, Hualei Wang

Virol Sin. 2023 Aug.;38(4): 635-638.

<https://doi.org/10.1016/j.virs.2023.05.012>

***In vitro* and *In vitro* efficacy of Molnupiravir against Zika virus infections**

Zhuang Wang, Shaokang Yang, Qingsong Dai, Xiaojia Guo, Yuexiang Li, Wei Li, Xiaotong Yang, Jingjing Yang, Xintong Yan, Huimin Tao, Chongda Luo, Song Li, Xingjuan Chen, Ruiyuan Cao, Wu Zhong

Viol Sin. 2023 Aug.;38(4): 639-642.

<https://doi.org/10.1016/j.virs.2023.05.011>

Migrasomes released by HSV-2-infected cells serve as a conveyance for virus spread

Yalan Liu, Zhiyuan Zhu, Yuncheng Li, Mengshi Yang, Qinxue Hu

Viol Sin. 2023 Aug.;38(4): 643-645.

<https://doi.org/10.1016/j.virs.2023.06.001>

Genetic characterization of rarely reported GII.3[P25] norovirus strain detected in patients with acute gastroenteritis in Huzhou, China, 2021

Peng Zhang, Deshun Xu, Teng Liu, Liping Chen, Lei Ji

Viol Sin. 2023 Aug.;38(4): 646-649.

<https://doi.org/10.1016/j.virs.2023.06.008>

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Dear Dr. Lisa E Gralinski,

We would like to share with you the latest issue published in [Virologica Sinica](#). Here are the articles in this issue.

About the cover: In this issue, Si et al. demonstrated that HTNV infection blocked JAK/STAT signaling by activating the receptor-interacting protein kinase 3 (RIPK3), but not triggering necroptosis. RIPK3 ablation efficiently promoted the expression of IFN-stimulated genes (ISG) and restricted viral replication *in vitro*. RIPK3 knockout mice also acquired prompt HTNV clearance ability with strengthened systemic inflammatory responses. Further investigation indicated that RIPK3 interfered with IFN pathway by binding to and incapacitating STAT1 during late HTNV infection stage. The cover image illustrates the possible immune evasion process of HTNV by manipulating RIPK3 traps to impede STAT1-mediate antiviral effects. See page 741–754 for details.

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Research Articles

Diversity and independent evolutionary profiling of rodent-borne viruses in Hainan, a tropical island of China

Youyou Li, Chuanning Tang, Yun Zhang, Zihan Li, Gaoyu Wang, Ruoyan Peng, Yi Huang, Xiaoyuan Hu, Henan Xin, Boxuan Feng, Xuefang Cao, Yongpeng He, Tonglei Guo, Yijun He, Haoxiang Su, Xiuji Cui, Lina Niu, Zhiqiang Wu, Jian Yang, Fan Yang, Gang Lu, Lei Gao, Qi Jin, Meifang Xiao, Feifei Yin, Jiang Du

Viol Sin. 2023 Oct.;38(5):651-662.

<https://doi.org/10.1016/j.virs.2023.08.003>

Epizootiological surveillance of porcine circoviruses in free-ranging wild boars in China

Wenjie Gong, Haiying Du, Tong Wang, Heting Sun, Peng Peng, Siyuan Qin, Haidong Geng, Zheng Zeng, Wangwang Liang, Hongquan Ling, Changchun Tu, Zhongzhong Tu

Viol Sin. 2023 Oct.;38(5):663-670.

<https://doi.org/10.1016/j.virs.2023.08.008>

Changing predominance of norovirus strains in children with acute gastroenteritis in Shanghai, 2018–2021

Lijuan Lu, Yuanyun Ao, Ran Jia, Huaqing Zhong, Pengcheng Liu, Menghua Xu, Liyun Su, Lingfeng Cao, Jin Xu

Virol Sin. 2023 Oct.;38(5):671-679.

<https://doi.org/10.1016/j.virs.2023.08.005>

HBV precore G1896A mutation promotes growth of hepatocellular carcinoma cells by activating ERK/MAPK pathway

Baoxin Zhao, Hongxiu Qiao, Yan Zhao, Zhiyun Gao, Weijie Wang, Yan Cui, Jian Li, Zhanjun Guo, Xia Chuai, Sandra Chiu

Virol Sin. 2023 Oct.;38(5):680-689.

<https://doi.org/10.1016/j.virs.2023.06.004>

miR-204 suppresses porcine reproductive and respiratory syndrome virus (PRRSV) replication via inhibiting LC3B mediated autophagy

Yao Yao, Sihan Li, Yingqi Zhu, Yangyang Xu, Siyuan Hao, Shuyuan Guo, Wen-Hai Feng

Virol Sin. 2023 Oct.;38(5):690-698.

<https://doi.org/10.1016/j.virs.2023.07.004>

Long noncoding RNA 1392 regulates MDA5 by interaction with ELAVL1 to inhibit coxsackievirus B5 infection

Jing Li, Jinwei Li, Peiying Teng, Fan Yang, Jihong Zhang, Bo Sun, Wei Chen

Virol Sin. 2023 Oct.;38(5):699-708.

<https://doi.org/10.1016/j.virs.2023.08.001>

Autophagy induced by human adenovirus B7 structural protein VI inhibits viral replication

Linlin Zhang, Yali Duan, Wei Wang, Qi Li, Jiao Tian, Yun Zhu, Ran Wang, Zhengde Xie

Virol Sin. 2023 Oct.;38(5):709-722.

<https://doi.org/10.1016/j.virs.2023.08.002>

Inactivated SARS-CoV-2 booster vaccine enhanced immune responses in patients with chronic liver diseases

Yongmei Liu, Jianhua Lu, Haoting Zhan, Wenfang Yuan, Xiaomeng Li, Haiyan Kang, Haolong Li, Yongliang Chen, Linlin Cheng, Xingli Sun, Haojie Zheng, Wei Wang, Erhei Dai, Yongzhe Li

Virol Sin. 2023 Oct.;38(5):723-734.

<https://doi.org/10.1016/j.virs.2023.07.005>

Abnormal liver function in children hospitalized with acute respiratory infection of adenoviruses: a retrospective study

Xingui Tian, Xiao Li, Shuyan Qiu, Rong Zhou, Wenkuan Liu

Virol Sin. 2023 Oct.;38(5):735-740.

<https://doi.org/10.1016/j.virs.2023.07.007>

RIPK3 promotes hantaviral replication by restricting JAK-STAT signaling without triggering necroptosis

Yue Si, Haijun Zhang, Ziqing Zhou, Xudong Zhu, Yongheng Yang, He Liu, Liang Zhang, Linfeng Cheng, Kerong Wang, Wei Ye, Xin Lv, Xijing Zhang, Wugang Hou, Gang Zhao, Yingfeng Lei, Fanglin Zhang, Hongwei Ma
Virol Sin. 2023 Oct.;38(5):741-754.
<https://doi.org/10.1016/j.virs.2023.08.006>

Enterovirus D68 infection upregulates SOCS3 expression to inhibit JAK-STAT3 signaling and antagonize the innate interferon response of the host

Yuling Zhang, Leling Xu, Zhe Zhang, Xin Su, Zhiyun Wang, Tao Wang
Virol Sin. 2023 Oct.;38(5):755-766.
<https://doi.org/10.1016/j.virs.2023.08.007>

Development of a novel virus-like particle-based vaccine for preventing tick-borne encephalitis virus infection

Jielin Tang, Muqing Fu, Chonghui Xu, Bao Xue, Anqi Zhou, Sijie Chen, He Zhao, Yuan Zhou, Jizheng Chen, Qi Yang, Xinwen Chen
Virol Sin. 2023 Oct.;38(5):767-777.
<https://doi.org/10.1016/j.virs.2023.06.003>

Identification of a receptor tyrosine kinase inhibitor CP-724714 inhibits SARS-CoV related swine diarrhea coronaviruses infection *in vitro*

Ling Zhou, Cheng Li, Ruiyu Zhang, Qianniu Li, Yuan Sun, Yaoyu Feng, Tian Lan, Jingyun Ma
Virol Sin. 2023 Oct.;38(5):778-786.
<https://doi.org/10.1016/j.virs.2023.06.010>

Nanobodies with cross-neutralizing activity provide prominent therapeutic efficacy in mild and severe COVID-19 rodent models

Qiuxue Han, Shen Wang, Zhenshan Wang, Cheng Zhang, Xinyue Wang, Na Feng, Tiecheng Wang, Yongkun Zhao, Hang Chi, Feihu Yan, Xianzhu Xia
Virol Sin. 2023 Oct.;38(5):787-800.
<https://doi.org/10.1016/j.virs.2023.07.003>

Characterization of bacteriophage BUCT631 lytic for K1 *Klebsiella pneumoniae* and its therapeutic efficacy in *Galleria mellonella* larvae

Pengjun Han, Mingfang Pu, Yahao Li, Huahao Fan, Yigang Tong
Virol Sin. 2023 Oct.;38(5):801-812.
<https://doi.org/10.1016/j.virs.2023.07.002>

Genomic similarity and antibody-dependent enhancement of immune serum potentially affect the protective efficacy of

commercial MLV vaccines against NADC30-like PRRSV

Yang Li, Lele Xu, Dian Jiao, Zifang Zheng, Zhihao Chen, Yang Jing, Zhiwei Li, Zhiqian Ma, Yingtong Feng, Xuyang Guo, Yumiao Wang, Yuan He, Haixue Zheng, Shuqi Xiao

Viol Sin. 2023 Oct.;38(5):813-826.

<https://doi.org/10.1016/j.virs.2023.08.010>

Letters

Comparative study of the pathogenicity of the mosquito origin strain and duck origin strain of Tembusu virus in ducklings and three-week-old mice

Xiaoli Wang, Yu He, Jiaqi Guo, Zhen Wu, Andres Merits, Mingshu Wang, Renyong Jia, Dekang Zhu, Mafeng Liu, Xinxin Zhao, Qiao Yang, Ying Wu, Shaqiu Zhang, Juan Huang, Xumin Ou, Qun Gao, Di Sun, Anchun Cheng, Shun Chen

Viol Sin. 2023 Oct.;38(5):827-831.

<https://doi.org/10.1016/j.virs.2023.07.006>

Natural circulation of tick-borne severe fever with thrombocytopenia syndrome virus in the city ecosystem, China

Xing Zhang, Chaoyue Zhao, Xiaoxi Si, Qiang Hu, Aihua Zheng

Viol Sin. 2023 Oct.;38(5):832-835.

<https://doi.org/10.1016/j.virs.2023.08.004>

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Dear Dr. Gralinski,

We are delighted to share with you the latest issue of *Virologica Sinica*. Kindly find the articles listed below. Your comments and suggestions are appreciated.

About the Cover

HBx/NF- κ B pathway plays an important role in HBV replication. However, whether NF- κ B-interacting long noncoding RNA (NKILA), a suppressor of NF- κ B activation, regulates HBV replication remains largely unknown. In this issue, Zhang et al. observed a negative correlation between NKILA expression level and HBV viral loads in HBV-positive patients, discovered that NKILA inhibits p65 translocation into the nucleus and reduces I κ B α phosphorylation levels, and further showed NKILA could interrupt the interaction between HBx and p65, thereby suppressing HBV replication and HBx-induced NF- κ B activation. The cover image illustrates the role of lncRNA NKILA in inhibiting HBV replication, incorporating elements from the legend of Chinese New Year. The prodigious man (human defense system) tied the head (HBx) of the beast (HBV) with a magic red silk strip (lncRNA NKILA) to protect people away from the attack. (Kindly provided by Prof. Hong Wang and Prof. Wenyan Zhang). See pages 44–55 for details.

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Review Articles

Single-cell RNA sequencing to understand host-virus interactions

Jia-Tong Chang, Li-Bo Liu, Pei-Gang Wang, Jing An

Virol Sin. 2024 Feb.; 39(1):1-8.

<https://doi.org/10.1016/j.virs.2023.11.009>

Classifying hepatitis B therapies with insights from covalently closed circular DNA dynamics

Jie-Li Hu, Ai-Long Huang

Virol Sin. 2024 Feb.; 39(1):9-23.

<https://doi.org/10.1016/j.virs.2023.12.005>

Interconnection of cellular autophagy and endosomal vesicle trafficking and its role in hepatitis B virus replication and

release

Jia Li, Yong Lin, Xueyu Wang, Mengji Lu

Virol Sin. 2024 Feb.; 39(1):24-30.

<https://doi.org/10.1016/j.virs.2024.01.001>

Research Articles

Ancient dormant virus remnant ERVW-1 drives ferroptosis via degradation of SLC3A2/GPX4 pathway in recent-onset schizophrenia

Dongyan Zhang, Xiulin Wu, Xing Xue, Wenshi Li, Ping Zhou, Zhao Lv, Kexin Zhao, Fan Zhu

Virol Sin. 2024 Feb.; 39(1):31-43.

<https://doi.org/10.1016/j.virs.2023.09.001>

LncRNA NKILA inhibits HBV replication by repressing NF- κ B signalling activation

Xi Zhang, Yuanyuan Li, Chen Huan, Yubao Hou, Rujia Liu, Hongyun Shi, Peng Zhang, Baisong Zheng, Yingchao Wang, Hong Wang, Wenyan Zhang

Virol Sin. 2024 Feb.; 39(1):44-55.

<https://doi.org/10.1016/j.virs.2023.10.002>

Mutual antagonism of mouse-adaptation mutations in HA and PA proteins on H9N2 virus replication

Liping Ma, Huabin Zheng, Xianliang Ke, Rui Gui, Zhongzi Yao, Jiasong Xiong, Quanjiao Chen

Virol Sin. 2024 Feb.; 39(1):56-70.

<https://doi.org/10.1016/j.virs.2023.11.004>

Naturally occurring PAE206K point mutation in 2009 H1N1 pandemic influenza viruses impairs viral replication at high temperatures

Mengmeng Cao, Qiannan Jia, Jinghua Li, Lili Zhao, Li Zhu, Yufan Zhang, Shan Li, Tao Deng

Virol Sin. 2024 Feb.; 39(1):71-80.

<https://doi.org/10.1016/j.virs.2023.11.005>

HIF-1 α promotes virus replication and cytokine storm in H1N1 virus-induced severe pneumonia through cellular metabolic reprogramming

Xiaoxiao Meng, Yong Zhu, Wenyu Yang, Jiayang Zhang, Wei Jin, Rui Tian, Zhengfeng Yang, Ruilan Wang

Virol Sin. 2024 Feb.; 39(1):81-96.

<https://doi.org/10.1016/j.virs.2023.11.010>

Phosphorylation of PB2 at serine 181 restricts viral replication and virulence of the highly pathogenic H5N1 avian

influenza virus in mice

Jiao Hu, Zixiong Zeng, Xia Chen, Manyu Zhang, Zenglei Hu, Min Gu, Xiaoquan Wang, Ruyi Gao, Shunlin Hu, Yu Chen, Xiaowen Liu, Daxin Peng, Xiufan Liu

Virol Sin. 2024 Feb.; 39(1):97-112.

<https://doi.org/10.1016/j.virs.2023.12.003>

Hsp90 β is critical for the infection of severe fever with thrombocytopenia syndrome virus

Bo Wang, Leike Zhang, Fei Deng, Zhihong Hu, Manli Wang, Jia Liu

Virol Sin. 2024 Feb.; 39(1):113-122.

<https://doi.org/10.1016/j.virs.2023.11.008>

Drug repurposing screen identifies vidofludimus calcium and pyrazofurin as novel chemical entities for the development of hepatitis E interventions

Hongbo Guo, Dan Liu, Kuan Liu, Yao Hou, Chunyang Li, Qiudi Li, Xiaohui Ding, Monique M.A. Verstegen, Jikai Zhang, Lingli Wang, Yibo Ding, Renxian Tang, Xiucheng Pan, Kuiyang Zheng, Luc J.W. van der Laan, Qiuwei Pan, Wenshi Wang

Virol Sin. 2024 Feb.; 39(1):123-133.

<https://doi.org/10.1016/j.virs.2023.11.006>

Rapid identification of full-length genome and tracing variations of monkeypox virus in clinical specimens based on mNGS and amplicon sequencing

Changcheng Wu, Ruhan A, Sheng Ye, Fei Ye, Weibang Huo, Roujian Lu, Yue Tang, Jianwei Yang, Xuehong Meng, Yun Tang, Shuang Chen, Li Zhao, Baoying Huang, Zhongxian Zhang, Yuda Chen, Dongfang Li, Wenling Wang, Ke-jia Shan, Jian Lu, Wenjie Tan

Virol Sin. 2024 Feb.; 39(1):134-143.

<https://doi.org/10.1016/j.virs.2023.12.002>

Ferroptosis contributes to JEV-induced neuronal damage and neuroinflammation

Wenjing Zhu, Qi Li, Yong Yin, Huanchun Chen, Youhui Si, Bibo Zhu, Shengbo Cao, Zikai Zhao, Jing Ye

Virol Sin. 2024 Feb.; 39(1):144-155.

<https://doi.org/10.1016/j.virs.2023.12.004>

RNA barcode segments for SARS-CoV-2 identification from HCoV-229E and SARSr-CoV-2 lineages

Changqiao You, Shuai Jiang, Yunyun Ding, Shunxing Ye, Xiaoxiao Zou, Hongming Zhang, Zeqi Li, Fenglin Chen, Yongliang Li, Xingyi Ge, Xinhong Guo

Virol Sin. 2024 Feb.; 39(1):156-168.

<https://doi.org/10.1016/j.virs.2024.01.006>

Isolation and characterization of spike S2-specific monoclonal antibodies with reactivity to pan-coronaviruses

Yabin Hu, Jun Chen, Jing Yang, Zhanpeng Liu, Xiaoyue Zhang, Qian Wu, Lulu Liu, Shishan Teng, Rongzhang He, Bo Liu, Xingyu Zheng, Rui Lu, Dong Pan, You Wang, Liting Peng, Hongying Chen, Yi-Ping Li, Wenpei Liu, Xiaowang Qu

Viol Sin. 2024 Feb.; 39(1):169-172.

<https://doi.org/10.1016/j.virs.2023.10.008>

SARS-CoV-2 breakthrough infections following inactivated vaccine vaccination induce few neutralizing antibodies against the currently emerging Omicron XBB variants

Fan Shen, Chun Liang, Cui-Xian Yang, Ying Lu, An-Qi Li, Ying Duan, Mi Zhang, Ren-Rong Tian, Xing-Qi Dong, Yong-Tang Zheng, Wei Pang

Viol Sin. 2024 Feb.; 39(1):173-176.

<https://doi.org/10.1016/j.virs.2023.11.007>

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We are delighted to share with you the [latest issue of Virologica Sinica](#). Kindly find the articles listed below. Your comments and suggestions are appreciated.

Foot-and-mouth disease (FMD) is a highly contagious disease caused by the FMD virus (FMDV). Although the cell receptor for FMDV has been identified, the specific mechanism of FMDV internalization after infection remains unknown. In this issue, Zhang et al. demonstrate that kinesin family member 5B (KIF5B) plays a crucial role in FMDV internalization. KIF5B directly interacts with VP1 to facilitate FMDV internalization by regulating clathrin uncoating. Further evidence indicates that KIF5B also facilitates the transport of viral particles to early and late endosomes during the early stages of FMDV infection. The cover image depicts FMDV (red) 'hijacking' host cell protein KIF5B (yellow) to invade the host cell and is then transported by KIF5B to the endosomes for uncoating, releasing RNA for reproduction. Subsequently, FMDV wrests cell resources (blue) within the host cell to complete its own replication, assembly, and release processes, thus completing its life cycle (Kindly provided by Dr. Wei Zhang and Prof. Haixue Zheng). See page 378–389 for details..

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News and Views

Joint deletion of multifunctional *MGF505-7R* and *H240R* genes generates a safe and effective African swine fever virus attenuated live vaccine candidate

Changjiang Weng, Li Huang, Guangqiang Ye

Virol Sin. 2024 Jun.; 39(3): 355-357.

<https://doi.org/10.1016/j.virs.2024.04.007>

Research Articles

Evolutionary dynamics and comparative pathogenicity of clade 2.3.4.4b H5 subtype avian influenza viruses, China, 2021–2022

Siru Lin, Junhong Chen, Ke Li, Yang Liu, Siyuan Fu, Shumin Xie, Aimin Zha, Aiguo Xin, Xinyu Han, Yuting Shi, Lingyu Xu, Ming Liao, Weixin Jia

Virol Sin. 2024 Jun.; 39(3): 358-368.

Risk of infection with arboviruses in a healthy population in Pakistan based on seroprevalence

Shengyao Chen, Muhammad Saqib, Hafiz Sajid Khan, Yuan Bai, Usman Ali Ashfaq, Muhammad Khalid Mansoor, Abulimti Moming, Jing Liu, Min Zhou, Saifullah Khan Niazi, Qiaoli Wu, Awais-Ur-Rahman Sial, Shuang Tang, Muhammad Hassan Sarfraz, Aneela Javed, Sumreen Hayat, Mohsin Khurshid, lahtasham Khan, Muhammad Ammar Athar, Zeeshan Taj, Bo Zhang, Fei Deng, Ali Zohaib, Shu Shen

Virol Sin. 2024 Jun.; 39(3): 369-377.

<https://doi.org/10.1016/j.virs.2024.04.001>

KIF5B-mediated internalization of FMDV promotes virus infection

Wei Zhang, Fan Yang, Yang Yang, Weijun Cao, Wenhua Shao, Jiali Wang, Mengyao Huang, Zhitong Chen, Xiaoyi Zhao, Weiwei Li, Zixiang Zhu, Haixue Zheng

Virol Sin. 2024 Jun.; 39(3): 378-389.

<https://doi.org/10.1016/j.virs.2024.03.005>

Crucial role played by CK8+ cells in mediating alveolar injury remodeling for patients with COVID-19

Yufeng Li, Hengrui Hu, Jia Liu, Longda Ma, Xi Wang, Liang Liu, Qian Liu, Liang Ren, Jiang Li, Fei Deng, Zhihong Hu, Yiwu Zhou, Manli Wang

Virol Sin. 2024 Jun.; 39(3): 390-402.

<https://doi.org/10.1016/j.virs.2024.03.007>

Pseudorabies virus manipulates mitochondrial tryptophanyl-tRNA synthetase 2 for viral replication

Xiu-Qing Li, Meng-Pan Cai, Ming-Yang Wang, Bo-Wen Shi, Guo-Yu Yang, Jiang Wang, Bei-Bei Chu, Sheng-Li Ming

Virol Sin. 2024 Jun.; 39(3): 403-413.

<https://doi.org/10.1016/j.virs.2024.04.003>

Characterization of humoral immune responses against SARS-CoV-2 accessory proteins in infected patients and mouse model

Yuming Li, Yanhong Tang, Xiaoqian Wang, Airu Zhu, Dongdong Liu, Yiyun He, Hu Guo, Jie Zheng, XinZhuo Liu, Fengyu Chi, Yanqun Wang, Zhen Zhuang, Zhaoyong Zhang, Donglan Liu, Zhao Chen, Fang Li, Wei Ran, Kuai Yu, Dong Wang, Liyan Wen, Jianfen Zhuo, Yanjun Zhang, Yin Xi, Jingxian Zhao, Jincun Zhao, Jing Sun

Virol Sin. 2024 Jun.; 39(3): 414-421.

<https://doi.org/10.1016/j.virs.2024.04.005>

Integration of HiBiT into enteroviruses: A universal tool for advancing enterovirus virology research

Rui Yu, Xiaohong Li, Peng Zhang, Minghao Xu, Jitong Zhao, Jingjing Yan, Chenli Qiu, Jiayi Shu, Shuo Zhang, Miaomiao Kang, Xiaoyan Zhang, Jianqing Xu, Shuye Zhang
Virol Sin. 2024 Jun.; 39(3): 422-433.
<https://doi.org/10.1016/j.virs.2024.03.004>

Establishment and application of a surrogate model for human Ebola virus disease in BSL-2 laboratory

Wanying Yang, Wujian Li, Wujie Zhou, Shen Wang, Weiqi Wang, Zhenshan Wang, Na Feng, Tiecheng Wang, Ying Xie, Yongkun Zhao, Feihu Yan, Xianzhu Xia
Virol Sin. 2024 Jun.; 39(3): 434-446.
<https://doi.org/10.1016/j.virs.2024.03.010>

An optimized high-throughput SARS-CoV-2 dual reporter trans-complementation system for antiviral screening in vitro and in vivo

Yingjian Li, Xue Tan, Jikai Deng, Xuemei Liu, Qianyun Liu, Zhen Zhang, Xiaoya Huang, Chao Shen, Ke Xu, Li Zhou, Yu Chen
Virol Sin. 2024 Jun.; 39(3): 447-458.
<https://doi.org/10.1016/j.virs.2024.03.009>

Development of a Měnglà virus minigenome and comparison of its polymerase complex with those of other filoviruses

Shi-Zhe Xie, Ke Yao, Bei Li, Cheng Peng, Xing-Lou Yang, Zheng-Li Shi
Virol Sin. 2024 Jun.; 39(3): 459-468.
<https://doi.org/10.1016/j.virs.2024.03.011>

Function investigation of p11.5 in ASFV infection

Dan Yin, Bin Shi, Renhao Geng, Yingnan Liu, Lang Gong, Hongxia Shao, Kun Qian, Hongjun Chen, Aijian Qin
Virol Sin. 2024 Jun.; 39(3): 469-477.
<https://doi.org/10.1016/j.virs.2024.05.007>

Nanobodies against African swine fever virus p72 and CD2v proteins as reagents for developing two cELISAs to detect viral antibodies

Jiahong Zhu, Qingyuan Liu, Liuya Li, Runyu Zhang, Yueting Chang, Jiakai Zhao, Siyu Liu, Xinyu Zhao, Xu Chen, Yani Sun, Qin Zhao
Virol Sin. 2024 Jun.; 39(3): 478-489.
<https://doi.org/10.1016/j.virs.2024.04.002>

DNA vaccine prime and replicating vaccinia vaccine boost induce robust humoral and cellular immune responses against MERS-CoV in mice

Xiuli Shen, Shuhui Wang, Yanling Hao, Yuyu Fu, Li Ren, Dan Li, Wenqi Tang, Jing Li, Ran Chen, Meiling Zhu, Shuo Wang, Ying

Liu, Yiming Shao

Virol Sin. 2024 Jun.; 39(3): 490-500.

<https://doi.org/10.1016/j.virs.2024.05.005>

Calmodulin-like 5 promotes PEDV replication by regulating late-endosome synthesis and innate immune response

Wen-Jun Tian, Xiu-Zhong Zhang, Jing Wang, Jian-Feng Liu, Fu-Huang Li, Xiao-Jia Wang

Virol Sin. 2024 Jun.; 39(3): 501-512.

<https://doi.org/10.1016/j.virs.2024.05.006>

Letters

Severe fever with thrombocytopenia syndrome virus infection attributed to cat contact: A case report in Beijing, China

Shuo Zhang, Yu Leng, Fa-Xue Zhang, Bo-Kang Fu, Bing-Zheng Wu, Jia-Hao Chen, Ning Cui, Ning Zhao, Wei Liu, Hao Li

Virol Sin. 2024 Jun.; 39(3): 513-515.

<https://doi.org/10.1016/j.virs.2024.03.006>

A lethal mice model of recombinant vesicular stomatitis viruses for EBOV-targeting prophylactic vaccines evaluation

Hong-Qing Zhang, Zhe-Rui Zhang, Cheng-Lin Deng, Zhi-Ming Yuan, Bo Zhang

Virol Sin. 2024 Jun.; 39(3): 516-519.

<https://doi.org/10.1016/j.virs.2024.03.008>

Genetic characteristics of H1N1 influenza virus outbreak in China in early 2023

Xuanxuan Li, Zefeng Dong, Jiaming Li, Chuanran Dou, Deyu Tian, Zhenghai Ma, Wenjun Liu, George F. Gao, Yuhai Bi

Virol Sin. 2024 Jun.; 39(3): 520-523.

<https://doi.org/10.1016/j.virs.2024.05.003>

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Influenza A virus (IAV) possesses a broad host range and undergoes rapid genomic variation, leading to the continuous emergence of novel viruses with significant antigenic variations and cross-species transmission potential. Understanding the evolutionary patterns and underlying mechanisms of all IAVs is crucial for effective prevention and control. However, current genetic clustering methods, such as phylogenetic-based and genetic distance-based approaches, lack phylogenetic information, which hinders the identification of complex events such as reassortments. In this issue, Ding et al. developed a novel genotype identification method, named FluTyping, to enhance the investigation of IAV genotype-based evolution. Based on both genetic distance and phylogenetic relationships, FluTyping established a comprehensive set of classification for all IAVs using whole genome sequences, offering a macro perspective of IAVs' genetic diversity patterns and their restriction factors. The cover image depicts IAVs with multi-genotypes co-circulation patterns show region-specific dominant genotypes, and the restriction of IAV transmission within specific regions contributes to the prevalence of certain genotypes (Kindly designed and provided by Dr. Xiao Ding, Prof. Aiping Wu and Prof. Taijiao Jiang). See page 525–536 for details.

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Research Articles

Transmission restriction and genomic evolution co-shape the genetic diversity patterns of influenza A virus

Xiao Ding, Jingze Liu, Taijiao Jiang, Aiping Wu

Viol Sin. 2024 Aug.; 39(4): 525-536.

<https://doi.org/10.1016/j.virs.2024.02.005>

RNA viromes of *Dermacentor nuttalli* ticks reveal a novel uukuvirus in Qīnghǎi Province, China

Yaohui Fang, Jun Wang, Jianqing Sun, Zhengyuan Su, Shengyao Chen, Jian Xiao, Jun Ni, Zhihong Hu, Yubang He, Shu Shen, Fei Deng

Viol Sin. 2024 Aug.; 39(4): 537-545.

<https://doi.org/10.1016/j.virs.2024.04.006>

Continued evolution of H10N3 influenza virus with adaptive mutations poses an increased threat to mammals

Shiping Ding, Jiangtao Zhou, Junlong Xiong, Xiaowen Du, Wenzhuo Yang, Jinyu Huang, Yi Liu, Lihong Huang, Ming Liao, Jiahao Zhang, Wenbao Qi

Virol Sin. 2024 Aug.; 39(4): 546-555.

<https://doi.org/10.1016/j.virs.2024.06.005>

Diverse genotypes of norovirus genogroup I and II contamination in environmental water in Thailand during the COVID-19 outbreak from 2020 to 2022

Kattareeya Kumthip, Pattara Khamrin, Aksara Thongprachum, Rungrana Malasao, Arpaporn Yodmeeklin, Hiroshi Ushijima, Niwat Maneekarn

Virol Sin. 2024 Aug.; 39(4): 556-564.

<https://doi.org/10.1016/j.virs.2024.05.010>

Individual virome analysis reveals the general co-infection of mammal-associated viruses with SARS-related coronaviruses in bats

Hao-Rui Si, Ke Wu, Jia Su, Tian-Yi Dong, Yan Zhu, Bei Li, Ying Chen, Yang Li, Zheng-Li Shi, Peng Zhou

Virol Sin. 2024 Aug.; 39(4): 565-573.

<https://doi.org/10.1016/j.virs.2024.06.008>

NSUN2 mediates distinct pathways to regulate enterovirus 71 replication

Lishi Liu, Zhen Chen, Kui Zhang, Haojie Hao, Li Ma, Haizhou Liu, Baocheng Yu, Shuang Ding, Xueyan Zhang, Miao Zhu, Xiang Guo, Yi Liu, Haibin Liu, Fang Huang, Ke Peng, Wuxiang Guan

Virol Sin. 2024 Aug.; 39(4): 574-586.

<https://doi.org/10.1016/j.virs.2024.05.002>

Pseudorabies virus VHS protein abrogates interferon responses by blocking NF- κ B and IRF3 nuclear translocation

Zhenfang Yan, Jiayu Yue, Yaxin Zhang, Zhengyang Hou, Dianyu Li, Yanmei Yang, Xiangrong Li, Adi Idris, Huixia Li, Shasha Li, Jingying Xie, Ruofei Feng

Virol Sin. 2024 Aug.; 39(4): 587-599.

<https://doi.org/10.1016/j.virs.2024.05.009>

Identification of residues in Lassa virus glycoprotein 1 involved in receptor switch

Jiao Guo, Yi Wan, Yang Liu, Xiaoying Jia, Siqi Dong, Gengfu Xiao, Wei Wang

Virol Sin. 2024 Aug.; 39(4): 600-608.

<https://doi.org/10.1016/j.virs.2024.06.001>

The binding and structural basis of fox ACE2 to RBDs from different sarbecoviruses

Junsen Chen, Junqing Sun, Zepeng Xu, Linjie Li, Xinrui Kang, Chunliang Luo, Qi Wang, Xueyang Guo, Yan Li, Kefang Liu, Ying Wu

Virol Sin. 2024 Aug.; 39(4): 609-618.

<https://doi.org/10.1016/j.virs.2024.06.004>

Structural and functional insights into the 2'-O-methyltransferase of SARS-CoV-2

Jikai Deng, Feiyu Gong, Yingjian Li, Xue Tan, Xuemei Liu, Shimin Yang, Xianying Chen, Hongyun Wang, Qianyun Liu, Chao Shen, Li Zhou, Yu Chen

Virol Sin. 2024 Aug.; 39(4): 619-631.

<https://doi.org/10.1016/j.virs.2024.07.001>

AIMP2 restricts EV71 replication by recruiting SMURF2 to promote the degradation of 3D polymerase

Junrui Ren, Lei Yu, Qiuhan Zhang, Pengyu Ren, Yumeng Cai, Xueyun Wang, Ke Lan, Shuwen Wu

Virol Sin. 2024 Aug.; 39(4): 632-644.

<https://doi.org/10.1016/j.virs.2024.06.009>

Design of antiviral AGO2-dependent short hairpin RNAs

Yuanyuan Bie, Jieling Zhang, Jiyao Chen, Yumin Zhang, Muhan Huang, Leike Zhang, Xi Zhou, Yang Qiu

Virol Sin. 2024 Aug.; 39(4): 645-654.

<https://doi.org/10.1016/j.virs.2024.05.001>

Detection of HBV DNA integration in plasma cell-free DNA of different HBV diseases utilizing DNA capture strategy

Zerui Yang, Jingyan Zeng, Yueyue Chen, Mengchun Wang, Hongchun Luo, Ai-Long Huang, Haijun Deng, Yuan Hu

Virol Sin. 2024 Aug.; 39(4): 655-666.

<https://doi.org/10.1016/j.virs.2024.06.003>

Measures of insulin resistance and beta cell function before and after treatment of HCV infection

Jizheng Chen, Pan Qiu, Tingfeng Zhao, Haowei Jiang, Kebinur Tursun, Sulaiman Ksimu, Xinwen Chen, Qian Wang

Virol Sin. 2024 Aug.; 39(4): 667-674.

<https://doi.org/10.1016/j.virs.2024.06.007>

A quadrivalent norovirus vaccine based on a chimpanzee adenovirus vector induces potent immunity in mice

Yihua Jiang, Lingjin Sun, Nan Qiao, Xiang Wang, Caihong Zhu, Man Xing, Hui Liu, Ping Zhou, Dongming Zhou

Virol Sin. 2024 Aug.; 39(4): 675-684.

<https://doi.org/10.1016/j.virs.2024.07.002>

Baicalein suppresses Coxsackievirus B3 replication by inhibiting caspase-1 and viral protease 2A

Yanyan Dong, Enze Shao, Siwei Li, Ruiqi Wang, Dan Wang, Lixin Wang, Hong Yang, Yingxia He, Tian Luan, Yang Chen, Yao Wang, Lexun Lin, Yan Wang, Zhaohua Zhong, Wenran Zhao

Virol Sin. 2024 Aug.; 39(4): 685-693.

<https://doi.org/10.1016/j.virs.2024.07.003>

Letters

Seroprevalence of neutralizing antibodies against HFMD associated enteroviruses among healthy individuals in Shanghai, China, 2022

Jiayu Wang, Wencheng Wu, Wei Wang, Jingyi Zhang, Jianwei Xiao, Mingyi Cai, Jiaying Guo, Run Li, Shuangli Zhu, Wanju Zhang, Min Chen, Zheng Teng

Virol Sin. 2024 Aug.; 39(4): 694-698.

<https://doi.org/10.1016/j.virs.2024.05.008>

Correlation between circulating T follicular helper cell levels after infection and a decreased risk of COVID-19 re-infection

Jinzhu Feng, Zeyu Pu, Rong Li, Yuzhuang Li, Xuwen Qin, Hui Zhang, Yiwen Zhang

Virol Sin. 2024 Aug.; 39(4): 699-701.

<https://doi.org/10.1016/j.virs.2024.06.002>

First complete genomic sequence analysis of canine distemper virus in wild boar

Tong Wang, Haiying Du, Na Feng, Yuhang Liu, Yu Xu, Heting Sun, Peng Peng, Siyuan Qin, Xiaotian Zhang, Yan Liu, Mingyuan Yu, Hongrui Liang, Biao He, Guoqiang Zhu, Changchun Tu, Zhongzhong Tu

Virol Sin. 2024 Aug.; 39(4): 702-704.

<https://doi.org/10.1016/j.virs.2024.05.004>

Coexistence of adeno-associated virus 2 with adenovirus 18 or herpesvirus may be associated with severe lingual papillomatosis in an immunocompromised individual

Jie-Mei Yu, Ze-Yin Liang, Yuan-Hui Fu, Xiang-Lei Peng, Yan-Peng Zheng, Yu-Jun Dong, Jin-Sheng He

Virol Sin. 2024 Aug.; 39(4): 705-707.

<https://doi.org/10.1016/j.virs.2024.06.006>

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Dear Dr. Gralinski,

We are delighted to share with you the [latest issue of *Virologica Sinica*](#). Kindly find the articles listed below. Your comments and suggestions are appreciated.

Severe fever with thrombocytopenia syndrome virus (SFTSV) is an emerging tick-borne virus responsible for the severe fever thrombocytopenia syndrome. Currently, no specific antiviral drugs have been approved for this disease. In this issue, Luo et al. investigated the inhibitory effects of vitamin D derivatives against SFTSV in cell lines and mouse models. The study further revealed synergistic effects of vitamin D derivatives combined with favipiravir (T-705) against SFTSV, as well as inhibitory effects on other viruses, including Dengue virus (DENV) and Ross River virus (RRV), thereby expanding the potential applications of vitamin D derivatives. The cover image illustrates that vitamin D derivatives (represented as the golden cudgel) can independently combat SFTSV and other viruses; however, in combination with T-705 (represented as Guanyin's vase), viruses can be eradicated more rapidly and thoroughly (Kindly provided by Prof. Jingjing Yang, Prof. Ruiyuan Cao, and Prof. Wu Zhong). See page 802–811 for details.

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Review

The unique immune evasion mechanisms of the mpox virus and their implication for developing new vaccines and immunotherapies

Dong Fang, Yan Liu, Dou Dou, Bin Su

Virol Sin. 2024 Oct.; 39(5): 709-718.

<https://doi.org/10.1016/j.virs.2024.08.008>

Research Articles

Circulation patterns and molecular characteristics of respiratory syncytial virus among hospitalized children in Tianjin, China, before and during the COVID-19 pandemic (2017–2022)

Mengzhu Hou, Guangping Liu, Chao Meng, Lili Dong, Yulian Fang, Lu Wang, Ning Wang, Chunquan Cai, Hanjie Wang

Virol Sin. 2024 Oct.; 39(5): 719-726.

<https://doi.org/10.1016/j.virs.2024.07.004>

A multi-center study on genetic variations in the fusion protein of respiratory syncytial virus from children with Acute Lower Respiratory Tract Infections in China during 2017–2021

Yiliang Fu, Fei Li, Yun Zhu, Luci Huang, Qiuping Li, Hanwen Zhang, Lili Zhong, Hailin Zhang, Zheng-Xiu Luo, Gen Lu, Jikui Deng, Lingfeng Cao, Ying Wu, Rong Jin, Lei Li, Lili Xu, Xiangpeng Chen, Zhengde Xie

Virol Sin. 2024 Oct.; 39(5): 727-736.

<https://doi.org/10.1016/j.virs.2024.09.002>

The spatiotemporal analysis of SARS-CoV-2 transmission in China since the termination of the dynamic zero-COVID policy

Jiaying Li, Jingqi Yang, Xiao Ding, Hangyu Zhou, Na Han, Aiping Wu

Virol Sin. 2024 Oct.; 39(5): 737-746.

<https://doi.org/10.1016/j.virs.2024.09.003>

Phylogenetic analyses and antigenic characterization of foot-and-mouth disease virus PanAsia lineage circulating in China between 1999 and 2023

Xiangle Zhang, Weimin Ma, Baohong Liu, Chaochao Shen, Fan Yang, Yamin Yang, Lv Lv, Jinyan Wu, Yongjie Liu, Youjun Shang, Jianhong Guo, Zixiang Zhu, Xiangtao Liu, Haixue Zheng, Jijun He

Virol Sin. 2024 Oct.; 39(5): 747-754.

<https://doi.org/10.1016/j.virs.2024.09.006>

Identification of a novel caspase cleavage motif AEAD

Yujie Fang, Zhou Gong, Miaomiao You, Ke Peng

Virol Sin. 2024 Oct.; 39(5): 755-766.

<https://doi.org/10.1016/j.virs.2024.08.001>

Antibacterial activity evaluation of a novel K3-specific phage against *Acinetobacter baumannii* and evidence for receptor-binding domain transfer across morphologies

Xiangkuan Zheng, Meihan Liu, Pei Li, Sixiang Xu, Long Chen, Guoxin Xu, Xiaoxiao Pang, Hong Du, Yishan Zheng, Xiang Huo, Zhongming Tan, Juan Li, Zhirong Li, Wei Zhang

Virol Sin. 2024 Oct.; 39(5): 767-781.

<https://doi.org/10.1016/j.virs.2024.08.002>

Single-cell RNA-sequencing reveals a profound immune cell response in human cytomegalovirus-infected humanized mice

An Wang, Xiao-Xu Zhu, Yuanyuan Bie, Bowen Zhang, Wenting Ji, Jing Lou, Muhan Huang, Xi Zhou, Yujie Ren

Virol Sin. 2024 Oct.; 39(5): 782-792.

<https://doi.org/10.1016/j.virs.2024.08.006>

Virome-wide analysis of histone modification mimicry motifs carried by viral proteins

Yang Xiao, Shuofeng Yuan, Ye Qiu, Xing-Yi Ge

Virol Sin. 2024 Oct.; 39(5): 793-801.

<https://doi.org/10.1016/j.virs.2024.09.004>

Antiviral activity of vitamin D derivatives against severe fever with thrombocytopenia syndrome virus *in vitro* and *in vivo*

Chongda Luo, Xintong Yan, Shaokang Yang, Sichen Ren, Yan Luo, Jiazheng Li, Ping Wang, Yunfeng Shao, Wei Li, Song Li, Jingjing Yang, Ruiyuan Cao, Wu Zhong

Virol Sin. 2024 Oct.; 39(5): 802-811.

<https://doi.org/10.1016/j.virs.2024.08.007>

Rational design of a DNA-launched live attenuated vaccine against human enterovirus 71

Rong-Rong Zhang, Meng-Jiao He, Chao Zhou, Yan-Peng Xu, Wei Tang, Tian-Shu Cao, Zheng-Jian Wang, Mei Wu, Tao Ming, Yi-Jiao Huang, Meng-Xu Sun, Hui Zhao, Yong-Qiang Deng, Xiao-Feng Li, Bin Wang, Qing Ye, Cheng-Feng Qin

Virol Sin. 2024 Oct.; 39(5): 812-820.

<https://doi.org/10.1016/j.virs.2024.09.008>

A novel vesicular stomatitis virus armed with IL-2 mimic for oncolytic therapy

Manman Wu, Yiwei Wang, Chuanjian Wu, Huang Huang, Xinyuan Zhou, Jun Wang, Sidong Xiong, Chunsheng Dong

Virol Sin. 2024 Oct.; 39(5): 821-832.

<https://doi.org/10.1016/j.virs.2024.09.007>

Letters

A bivalent Delta/BA.5 mRNA vaccine elicits broad immune responses against various lineages of SARS-CoV-2 including JN.1

Kangyin Li, Qi Liu, Yan Wu, Bihao Wu, Shaohong Chen, Xinghai Zhang, Xiaoying Jia, Rui Gong, Yucai Peng, Huajun Zhang, Sandra Chiu

Virol Sin. 2024 Oct.; 39(5): 833-835.

<https://doi.org/10.1016/j.virs.2024.08.003>

Trivalent SARS-CoV-2 virus-like particle vaccines exhibit broad-spectrum neutralization and protection against XBB.1 and BA.2.86 variants

Lu Zhang, Siyu Tian, Jun Dai, Yuanyuan Li, Yu Zhou, Yan Li, Jiao Xu, Shuyun Liu, Zhiwei Lin, Zhaoyong Zhang, Jiantao Chen, Peilan Wei, Jingxian Zhao, Jing Jin, Yanqun Wang, Jincun Zhao

Virol Sin. 2024 Oct.; 39(5): 836-839.

<https://doi.org/10.1016/j.virs.2024.08.005>

Rapid diagnosis of a fox's death case using nanopore sequencing reveals the infection with an Artic-like rabies virus

Yuhang Liu, Zhiqiang Liu, Jian Li, Xiaomin Yan, Weidi Xu, Le Yi, Changchun Tu, Biao He

Viol Sin. 2024 Oct.; 39(5): 840-842.

<https://doi.org/10.1016/j.virs.2024.08.010>

Meeting Report

The 2024 National Symposium on Insect Virology held in Qingdao

Jiali Si, Xi Wang, Manli Wang, Zhihong Hu

Viol Sin. 2024 Oct.; 39(5): 843-844.

<https://doi.org/10.1016/j.virs.2024.08.011>

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The live attenuated hepatitis A virus (HAV) vaccine H2 strain was developed through the passaging of a wild-type H2w isolate in cell cultures. Currently, the mechanism underlying its attenuation phenotype remain largely unknown. In this issue, Yan et al. reported the first full-length infectious cDNA clone of the H2 strain. The recovered H2ic virus closely resembles the original H2 strain both *in vitro* and *in vivo*. Furthermore, by utilizing a chimeric approach based on this reverse genetic system, the authors identified that mutations in the 2B, 2C, and 3A genes are primarily responsible for significantly enhancing virus growth in cultured cells, while mutations in the 3C and 3D genes have a lesser impact. The cover image highlights that the reverse genetic system of the H2 strain serves as a vital platform for advancing the genetic and functional analysis of the HAV life cycle and for facilitating vaccine development (Kindly designed and provided by Prof. Xiao-Feng Li and Cheng-Feng Qin). See page 812–891 for details.

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Mini Review

Ten computational challenges in human virome studies

Yifan Wu, Yongsong Peng

Virol Sin. 2024 Dec.; 39(6): 845-850.

<https://doi.org/10.1016/j.virs.2024.04.008>

Research Articles

Viral load dynamics in asymptomatic and symptomatic patients during Omicron BA.2 outbreak in Shanghai, China, 2022: A longitudinal cohort study

Jingwen Ai, Jiaxin Zhou, Yang Li, Feng Sun, Shijia Ge, Haocheng Zhang, Yanpeng Wu, Yan Wang, Yilin Zhang, Hongyu Wang, Jianpeng Cai, Xian Zhou, Sen Wang, Rong Li, Zhen Feng, Xiangyanyu Xu, Xuemei Yan, Yuchen Zhao, Juanjuan Zhang, Hongjie Yu, Wenhong Zhang

Virol Sin. 2024 Dec.; 39(6): 851-859.

<https://doi.org/10.1016/j.virs.2024.10.001>

Single-cell RNA sequencing reveals the diversity of the immunological landscape response to genital herpes

Siji Chen, Jiang Zhu, Chunting Hua, Chenxi Feng, Xia Wu, Can Zhou, Xianzhen Chen, Boya Zhang, Yaohan Xu, Zeyu Ma, Jianping He, Na Jin, Yinjing Song, Stijn van der Veen, Hao Cheng

Virol Sin. 2024 Dec.; 39(6): 860-874.

<https://doi.org/10.1016/j.virs.2024.10.003>

The first discovery of severe fever with thrombocytopenia virus in the center of metropolitan Beijing, China

Fei Yuan, Lianglong Zhu, Di Tian, Mengyu Xia, Ming-hao Zheng, Qing Zhang, Tingyu Zhang, Xing Zhang, Aihua Zheng

Virol Sin. 2024 Dec.; 39(6): 875-881.

<https://doi.org/10.1016/j.virs.2024.11.002>

Identification of mutations in viral proteins involved in cell adaptation using a reverse genetic system of the live attenuated hepatitis A virus vaccine H2 strain

Xiu-Li Yan, Jian Li, Qing-Qing Ma, Hong-Jiang Wang, Lin Li, Hui Zhao, Cheng-Feng Qin, Xiao-Feng Li

Virol Sin. 2024 Dec.; 39(6): 881-891.

<https://doi.org/10.1016/j.virs.2024.08.004>

Bis-benzylisoquinoline alkaloids inhibit flavivirus entry and replication by compromising endolysosomal trafficking and autophagy

Lihong Huang, Lele Liu, Junhai Zhu, Nanjun Chen, Jie Chen, Chuen-Fuk Chan, Fei Gao, Youqin Yin, Jiufeng Sun, Rongxin Zhang, Kehui Zhang, Wenbao Qi, Jianbo Yue

Virol Sin. 2024 Dec.; 39(6): 892-908.

<https://doi.org/10.1016/j.virs.2024.09.001>

Ferritin nanoparticle-based Nipah virus glycoprotein vaccines elicit potent protective immune responses in mice and hamsters

Shaohong Chen, Xinghai Zhang, Yanfeng Yao, Shengdong Wang, Kangyin Li, Baoyue Zhang, Tianxi Ye, Li Chen, Yan Wu, Entao Li, Bichao Xu, Pei Zhang, Xia Chuai, Yong Ran, Rui Gong, Huajun Zhang, Sandra Chiu

Virol Sin. 2024 Dec.; 39(6): 909-916.

<https://doi.org/10.1016/j.virs.2024.09.005>

Efficient and robust reverse genetics system for bovine rotavirus generation and its application for antiviral screening

Song-Kang Qin, Kuan-Hao Li, Ben-Jin Liu, Cun Cao, De-Bin Yu, Zhi-Gang Jiang, Jun Wang, Yu-Xin Han, Fang Wang, Ying-Lin Qi, Chao Sun, Li Yu, Ji-Tao Chang, Xin Yin

Virol Sin. 2024 Dec.; 39(6): 917-928.

Generation and characterization of a novel ovariole cell line derived from *Spodoptera frugiperda* in China with sensitivity to both SfMNPV and AcMNPV

Yan Tong, Wenyi Jin, Xuan Li, Lin Guo, Gang Luo, Qian Meng, Jihong Zhang, Qilian Qin, Huan Zhang

Viol Sin. 2024 Dec.; 39(6): 929-937.

<https://doi.org/10.1016/j.virs.2024.10.002>

Modulation of the unfolded protein response by white spot syndrome virus via wsv406 targeting BiP to facilitate viral replication

Shihan Chen, Qiqi Zhong, Xuzheng Liao, Haiyang Wang, Bang Xiao, Jianguo He, Chaozheng Li

Viol Sin. 2024 Dec.; 39(6): 938-950.

<https://doi.org/10.1016/j.virs.2024.10.005>

Case study: May human norovirus infection be associated with premature delivery?

Jiaying Cao, Yuetong Li, Feiyang Xue, Ziyang Sheng, Libo Liu, Yingying Zhang, Lele Wang, Liang Zeng, Yanmin Jiang, Dongying Fan, Fang Li, Jing An

Viol Sin. 2024 Dec.; 39(6): 951-962.

<https://doi.org/10.1016/j.virs.2024.10.004>

Construction and validation of a mouse model for studying severe human adenovirus infections

Dingbin Chen, Yuqian Yan, Ting Mei, Peipei Yang, Siqi Deng, Yiqiang Li, Tie Zhao, Ning Xin, Biyan Duan, Weifeng Liang, Yuemei Yang, Wei Zhao, Donald Seto, Junxian Ou, Qiwei Zhang

Viol Sin. 2024 Dec.; 39(6): 963-973.

<https://doi.org/10.1016/j.virs.2024.11.001>

Letters

A G3P[3] bat rotavirus can infect cultured human cholangiocytes and cause biliary atresia symptom in suckling mice

Pengfei Hao, Zhaoxia Pang, Qiaoqiao Qu, Chunmei Cui, Yuhang Jiang, Jing Chen, Zihan Gao, Zhiqiang Xu, Letian Li, Ningyi Jin, Chang Li

Viol Sin. 2024 Dec.; 39(6): 974-976.

<https://doi.org/10.1016/j.virs.2024.09.009>

News and Views

Bibliometric analysis of virology advancements in the 21st century

Lili Ma, Wei Pan, Jiali Si

Virol Sin. 2024 Dec.; 39(6): 977-980.
<https://doi.org/10.1016/j.virs.2024.08.009>

Pandemic preparedness of effective vaccines for the outbreak of newly H5N1 highly pathogenic avian influenza virus

Feixia Gao, Qi Wang, Chenchen Qiu, Jian Luo, Xiuling Li

Virol Sin. 2024 Dec.; 39(6): 981-985.
<https://doi.org/10.1016/j.virs.2024.11.005>

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2024 Reviewer Acknowledgment

[https://doi.org/10.1016/S1995-820X\(24\)00202-5](https://doi.org/10.1016/S1995-820X(24)00202-5)

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Seasonal influenza A viruses (IAVs) and influenza B viruses (IBVs) are common causes of human respiratory diseases. Vaccines are the most effective means of preventing influenza infections. However, the protective effects of existing IBV vaccines against mutated strains have not been comprehensively evaluated. In this issue, Zhang et al. systematically analyzed the antigenicity of hemagglutinin protein from circulating B/Victoria and B/Yamagata IBV strains. They found that the recommended IBV vaccine strains showed strong neutralization activity against the epidemic virus strains within the same year. Analyses on mutation sites indicated that key amino acid substitutions, such as R141G, D197N, and R203K, could significantly affect the antigenicity of B/Victoria vaccine strains, highlighting the need for vigilant monitoring. The cover image shows the game between the evolution of influenza virus and the human immune system (Kindly designed and provided by Prof. Weijin Huang). See page 80–91 for details.

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Review

Insights into recent advancements in human and animal rotavirus vaccines: Exploring new frontiers

Ahmed H. Ghonaim, Sherin R. Rouby, Wedad M. Nageeb, Ashraf Ahmed Elgendy, Rong Xu, Changsheng Jiang, Noha H.

Ghonaim, Qigai He, Wentao Li

Virol. Sin. 2025 Feb.; 40(1):1-14.

<https://doi.org/10.1016/j.virs.2024.12.001>

Research Articles

Gene flow and its sporadic spillover: H10 and N5 avian influenza viruses from wild birds and the H10N5 human cases in China

Weijie Chen, Shuiping Lu, Haiyan Xiong, Zhiyu Xiang, Yuxi Wang, Jingjing Hu, Yue Pan, Yanjiao Li, Qile Gao, Qi Chen, Siru Hu, Weibing Wang, Chenglong Xiong

Virol. Sin. 2025 Feb.; 40(1):15-23.

<https://doi.org/10.1016/j.virs.2024.12.002>

A low pathogenic avian influenza A/Mallard/South Korea/KNU2019-34/2019 (H1N1) virus has the potential to increase the mammalian pathogenicity

Jaemoo Kim, Jungho Kim, Suhyeon Heo, Chang-Hun Yeom, Bao Tuan Duong, Haan Woo Sung, Seon-Ju Yeo, Hyun Park, Haryoung Poo, Jihyun Yang

Viol. Sin. 2025 Feb.; 40(1):24-34.

<https://doi.org/10.1016/j.virs.2024.12.005>

PB2 627V and HA 217 sites synergistically affect the lethality of H9N2 in mice

Lingcai Zhao, Miao Tian, Xifeng Hu, Menglu Fan, Chenglin Hou, Jihui Ping

Viol. Sin. 2025 Feb.; 40(1):35-49.

<https://doi.org/10.1016/j.virs.2024.12.003>

Comparative analysis between genotypes of adenovirus isolates from hospitalized children with acute respiratory tract infections and clinical manifestations in Wuhan, China, from June 2022 to September 2023

Chunchen Wu, Yanfang Zhang, Ao Liang, Xiaoxue Wu, Yaqi Zhu, Zhaoxuan Huang, Jun Wang, Yali Deng, Lixian Pan, Anbang Wang, Fei Deng, Jianbo Xia

Viol. Sin. 2025 Feb.; 40(1):50-60.

<https://doi.org/10.1016/j.virs.2024.12.004>

Zika virus infections and associated risk factors among pregnant women in Gombe, Nigeria

Oderinde Soji Bamidele, Abdulbasi Bakoji, Samaila Jackson Yaga, Kunle Ijaya, Bukar Mohammed, Ismaila Yunusa Yuguda, Marycelin M. Baba

Viol. Sin. 2025 Feb.; 40(1):61-70.

<https://doi.org/10.1016/j.virs.2024.12.008>

Discovery and characterization of a novel carlavirus in *Ligularia jaluensis* plants

Shifang Fei, Jiaping Yu, Yali Zhou, Yi Xie, Li Xie, Shuai Fu, Jianxiang Wu

Viol. Sin. 2025 Feb.; 40(1):71-79.

<https://doi.org/10.1016/j.virs.2024.11.003>

Antigenic analysis of the influenza B virus hemagglutinin protein

Mengyi Zhang, Chaoying Yang, Xi Wu, Yifei Wang, Lijie Wang, Qianqian Cui, Jincheng Tong, Yimeng An, Meina Cai, Shishi Cheng, Qi Jiang, Yulin Wang, Chenyan Zhao, Youchun Wang, Weijin Huang

Viol. Sin. 2025 Feb.; 40(1):80-91.

<https://doi.org/10.1016/j.virs.2024.08.012>

CRTC3 restricts SARS-CoV-2 replication and is antagonized by CREB

Li Yang, Xiao-Tao Zeng, Rong-Hua Luo, Ying Tang, Si-Xue Ren, Xin-Yan Long, Xiang-Hui Fu, Wan-Jiang Zhang, Hai-Yan Ren, Yong-Tang Zheng, Wei Cheng

Virol. Sin. 2025 Feb.; 40(1):92-108.

<https://doi.org/10.1016/j.virs.2024.12.006>

Random forest algorithm reveals novel sites in HA protein that shift receptor binding preference of the H9N2 avian influenza virus

Yuncong Yin, Wen Li, Rujian Chen, Xiao Wang, Yiting Chen, Xinyuan Cui, Xingbang Lu, David M. Irwin, Xuejuan Shen, Yongyi Shen

Virol. Sin. 2025 Feb.; 40(1):109-117.

<https://doi.org/10.1016/j.virs.2024.12.010>

Patterns of liver fibrosis evolution in Chinese HIV/HBV co-infected adults following 5-year antiretroviral treatment: A longitudinal study using non-invasive APRI and Fib-4 scores

Qingrong Zhang, Lijun Sun, Yuxuan Liang, Wenlu Zou, Jingtao Huang, Yuan Zhang, Yi Jin, Na Zhou, Jiangzhu Ye, Huachun Zou, Hao Wu, Tong Zhang, Bin Su, Taiyi Jiang, Haitao Chen

Virol. Sin. 2025 Feb.; 40(1):118-124.

<https://doi.org/10.1016/j.virs.2024.12.009>

The potential mechanisms and material basis of Fuzheng Jiedu decoction broad-spectrum inhibiting coronaviruses

Ke Liu, Bixia Hong, Shi-Ting He, Siying Du, Jiayi Ke, Lili Tian, Tao Tao, Yihan Zhang, Kelin Li, Han Chang, Mengzhe Li, Xiaoping An, Lihua Song, Zhongde Zhang, Liang Liu, Hudan Pan, Huahao Fan, Yigang Tong

Virol. Sin. 2025 Feb.; 40(1):125-136.

<https://doi.org/10.1016/j.virs.2024.12.007>

Letters

Geographical distribution and characterization of Jingmen tick virus in wild boars in China

Tong Wang, Yu Guo, Yu Xu, Heting Sun, Peng Peng, Siyuan Qin, Guoqiang Zhu, Changchun Tu, Zhongzhong Tu

Virol. Sin. 2025 Feb.; 40(1):137-140.

<https://doi.org/10.1016/j.virs.2024.12.011>

Distinct tropisms of HCMV and SARS-CoV-2 in lung tissue of a patient with advanced HIV disease

Jingjing Xu, Bo Yang, Ye Zheng, Yuexiang Yang, Min-Hua Luo, Yun Ling, Xiaohong Fan, Han Cheng

Virol. Sin. 2025 Feb.; 40(1):141-143.

<https://doi.org/10.1016/j.virs.2025.01.001>

Rapid preparation and characterization of pansarbecovirus mRNA vaccine candidates based on the receptor binding domain

Mei Wu, Tian-Shu Cao, Xiao-Chuan Xiong, Tao Ming, Pan-Deng Shi, Rong-Rong Zhang, Qing Ye, Cheng-Feng Qin

Virol. Sin. 2025 Feb.; 40(1):144-146.

<https://doi.org/10.1016/j.virs.2024.11.004>

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Zika virus (ZIKV), a significant mosquito-borne orthoflavivirus, has emerged as a major global health concern. However, comprehensive research on mosquito-to-mosquito transmission patterns of ZIKV remains limited. To explore how ZIKV transmits within mosquitoes, Wang et al. conducted a systematic laboratory investigation to assess the ability of ZIKV spread among mosquitoes and its impact on mosquito development. The study revealed that ZIKV can be transmitted both vertically and horizontally among *Aedes aegypti* mosquitoes, through oviposition and contact between mosquitoes of the same or opposite sex. Additionally, ZIKV infection resulted in a reduction in the number of mosquito eggs but an increase in the size of mosquito eggs, while altered levels of hormone related genes were also observed. The cover image illustrates ZIKV transmissions among mosquitoes, highlighting the significant threat it poses to humans. See page 192–205 for details.

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Review

Current antiviral therapies and promising drug candidates against respiratory syncytial virus infection

Ziheng Feng, Zhengde Xie, Lili Xu

Viol. Sin. 2025 Apr.; 40(2):147-156.

<https://doi.org/10.1016/j.virs.2025.01.003>

Research Articles

Epidemiological and molecular characteristics of human parainfluenza virus in southern China during 2016-2020

Yizhe Li, Minjie Liu, Jingyao Liang, Hengming Ye, Mingcui Lyu, Delin Chen, Linyue Liang, Shuqing Zhang, Kexin Zhang, Shu An, Wenle Zhou, Jueheng Wu, Xun Zhu, Zhenjian He

Viol. Sin. 2025 Apr.; 40(2):157-165.

<https://doi.org/10.1016/j.virs.2025.03.004>

Virus profiling of bronchoalveolar lavage fluid in hospitalized non-COVID-19 adult patients with pulmonary infection from

November 2020 to November 2021

Virus profiling of bronchoalveolar lavage fluid in hospitalized non-COVID-19 adult patients with pulmonary infection from November 2020 to November 2021

Viol. Sin. 2025 Apr.; 40(2):166-175.

<https://doi.org/10.1016/j.virs.2025.03.005>

Phylogenitc analysis and immunogenicity comparison of porcine genotype G9 rotavirus in China from 2020-2023

Yudi Pan, Zixin Li, Qian Miao, Hongyan Shi, Longjun Guo, Li Feng, Jin Tian

Viol. Sin. 2025 Apr.; 40(2):176-185.

<https://doi.org/10.1016/j.virs.2025.02.003>

Identification and genetic analysis of new ephemeroviruses in wild boars in China

Zhongzhong Tu, Tong Wang, Yu Xu, Heting Sun, Peng Peng, Siyuan Qin, Changchun Tu

Viol. Sin. 2025 Apr.; 40(2):186-191.

<https://doi.org/10.1016/j.virs.2025.02.002>

Zika virus transmission in *Aedes aegypti*: A systematic study on the ability of mosquitoes to transmit the virus horizontally and vertically

Xugang Wang, Chaonan Qian, Chenxi Zhang, Siyun Hu, Muhammad Asad, Chengjie Yang, Bingrui Liao, Xiaotong Guo, Chen Zhang, Quanzhi Li, Xinyao Li, Qiuying Huang, Youhui Si, Bibo Zhu, Shengbo Cao, Jing Ye

Viol. Sin. 2025 Apr.; 40(2):192-205.

<https://doi.org/10.1016/j.virs.2025.02.001>

***In vivo* quantitative proteomic analysis of porcine alveolar macrophages in PRRSV-infected pigs**

Ying Wei, Chuangchao Zou, Siying Zeng, Ouyang Peng, Guangli Hu, Yihui Huang, Qiuping Xu, Fangyu Hu, Yongchang Cao, Hao Zhang

Viol. Sin. 2025 Apr.; 40(2):206-216.

<https://doi.org/10.1016/j.virs.2025.03.002>

Host factor Naf1 restricts HIV-1 infection of myeloid cells and compromises the capacity of dendritic cell to prime CD4⁺ T cell

Chengzuo Xie, Xia Jin, Wan-Wei Li, Jian-Hua Wang

Viol. Sin. 2025 Apr.; 40(2):217-224.

<https://doi.org/10.1016/j.virs.2025.03.007>

The SARS-CoV-2 NSP4 T492I mutation promotes double-membrane vesicle formation to facilitate transmission

Pei Wang, Buyun Tian, Ke Xiao, Wei Ji, Zonghong Li

Virol. Sin. 2025 Apr.; 40(2):225-235.

<https://doi.org/10.1016/j.virs.2025.03.010>

Structure-function insights into the dual role of African swine fever virus pB318L: A typical geranylgeranyl-diphosphate synthase and a nuclear import protein

Hai-Fan Zhao, Ying Wang, Xiao-Hong Liu, Xian-Hui Liu, Zhi Geng, Zeng-Qiang Gao, Li Huang, Chang-Jiang Weng, Yu-Hui Dong, Heng Zhang

Virol. Sin. 2025 Apr.; 40(2):236-246.

<https://doi.org/10.1016/j.virs.2025.03.013>

***Artemisia annua* L. leaf extracts suppress influenza virus infection by targeting the viral nucleoprotein and blocking mitochondria-mediated apoptosis**

Xiwen Zhao, Xuan Dai, Fuyi Wang, Chenyang Li, Xun Song, Yingying Han, Chaowei Zhang, Lu Wang, Zhendan He, Rongping Zhang, Liang Ye

Virol. Sin. 2025 Apr.; 40(2):247-259.

<https://doi.org/10.1016/j.virs.2025.03.001>

Qingqi Guxue Decoction induces S cell cycle arrest to inhibit replication of severe fever with thrombocytopenia syndrome virus

Qingqi Guxue Decoction induces S cell cycle arrest to inhibit replication of severe fever with thrombocytopenia syndrome virus

Virol. Sin. 2025 Apr.; 40(2):260-274.

<https://doi.org/10.1016/j.virs.2025.03.011>

Development of a reporter HBoV1 strain for antiviral drug screening and life cycle studies

Jielin Tang, Sijie Chen, Yi Zhong, Yijun Deng, Dan Huang, Junjun Liu, Yi Zheng, Jiyuan Xu, Bao Xue, Fan Wang, Yuan Zhou, Hanzhong Wang, Qi Yang, Xinwen Chen

Virol. Sin. 2025 Apr.; 40(2):275-283.

<https://doi.org/10.1016/j.virs.2025.03.009>

Letters

Characterization of novel highly pathogenic avian influenza A(H5N6) clade 2.3.4.4b virus in wild birds, East China, 2024

Renjie Sun, Xiaoxiao Feng, Jing Huang, Fangyu Zheng, Ronghui Xie, Chuanliang Zhang, Hongli Zhang, Yin Xue, Aijun Liu, Xiaobing Huang, Lin Yuan, Lingyan Zhao

Virol. Sin. 2025 Apr.; 40(2):284-287.

<https://doi.org/10.1016/j.virs.2025.01.002>

Evaluating the performance of the PREDAC method in flu vaccine recommendations over the past decade (2013-2023)

Yousong Peng, Lei Yang, Weijuan Huang, Mi Liu, Xiao Ding, Xiangjun Du, Yuelong Shu, Taijiao Jiang, Dayan Wang

Viol. Sin. 2025 Apr.; 40(2):288-291.

<https://doi.org/10.1016/j.virs.2025.01.004>

Sphingomyelin phosphodiesterase 3 as a novel host factor inhibiting hepatitis B virus transcription

Chen Li, Meng Zhou, Kaitao Zhao, Wenbo Liu, Chengliang Zhu, Xiaoming Cheng, Yuchen Xia

Viol. Sin. 2025 Apr.; 40(2):292-295.

<https://doi.org/10.1016/j.virs.2025.02.004>

Identification of an immunodominant neutralizing epitope of porcine astrovirus type 5 capsid protein

Yixin Hu, Zehui Li, Chenlin Hao, Hao Lu, Yunfei Xing, Kexin Liu, Xiaohui Jin, Zhanyong Wei

Viol. Sin. 2025 Apr.; 40(2):296-299.

<https://doi.org/10.1016/j.virs.2025.03.003>

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Dear Dr. Gralinski,

We are delighted to share with you the [latest issue of *Virologica Sinica*](#). Kindly find the articles listed below. Your comments and suggestions are appreciated.

Porcine epidemic diarrhea virus (PEDV) is a devastating enteric coronavirus in piglets. This virus can cause up to 100% mortality in piglets within two weeks of age, posing a significant threat to the swine industry. Recent virome analyses have identified several PEDV-like coronaviruses in bats, indicating potential cross-species infectivity. In this issue, Chen et al. detected the nucleic acid of PEDV in pig farm rat fecal samples. Subsequent animal challenge experiments showed that PEDV can cause systemic infections in neonatal mice and rats, with morbidity and mortality highly influenced by inoculation routes and doses. Unlike pigs, where PEDV targets the intestine, the brain and lungs were the primary organs affected in rodents. Moreover, the cerebral tropism of PEDV was first verified in piglets. This study provides robust evidence supporting the potential cross-species infection of PEDV. The cover depicts the possible PEDV transmission chain linked by the coexistence of rats and pigs on farms (Kindly designed and provided by Prof. Guangliang Liu and Dr. Jianing Chen). See page 301–313 for details.

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Research Articles

Insights into cross-species infection: Porcine epidemic diarrhea virus infections in the rodent

Jianing Chen, Zemei Wang, Shengyu Lin, Mengling Gao, Yongheng Shao, Shuxian Li, Qingbo Chen, Yaru Cui, Yonghao Hu, Guangliang Liu

Virol. Sin. 2025 Jun.; 40(3):301-313.

<https://doi.org/10.1016/j.virs.2025.03.012>

Decoding the virome reveals diverse novel viruses in tree shrews (*Tupaia belangeri*) in Yunnan Province

Zhong-Hao Lian, Zhi You, Pei-Yu Han, Ye Qiu, Yun-Zhi Zhang, Xing-Yi Ge

Virol. Sin. 2025 Jun.; 40(3):314-323.

<https://doi.org/10.1016/j.virs.2025.05.011>

The SARS-CoV-2 3CL protease inhibits pyroptosis through the cleavage of gasdermin D

Yecheng Zhang, Xinlei Ji, Dan Huang, Gen Lu, Xinwen Chen

Virol. Sin. 2025 Jun.; 40(3):324-332.

<https://doi.org/10.1016/j.virs.2025.03.006>

Differential susceptibility of immunodeficient mice to MPXV infection and the impact of various inoculation routes

Xiaohan Wang, Shaowen Shi, Xiaoxuan Nie, Yongyang Sun, Jinglei Hu, Manlin He, Wenhao Ren, Yuxing Wang, Zhendong Guo, Gonghe Li, Changbo Ou, Xiao Li, Zongzheng Zhao

Virol. Sin. 2025 Jun.; 40(3):333-339.

<https://doi.org/10.1016/j.virs.2025.04.001>

Viral pseudo-enzyme facilitates KSHV lytic replication via suppressing PFAS-mediated RTA deamidation

Yang Xu, Qiushi Zhang, Guoli Hou, Liang Hu, Tiaoyi Xiao, Xinyu Liang, Deliang Li, Junhua Li

Virol. Sin. 2025 Jun.; 40(3):340-348.

<https://doi.org/10.1016/j.virs.2025.04.005>

Characterization of a SARS-CoV-2 infection model in golden hamsters with diabetes mellitus

Hao-Feng Lin, Ren-Di Jiang, Rui-Xin Qin, Bing Yao, Wen-Tao Zeng, Yun Gao, Ai-Min Shi, Jian-Min Li, Mei-Qin Liu

Virol. Sin. 2025 Jun.; 40(3):349-360.

<https://doi.org/10.1016/j.virs.2025.05.001>

Elevated interferon-induced transmembrane protein 3 in platelets and megakaryocytes suppresses Crimean-Congo hemorrhagic fever viral infection by interacting with glycoprotein Gc

Jingyuan Zhang, Yaohui Fang, Chenhui Lin, Xiaoli Wu, Chaoxiong Yue, Fei Deng, Shu Shen

Virol. Sin. 2025 Jun.; 40(3):361-373.

<https://doi.org/10.1016/j.virs.2025.05.002>

Host factor RBM25 promotes HBV replication through Yin Yang 1-mediated cccDNA transcription

Yukun Li, Tianhao Mao, Liwei Zheng, Zhao Zhou, Qianqian Jiang, Xinyu Du, Ziyuan Ma, Xin Liu, Ting Zhang, Guochao Wei, Lin Wang, Yongzhen Liu, Xiaojing Zhang, Shourong Liu, Xiangmei Chen, Fengmin Lu

Virol. Sin. 2025 Jun.; 40(3):374-387.

<https://doi.org/10.1016/j.virs.2025.05.004>

Nucleophosmin 1 inhibits the replication of influenza A virus by competitively binding viral RNA with viral proteins

Yingying Yu, Qian Wang, Yanli Wei, Junwen Liu, Guangwen Wang, Zhengxiang Wang, Wentao Shen, Lu Han, Chengjun Li, Cao-Qi Lei, Shuai Xu, Qiyun Zhu

Virol. Sin. 2025 Jun.; 40(3):388-400.

<https://doi.org/10.1016/j.virs.2025.04.007>

Human endogenous retrovirus W family envelope protein (ERVWE1) regulates macroautophagy activation and micromitophagy inhibition via NOXA1 in schizophrenia

Jiahang Zhang, Huiling Wang, Xing Xue, Xiulin Wu, Wenshi Li, Zhao Lv, Yaru Su, Mengqi Zhang, Kexin Zhao, Xu Zhang, Chen Jia, Fan Zhu

Virol. Sin. 2025 Jun.; 40(3):401-418.

<https://doi.org/10.1016/j.virs.2025.05.007>

Compromised efferocytosis during aging is related to COVID-19 severity in mice

Xianliang Ke, Xian Lin, Jin Wang, Minqi Chen, Xiaoqin Jian, Chang Ye, Quanjiao Chen

Virol. Sin. 2025 Jun.; 40(3):419-429.

<https://doi.org/10.1016/j.virs.2025.05.008>

***Scutellaria barbata* D. Don extracts alleviate SARS-CoV-2 induced acute lung injury by inhibiting virus replication and bi-directional immune modulation**

Yan Ran, Zinuo Chen, Carolina Q. Sacramento, Lingyuan Fan, Qinghua Cui, Lijun Rong, Ruikun Du

Virol. Sin. 2025 Jun.; 40(3):430-438.

<https://doi.org/10.1016/j.virs.2025.04.004>

Eltrombopag, an FDA-approved drug, inhibits dengue virus type 2 by targeting NS2B-NS3 protease

Xuerui Zhu, Xiao Gao, Yan Wu, Jia Lu, Xinlan Chen, Chenshu Zhao, Haoyu Li, Zhongfa Zhang, Shuwen Liu, Gengfu Xiao, Xiaoyan Pan

Virol. Sin. 2025 Jun.; 40(3):419-429.

<https://doi.org/10.1016/j.virs.2025.05.009>

Severe enterovirus A71 infection is associated with dysfunction of T cell immune response and alleviated by Astragaloside A

Chong Wang, Muhan Huang, Bingyu Guo, Xi Zhou, Zongqiang Cui, Yi Xu, Yujie Ren

Virol. Sin. 2025 Jun.; 40(3):451-461.

<https://doi.org/10.1016/j.virs.2025.05.010>

Development and immunoprotection assessment of novel vaccines for avian infectious bronchitis virus

Benli Huang, Sheng Chen, Zhanxin Wang, Keyu Feng, Yutao Teng, Ruoying Li, Guanming Shao, Jiaqian Rao, Xinheng Zhang, Qingmei Xie

Virol. Sin. 2025 Jun.; 40(3):462-476.

<https://doi.org/10.1016/j.virs.2025.03.008>

Clofazimine targeting the spike protein and RdRp exhibits highly efficient antiviral activity against porcine epidemic diarrhea virus *in vitro*

Shuting Zhou, Junrui Zhu, Houde Zhao, Zixin Huang, Kangqi Zheng, Fan Xia, Yufan Xu, Guocheng Zhao, Jijie Jiang, En Zhang, Haoyang Nian, Li Cui, Tao Sun, Xiangfeng Wang, Yanjun Zhou, Zhibiao Yang, Zhe Wang

Virol. Sin. 2025 Jun.; 40(3):477-490.

<https://doi.org/10.1016/j.virs.2025.05.012>

Letters

Coadministration of ribavirin and arenaviral entry inhibitor LHF-535 enhances antiviral benefit against authentic lassa virus

Cheng Peng, Jialing Hu, Yuan Bai, Wei Wu, Wenting Mao, Yang Liu, Yi Wan, Lei Zhang, Wei Li, Tingting Tian, Tiezhu Liu, Yanhai Wang, Mifang Liang, Jun Han, Zhiming Yuan, Jiandong Li, Chao Shan, Fei Deng, Wei Wang

Virol. Sin. 2025 Jun.; 40(3):491-494.

<https://doi.org/10.1016/j.virs.2025.04.003>

A noninfectious pseudovirus system for an emerging orthoflavivirus

Yanfan Shi, Yu He, Xiaoli Wang, Zhen Wu, Tao Wang, Mingshu Wang, Renyong Jia, Dekang Zhu, Mafeng Liu, Xinxin Zhao, Qiao Yang, Ying Wu, Shaiqiu Zhang, Juan Huang, Xumin Ou, Di Sun, Anchun Cheng, Shun Chen

Virol. Sin. 2025 Jun.; 40(3):495-498.

<https://doi.org/10.1016/j.virs.2025.04.006>

A mouse model of Crimean-Congo hemorrhagic fever virus-induced coagulopathy

Hui Zhang, Ziyang Jiang, Haidang Liao, Jiang Li, Manli Wang, Yiwu Zhou, Zhihong Hu, Jia Liu

Virol. Sin. 2025 Jun.; 40(3):499-502.

<https://doi.org/10.1016/j.virs.2025.04.008>

Mutational landscapes of NITD008-resistant EV71 variants revealed through population sequencing

Fang Yu, Qiu-Yan Zhang, Zhe-Rui Zhang, Cheng-Lin Deng, Bo Zhang

Virol. Sin. 2025 Jun.; 40(3):503-505.

<https://doi.org/10.1016/j.virs.2025.05.003>

Corrigendum

Corrigendum to “Evaluating the performance of the PREDAC method in flu vaccine recommendations over the past decade (2013–2023)” [Virol. Sin. 40 (2025) 288–291]

Yousong Peng, Lei Yang, Weijuan Huang, Mi Liu, Xiao Ding, Xiangjun Du, Yuelong Shu, Taijiao Jiang, Dayan Wang

Virol. Sin. 2025 Jun.; 40(3):506-507.

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<http://link.springer.com/journal/12250>

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Dear Dr. Gralinski,

We are delighted to share with you the [latest issue of *Virologica Sinica*](#). Kindly find the articles listed below. Your comments and suggestions are appreciated.

Mammals serve as vital reservoirs for human infectious diseases, with viral spillover events closely linked to ecological and climatic determinants. To elucidate the diversity and transmission dynamics of mammalian viruses, Shi et al. conducted a comprehensive meta-transcriptomic investigation across multiple small mammals—including bats, rodents, hedgehogs, and shrews—across 20 species in southern China. The study uncovered an extensive diversity of vertebrate-associated viruses, including numerous novel variants, with viral composition demonstrating significant variation across host species and geographical regions. This variation was principally governed by host taxonomic and ecological characteristics. The study identified bats as key hubs in viral transmission networks, with evidence of cross-species virus sharing. The cover image illustrates viral transmission networks among mammals in different ecological environment (Kindly designed and provided by Prof. Guangwen Cao and Dr. Yiwei Shi). See page 520–534 for details.

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Review

The coronavirus 3CL protease: Unveiling its complex host interactions and central role in viral pathogenesis

Yecheng Zhang, Xinlei Ji, Dan Huang, Gen Lu, Xinwen Chen

Viol. Sin. 2025 Aug.; 40(4):509-519.

<https://doi.org/10.1016/j.virs.2025.07.002>

Research Articles

Virome diversity in small mammals from south China: Insights into virus evolution, transmission, and ecology

Yiwei Shi, Letian Fang, Cixiu Li, Peng Li, Jiluo Liu, Yifan Chen, Yue Zhao, Zishuai Li, Shuqi Liu, Yibo Ding, Xinyu Zhou, Dongming Jiang, Jiaying Shen, Zihan Zhang, Junheng Lyu, Rui Pu, Xiaojie Tan, Jianhua Yin, Weifeng Shi, Guangwen Cao

Viol. Sin. 2025 Aug.; 40(4): 520—534.

<https://doi.org/10.1016/j.virs.2025.06.004>

Epidemiological and genomic surveillance of influenza A virus (pdm09 H1N1 and H3N2) strains from 2017 to 2025 in Tianjin, China

Mingkun Wu, Liru Guo, Mei Kong, Ming Zou, Xiaochang Liu, Xiaoyan Li

Viol. Sin. 2025 Aug.; 40(4): 535—545.

<https://doi.org/10.1016/j.virs.2025.07.011>

The slow progression of Japanese encephalitis in aged mice is likely associated to B cell recruitment in the brain

Zheng-Ran Song, Yi-Lin Yang, Yang Zhou, Li-Bo Liu, Fei-Yang Xue, Lin-Shen-Yang Liu, Na Gao, Dong-Ying Fan, Yi-Song Wang, Jing An, Pei-Gang Wang

Viol. Sin. 2025 Aug.; 40(4): 546—559.

<https://doi.org/10.1016/j.virs.2025.05.013>

SARS-CoV-2-encoded miR-nsp3-3p promotes pulmonary fibrosis by inhibiting expression of ALCAM

Yang Yang, Qiuyue Wu, Xueyan Liu, Hongjian Zhou, Jianzhen Lei, Lan Luo, Xinyi Xia

Viol. Sin. 2025 Aug.; 40(4): 560—570.

<https://doi.org/10.1016/j.virs.2025.06.007>

STAT5-c-Myc-axis regulates B cell metabolism in vaccinated individuals and COVID-19 recovered patients

Lu Yang, Linhua Wang, Qian Liu, Xu Zhang, Yuexin Luo, Junbiao Xue, Xinpu Yang, Maria G. Byazrova, Alexander V. Filatov, Sheng-Ce Tao, Wei Xiao, Chaohong Liu

Viol. Sin. 2025 Aug.; 40(4): 571—578.

<https://doi.org/10.1016/j.virs.2025.07.003>

Clinical outcomes after HBsAg clearance in chronic hepatitis B patients treated with Peg-IFN α : A study with an 11- to 173-month follow-up

Wen Deng, Hongxiao Hao, Ziyu Zhang, Xinxin Li, Weihua Cao, Yaqin Zhang, Shiyu Wang, Zixuan Gao, Linmei Yao, Shuojie Wang, Xin Wei, Wei Yi, Linqing Zhao, Yao Xie, Minghui Li

Viol. Sin. 2025 Aug.; 40(4): 579—586.

<https://doi.org/10.1016/j.virs.2025.06.008>

Isolation and identification of a newly discovered broad-spectrum *Acinetobacter baumannii* phage and therapeutic validation against pan-resistant *Acinetobacter baumannii*

Miaomiao Lin, Lele Xiong, Wen Li, Lingyan Xiao, Wei Zhang, Xiaogui Zhao, Yishan Zheng

Viol. Sin. 2025 Aug.; 40(4): 587—600.

<https://doi.org/10.1016/j.virs.2025.06.003>

Identification of a novel ectromelia virus from rodent: Implications for use as an *in vivo* infection model for vaccine and

antiviral research

Shuting Huo, Changcheng Wu, Zhenyong Qi, Jiwei Sun, Xin Meng, Jingdong Song, Zhongxian Zhang, Liye Jin, Chang Shu, Zhifeng Lin, Weibang Huo, Yao Deng, Li Zhao, Jiandong Li, Wenjie Tan

Virol. Sin. 2025 Aug.; 40(4): 601—612.

<https://doi.org/10.1016/j.virs.2025.07.001>

Rapid and accurate detection of infectious SARS-CoV-2 by viral receptor capture combined with loop-mediated isothermal amplification

Zixiao Yang, Xinrong Zhou, Xikui Sun, Liu Cao, Tiefeng Xu, Kun Li, Hongchao Liu, Yanxi Ji, Lihong Liu, Konstantin I. Ivanov, Zhonghan Yang, Deyin Guo, Chun-Mei Li

Virol. Sin. 2025 Aug.; 40(4): 613—623.

<https://doi.org/10.1016/j.virs.2025.06.006>

Identification of PEDV inhibitors targeting 3CL protease

Ang Tian, Shutong Shi, Siying Zou, Shuaiyin Guan, Hao Wu, Zhen Li, Huanchun Chen, Yunfeng Song

Virol. Sin. 2025 Aug.; 40(4): 624—635.

<https://doi.org/10.1016/j.virs.2025.06.002>

Single-cycle Rift Valley fever virus particles from stable replicon cells enable discovery of antiviral CNX-1351 for multiple RNA viruses

Zhichao Gao, Hongyuan Guo, Ziqiao Wang, Pengcheng Wang, Xinran Sun, Shimei Zhang, Fei Feng, Chao Shan, Youhua Xie, Rong Zhang

Virol. Sin. 2025 Aug.; 40(4): 636—646.

<https://doi.org/10.1016/j.virs.2025.06.009>

Quercetin inhibits herpes simplex virus 1 replication in corneal epithelium and suppresses keratitis progression

Yubin Yu, Sihao Liu, Qinghua Liu, Xiuping Liu, Kaili Wu

Virol. Sin. 2025 Aug.; 40(4): 647—657.

<https://doi.org/10.1016/j.virs.2025.07.007>

ARRDC3 promotes lysosome-mediated YAP degradation to inhibit enterovirus replication

Xia Huang, Siyuan Wang, Yan Huang, Yue Wang, Guangchao Zang, Yan Liang, Juntong Liu, Xinyue Han, Jingjing Liao, Tingting Chen, Nan Lu, Guangyuan Zhang

Virol. Sin. 2025 Aug.; 40(4): 658—668.

<https://doi.org/10.1016/j.virs.2025.07.009>

Thermal tolerance and inactivation of Ebola virus

Xiaoxiao Gao, Cheng Peng, Rongjuan Pei

Virol. Sin. 2025 Aug.; 40(4):669-671.

<https://doi.org/10.1016/j.virs.2025.07.004>

First isolation and genomic characterization of a novel inter-genotype recombinant feline calicivirus from domestic cats: Implications for viral evolution

Xiaomei Tan, Liangliang Lin, Qi Zhang, Na Li, Ningning Dong, Shishi Wang, Wenqi Zhu, Maoqing Luo, Shuaisai Pang, Yanzhao Xu, Guangqing Liu, Chunchun Meng

Virol. Sin. 2025 Aug.; 40(4):672-675.

<https://doi.org/10.1016/j.virs.2025.06.005>

Isolation and phylogenetic analysis of swinepox virus from pigs in China

Nan Cao, Yamei Li, Xiangmin Li, Ping Qian

Virol. Sin. 2025 Aug.; 40(4): 676—679.

<https://doi.org/10.1016/j.virs.2025.07.006>

Co-circulation of all four DENV serotypes during 2016 outbreak in Sinaloa, Mexico: First report of DENV-4 in patients

Annete Itzel Apodaca-Medina, José Israel Torres-Avenidaño, Hipólito Castillo-Ureta, Edith Hilario Torres-Montoya, Sergio Alonso Durán-Pérez, Lorenzo Ulises Osuna-Martínez, María Elena Báez-Flores, José Guadalupe Rendón-Maldonado

Virol. Sin. 2025 Aug.; 40(4): 680—683.

<https://doi.org/10.1016/j.virs.2025.07.010>

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Dear Dr. Gralinski,

We are delighted to share with you the [latest issue of *Virologica Sinica*](#). Kindly find the articles listed below. Your comments and suggestions are appreciated.

Human coronavirus OC43 (HCoV-OC43), a typical type of coronavirus, causes the common cold in humans. Although the HCoV-OC43 virus has been identified for over 60 years, the specific mechanism of viral internalization post-infection remains unclear. In this issue, Li et al. investigate how sorting nexin 10 (SNX10) mediates HCoV-OC43 infection via interacting with the adaptor protein complex 2 μ 1 subunit (AP2M1). SNX10 can further promote lysosomal acidification and assist viral genome release. The cover image draws on the story of the Trojan Horse: For a long time, the Greek army (representing the virus) could not break through the walls of Troy (the host cell membrane). They thus feigned retreat and left a huge wooden horse (AP2M1). The Trojans (SNX10) took the house into the city as a trophy. When night fell (mimicking the acidic environment), the Greek soldiers hiding inside the horse rushed out (release the viral genome) and cooperated with the returning army to breach the walls of Troy (Kindly designed and provided by Prof. Shuwen Liu and Dr. Haobin Li). See page 755–768 for details.

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Review

HBV and host metabolic crosstalk: Reprogramming pathways for viral replication and pathogenesis

YanYing Yan, Zhiqiang Wei, Min Zheng, Mengji Lu, Xueyu Wang

Viol. Sin. 2025 Oct.; 40(5):685-693.

<https://doi.org/10.1016/j.virs.2025.09.008>

Research Articles

Genetic analysis of human adenovirus type 108 circulating in China during 2014—2024

Jinjin Wang, Ling Jing, Yali Duan, Junhong Ai, Yun Zhu, Ran Wang, Xiangpeng Chen, Gen Lu, Yun Sun, Changchong Li, Rong Jin, Yunxiao Shang, Yixiao Bao, Shuhua An, Yunlian Zhou, Limin Ning, Baoping Xu, Yuhai Bi, Zhengde Xie

Viol. Sin. 2025 Oct.; 40(5): 694—709.

<https://doi.org/10.1016/j.virs.2025.09.002>

Long-term surveillance of avian avulavirus in wild birds in China from 2003 to 2020

Qing An, Yi Li, Xinru Lv, Shunmeng Qu, Xiang Li, Shaoxia Lu, Weiguang Wang, Xuyang Zhao, Yuan Cui, Yang Zhou, Hongli Zhai, Ao Li, Fangyuan Chen, Yang Xiu, Xiangwei Zeng, Yajun Wang, Zhijun Hou, Cheng Cheng, Yulong Wang, Linna Liu, Hongliang Chai

Virol. Sin. 2025 Oct.; 40(5): 710—721.

<https://doi.org/10.1016/j.virs.2025.09.004>

Epidemiological, phylogenetic, and pathogenicity analysis of H4 subtype avian influenza viruses in China, 2011—2022

Qiuyan Mao, Junfeng Zhu, Shuo Liu, Cheng Peng, Tiantian Wu, Jie Tian, Xiaoqi Li, Jizhe Yang, Jinping Li, Guangyu Hou, Wenming Jiang, Hualei Liu

Virol. Sin. 2025 Oct.; 40(5): 722—734.

<https://doi.org/10.1016/j.virs.2025.09.005>

Phylogenomics and structural modelling feature accelerated evolution of Oropouche virus: 1955 to 2024

Yibo Ding, Jiajing Li, Xin Wang, Simone Malag^貌, Amaro Nunes Duarte-Neto, Xiaohui Ding, Fang Qin, Michela Deiana, Concetta Castilletti, Hongbo Guo, Qiuwei Pan, Wenshi Wang

Virol. Sin. 2025 Oct.; 40(5): 735—747.

<https://doi.org/10.1016/j.virs.2025.09.009>

Seasonal dynamics of hedgehog-borne ticks and severe fever with thrombocytopenia syndrome virus in Beijing's urban parks

Chunzheng Li, Hongyue Li, Yuanchi Ye, Lianglong Zhu, Aihua Zheng, Xing Zhang

Virol. Sin. 2025 Oct.; 40(5): 748—754.

<https://doi.org/10.1016/j.virs.2025.10.005>

SNX10 enhances HCoV-OC43 infection by facilitating viral entry and inhibiting virus-triggered autophagy

Haobin Li, Huiyi Guo, Binhao Rong, Haowei Li, Wenjiao Wu, Chan Yang, Shuwen Liu

Virol. Sin. 2025 Oct.; 40(5): 755—768.

<https://doi.org/10.1016/j.virs.2025.07.005>

Antigenic and structural insights into Langya henipavirus attachment glycoprotein

Yaohui Li, Xiaoyan Huang, Xiaodong Zai, Chenfeng Mao, Ruihua Li, Yamei Feng, Yue Zhang, Zhang Zhang, Jun Zhang, Junjie Xu

Virol. Sin. 2025 Oct.; 40(5): 769—777.

<https://doi.org/10.1016/j.virs.2025.08.005>

Ubiquitously expressed transcript isoform 2 (UXT-V2) restricts HSV-2 replication by targeting glycoprotein B for degradation through ubiquitin-proteasome pathway

Chuntian Li, Yuncheng Li, Ranqing Cheng, Miaomiao Li, Mudan Zhang, Zhiyuan Zhu, Ping Yang, Qinxue Hu, Yalan Liu
Virol. Sin. 2025 Oct.; 40(5): 778—792.
<https://doi.org/10.1016/j.virs.2025.08.004>

A safe and broad-spectrum SARS-CoV-2 mRNA vaccine with a new delivery system for in-situ expression

Weiyi Yu, Xianying Chen, Qiubing Chen, Peixuan Chen, Naizhang Liu, Yingjian Li, Xue Tan, Qiuhan Zhang, Yan Rao, Ming Guo, Zhixiang Huang, Xin Wang, Zhen Zhang, Wenjie Xiang, Yuzhen Zhang, Qianyun Liu, Hao Yin, Li Zhou, Yu Chen, Ke Lan
Virol. Sin. 2025 Oct.; 40(5): 793—803.
<https://doi.org/10.1016/j.virs.2025.09.001>

The pathogenic role and genomic characteristics of Epstein-Barr virus in vitreoretinal lymphoma

Xiaoqing Liu, Guangjie Jiang, Chianru Tan, Kun Chen, Zhewei Sun, Jiaying Du, Bei Wang, Fuqi Ai, Yimin Ma, Yueru Tian, Yong Guo, Ming Guan
Virol. Sin. 2025 Oct.; 40(5): 804—811.
<https://doi.org/10.1016/j.virs.2025.09.007>

Synthetic genomics-based generation of the tick-borne encephalitis virus Siberian subtype prototype strain and E51K-attenuated variant for vaccine development and antiviral screening

Tolganay Kulatay, Elena Sedova, Alexander Shevtsov, Gulzat Zauatbayeva, Bakytkali Ingirbay, Viktoriya Keyer, Zhanar Shakhmanova, Maral Zhumabekova, Yergali Abduraimov, Aralbek Rsaliyev, Nurgul Sikhayeva, Irina Kozlova, Mikhail Zaripov, Alexandr V. Shustov
Virol. Sin. 2025 Oct.; 40(5): 812—821.
<https://doi.org/10.1016/j.virs.2025.09.010>

African swine fever virus MGF360-9L degrades DDX20 through the Rab1A-dependent autophagy pathway to antagonize its antiviral effect

Lu He, Xuxu Fan, Zhaoyu Zhu, Danshi Pei, Yizhuo Wang, Xizhong Li, Qingfeng Ren, Haixue Zheng, Weiwei Li, Zixiang Zhu
Virol. Sin. 2025 Oct.; 40(5): 822—834.
<https://doi.org/10.1016/j.virs.2025.10.001>

Efficacy and safety of switching from lopinavir/ritonavir-based regimens to bictegravir/emtricitabine/tenofovir alafenamide in people living with HIV: A multicenter retrospective study

Jiantao Fu, Yifan Guo, Guoxiang Zheng, Zongxing Yang, Jinchuan Shi, Dingyan Yan, Jianhua Yu, Lijun Sun, Hongxin Zhao
Virol. Sin. 2025 Oct.; 40(5): 835—841.
<https://doi.org/10.1016/j.virs.2025.10.003>

Oncolytic Newcastle disease virus promotes tumor cell death via the anoikis effector Bit1 translocation

Yang Qu, Sainan He, Liya Shen, Ying Liao, Xusheng Qiu, Lei Tan, Cuiping Song, Ning Tang, Yingjie Sun, Chan Ding

Viol. Sin. 2025 Oct.; 40(5): 842—852.

<https://doi.org/10.1016/j.virs.2025.10.004>

Letters

Black swans as sentinel species for the emergence of clade 2.3.4.4b highly pathogenic avian influenza (H5N1) in Shanghai, China, 2024

Yuting Xu, Shihai Wu, Lei Ji, Jie Hu, Jin Wang, Ke Li, Yue Yuan, Gaojian Li, Guangjian Zhu, Panyu Hua, Qihong Miao, Hongxuan He, Guimei He

Viol. Sin. 2025 Oct.; 40(5): 853—855.

<https://doi.org/10.1016/j.virs.2025.07.008>

Antisera and antivirals targeting the conserved domains in SARS-CoV-2 S2 subunit are effective against ACE2-using MERSCoVs with spillover potential

Lujia Sun, Bianying Feng, Zezhong Liu, Jingqi Chen, Xiangwen Hao, Shuai Xia, Lu Lu, Qihong Man, Shibo Jiang, Xinling Wang

Viol. Sin. 2025 Oct.; 40(5): 856—859.

<https://doi.org/10.1016/j.virs.2025.09.003>

First identification of Tusavirus in calf intestinal tissue suggests interspecies transmission and genomic variation

Yang Song, Weiwei Gai, Jiabin Sun, Xiangyu Lv, Haojie Sang, Shuai Guo, Jingqiang Ren, Jingbo Zhai, Shubo Wen

Viol. Sin. 2025 Oct.; 40(5): 860—862.

<https://doi.org/10.1016/j.virs.2025.09.006>

Meeting Report

The 16th national virology symposium concludes: Sustaining academic exchanges and innovations in China's virology

Jiali Si, Ying Wu

Viol. Sin. 2025 Oct.; 40(5): 863—864.

<https://doi.org/10.1016/j.virs.2025.08.003>

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Dear Dr. Gralinski,

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Dengue virus (DENV), a mosquito-borne pathogen responsible for dengue fever, continues to pose a formidable global health challenge. Over the past five years, dengue fever has seen a steady global increase in cases, now being endemic in more than 100 countries and regions across tropical and subtropical areas of the Americas, Asia, Africa, and Australia. However, there are no commercially available vaccines or specific antiviral treatments against DENV. In this issue, *Virologica Sinica* presents a collection of articles highlighting recent advances in dengue virus studies, including a review on recent development of antiviral agents, identification of a host factor promoting zika virus and DENV2 infections via distinct mechanisms, and novel diagnostic biomarkers for differentiating dengue fever and dengue-associated neutropenia. The cover shows dengue virus particles, along with potential antiviral agents and biomarkers relevant to early diagnosis.

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Review

Antiviral agents for dengue virus

Yinghan Jiang, Yanran Wang, Yaqun Xu, Yuxin Tian, Mengyuan Zhao, Chenguang Shen, Yang Yang, Minghui Yang
Virol. Sin. 2025 Dec.; 40(6):865—873.

<https://doi.org/10.1016/j.virs.2025.11.009>

Research Articles

Adaptor protein complex 1 gamma 1 subunit is an important host factor involved in both Zika virus and dengue virus infections

Jinna Yang, Changbai Huang, Yao Feng, Junfang He, Yang Liu, Ping Zhang, Chao Liu
Virol. Sin. 2025 Dec.; 40(6): 874—883.

<https://doi.org/10.1016/j.virs.2025.07.012>

Deep data-independent acquisition-based plasma proteomic profiling unveils distinct molecular features in dengue fever

with neutropenia

Guanyong Ou, Jun Wang, Rongrong Zou, Dongmei Lai, Qi Qian, Xiaowen Liang, Yuelin Wang, Canghai Ma, Hao Liao, Shiyu Niu, Jing Yuan, Yingxia Liu, Yang Yang

Viol. Sin. 2025 Dec.; 40(6): 884—897.

<https://doi.org/10.1016/j.virs.2025.12.005>

Meta-transcriptomic analysis of tick virome diversity and ecological characteristics in Yunnan Province, southwestern China

Rong Xiang, Fengjuan Tian, Jing Li, Jihu Yang, Danni Zeng, Yilin Zhao, Zhi Luo, Miao Li, Chaobo Du, Wenqiang Shi, Chunfeng Luo, Xiaohe Liu, Yi Sun, Yigang Tong, Chunhong Du, Jiafu Jiang

Viol. Sin. 2025 Dec.; 40(6): 898—909.

<https://doi.org/10.1016/j.virs.2025.12.004>

Ubiquitin-specific protease 5 promotes EV-A71 replication by de-ubiquitinating MAVS and IRF3

Shumin Zhang, Yuan Fang, Shuai Ren, Xuhua Zhang, Chenggong Zheng, Zhipeng Qin, Wenqiang Wei, Huabin Zheng, Chuntian Li, Zekun Wang, Yujie Ren

Viol. Sin. 2025 Dec.; 40(6): 910—920.

<https://doi.org/10.1016/j.virs.2025.12.002>

RNA and ChIP-sequencing analysis reveals SOX3 suppresses antiviral innate immunity through the AKT1-PTEN signaling axis

Tanzeel Yousaf, Jianwen Chen, Wajeeha Naz, Jiaqi Xu, Ying Liu, Junsong Huang, Siqi Yang, Jing Zhang, Iram Amin, Mingxiong Guo, Yunlan Tang, Guihong Sun

Viol. Sin. 2025 Dec.; 40(6): 921—934.

<https://doi.org/10.1016/j.virs.2025.11.012>

Structural polymorphism of two-dimensional lattices assembled from baculoviral capsid proteins

Kexing Tian, Heya Na, Yan Fu, Tingting Chong, Chao Leng, Fanxing Meng, Yaozhou Liang, Manli Wang, Zhihong Hu, Xi Wang, Guibo Rao, Sheng Cao

Viol. Sin. 2025 Dec.; 40(6): 935—945.

<https://doi.org/10.1016/j.virs.2025.11.005>

Topoisomerase II α orchestrates secretion of IL-6 and IL-8 with human papillomavirus replication

Yanfei Liu, Zi Han, Paul Kaminski, Chengcheng Tao, Xiaoge Li, Mengmeng Liu, Yang Li, Ying Jia, Junfen Xu, Shiyuan Hong

Viol. Sin. 2025 Dec.; 40(6): 946—961.

<https://doi.org/10.1016/j.virs.2025.11.004>

A decreased proportion of naïve MAIT cells is associated with the incomplete immune reconstitution in antiretroviral therapy-treated HIV-1 patients

Jie Jia, Hong-Yi Zheng, Yu Zhao, Kai-Cheng Gao, Deshenyue Kong, Danfeng Lu, Ji-Qun Yang, Jun-Hong Mao, Xiuwen Wang, Kun-Hua Wang, Bin Su, Jian-Hua Wang, Yong-Tang Zheng, Yi-Qun Kuang

Viol. Sin. 2025 Oct.; 40(6): 962—976.

<https://doi.org/10.1016/j.virs.2025.12.003>

Oncolytic HSV-1 expressing GM-CSF and IL-12 enhances anti-tumor efficacy in immunocompetent murine melanoma model

Han Xiao, Qiran Yin, Jia Liu, Hengrui Hu, Jiang Li, Manli Wang, Zhihong Hu

Viol. Sin. 2025 Dec.; 40(6): 977—988.

<https://doi.org/10.1016/j.virs.2025.11.002>

Thapsigargin suppresses porcine hemagglutinating encephalomyelitis virus replication by disrupting host energy metabolism

Qianhan Jia, Zi Li, Yanfang Y, Zezhao Ca, Ruizhao Qi, Jing Zhan, Wenqi H, Junchao Sh

Viol. Sin. 2025 Dec.; 40(6): 989—1001.

<https://doi.org/10.1016/j.virs.2025.11.006>

Improvement in UV resistance of entomopathogenic viruses by coating silica nanoparticles on occlusion bodies surface

Jia Wang, Zhongqiang Wu, Xiaoqin Yang, Chengfeng Lei, Xiulian Sun

Viol. Sin. 2025 Dec.; 40(6): 1002—1010.

<https://doi.org/10.1016/j.virs.2025.11.008>

Predicting mortality risk of severe fever with thrombocytopenia syndrome: A multi-center retrospective cohort study

Xue-Geng Hong, Hong-Han Ge, Ning Cui, Yan-Li Xu, Xin Yang, Jia-Hao Chen, Xiao-Hong Yin, Yi-Mei Yuan, Chao Zhou, Hao Li, Xiao-Ai Zhang, Ming Yue, Ling Lin, Wei Liu

Viol. Sin. 2025 Dec.; 40(6): 1011—1020.

<https://doi.org/10.1016/j.virs.2025.12.008>

Neutralization of Crimean-Congo hemorrhagic fever pseudotyped virions with heavy chain antibodies

Kewen Qian, Yu Zhang, Zhihao Li, Wei Ye, Yue Cui, Zheng Zhu, Zhengshan Chen, Jianrong Wang, Jin Han, Ping Huang, Pu Fan, Peng Lv, Ting Fang, Guanying Zhang, Changming Yu, Yunzhu Dong, Wujian Li, Fanglin Zhang, Xiangyang Chi

Viol. Sin. 2025 Dec.; 40(6): 1021—1036.

<https://doi.org/10.1016/j.virs.2025.12.001>

An adenovirus-vectored recombinant vaccine confers passive immunity protection from swine acute diarrhea syndrome coronavirus challenge in neonatal mice

Yu Zhang, Yueyue Duan, Xueliang Zhu, Lei Shi, Juan Zhang, Wenquan Mao, Luyao Li, Cong Yuan, Maowen Sun, Haixue Zheng, Qi Wang

Viol. Sin. 2025 Dec.; 40(6): 1037—1044.

<https://doi.org/10.1016/j.virs.2025.12.007>

Letters

Genomic characterization of three unclassified rhabdoviruses from mosquitoes in Malaysia and Central Africa

Dong-Sheng Luo, Zhi-Jian Zhou, Xing-Yi Ge, Hervé Bourhy, Efsthios S. Giotis, Marc Grandadam, Zheng-Li Shi, Laurent Dacheux

Viol. Sin. 2025 Dec.; 40(6): 1045—1049.

<https://doi.org/10.1016/j.virs.2025.11.003>

A dual monoclonal antibody-based sandwich ELISA for detection of potent vaccine immunogen against Coxsackievirus B1

Hao Chen, Rui Zhu, Yuanyuan Wu, Zhifeng Ke, Yubo Wu, Dongqing Zhang, Yuxiang Zou, Jiaying Wu, Xuejun Feng, Zhichao Yin, Mujin Fang, Ningshao Xia, Longfa Xu, Tong Cheng

Viol. Sin. 2025 Dec.; 40(6): 1050—1053.

<https://doi.org/10.1016/j.virs.2025.11.007>

Specific and visual detection of EBOV based on a one-pot RT-RAA-CRISPR/Cas12a assay

Zanheng Huang, Pei Huang, Zengguo Cao, Tianyi Zhang, Kaikai Jin, Meihui Liu, Yujie Bai, Zhiyuan Gong, Xuemeng Li, Yuanyuan Li, Haili Zhang, Hualei Wang

Viol. Sin. 2025 Dec.; 40(6): 1054—1057.

<https://doi.org/10.1016/j.virs.2025.11.011>

News and Views

The effectiveness of two doses of Hecolin vaccine in response to outbreaks in resource-limited settings

Fan Zhang, Jianbo Xia, Ling Wang

Viol. Sin. 2025 Dec.; 40(6): 1058—1060.

<https://doi.org/10.1016/j.virs.2025.11.001>

Bibliometric analysis of global research output on viral vaccines and antivirals in the 21st century

Lili Ma, Wei Pan, Miaomiao Yan, Jiali Si

Viol. Sin. 2025 Dec.; 40(6): 1061—1065.

<https://doi.org/10.1016/j.virs.2025.08.002>

Corrigendum

Corrigendum to “Insights into recent advancements in human and animal rotavirus vaccines: Exploring new frontiers” [Virol. Sin. 40 (2025) 1–14]

Ahmed H. Ghonaim, Sherin R. Rouby, Wedad M. Nageeb, Ashraf Ahmed Elgendy, Rong Xu, Changsheng Jiang, Noha H. Ghonaim, Qigai He, Wentao Li

Virol. Sin. 2025 Dec.; 40(6): 1066—1067.

<https://doi.org/10.1016/j.virs.2025.10.002>

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Dear Dr. Gralinski, Lisa E,

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In late 2024, northern China experienced an unexpected surge in human metapneumovirus (hMPV) cases, raising questions about potential novel variants. Kang et al. conducted genomic and evolutionary analyses of hMPV from 2014 to 2024, using data from the Beijing Respiratory Pathogen Surveillance System (RPSS) across 35 sentinel hospitals. They identified lineage I of clade B2 as the main cause of the hMPV outbreak in Beijing from November to December 2024, with no novel variants detected. This study emphasizes the importance of continuous genomic surveillance of respiratory viruses and strengthens preparedness for emerging and re-emerging infectious diseases. The cover image uses a deep-rooted tree to represent the surveillance system, which encompasses epidemiological surveys, medical records, and laboratory test results, with colored leaves and branches illustrating genotype shifts (Kindly designed and provided by Prof. Quanyi Wang and Dr. Lu Kang). See page 48–57 for details.

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Reviews

Current status of dengue fever epidemics and vaccine development

Shiqi He, Dongying Fan, Yuqing Guo, Yuheng Guan, Ziyang Sheng, Na Gao, Jing An

Viol. Sin. 2026 Jan.; 41(1):1–9.

<https://doi.org/10.1016/j.virs.2026.01.001>

The role of T cells in influenza infection and vaccination

Yuxuan Li, Chenxi Zhu, Yi Wang, Heather Miller, Kamel Benlagha, Maria G. Byazrova, Alexander Filatov, Lu Yang, Chaohong Liu

Viol. Sin. 2026 Jan.; 41(1):10–22.

<https://doi.org/10.1016/j.virs.2026.02.005>

Advances in human respiratory organoid models for studying the pathogenesis and intervention strategies of COVID-19

Zeping Shan, Jiarui Li, Zihui Ye, Yuyue Chen, Jie Chen, Yüewen Chen, Xiaofan Wang, Chong Gao, Shibo Jiang, Naru Zhang
Virol. Sin. 2026 Jan.; 41(1):23–34.
<https://doi.org/10.1016/j.virs.2026.02.002>

Research Articles

Metatranscriptomics profiling reveals rodent- and shrew-borne viral diversity and evolutionary relationships in Guangzhou, China

Shuangshuang Chen, Wanping Li, Lirui Fan, Conghui Xu, Sixuan Liu, Hongye Li, Peiwen Liu, Wei Zhu, Xinwei Wu, Pengzhe Qin, Juntao Li, Xiaowei Ma, Yuehong Wei
Virol. Sin. 2026 Jan.; 41(1):35–47.
<https://doi.org/10.1016/j.virs.2025.12.009>

Genomic evidence of HMPV resurgence in Beijing: Clade B2 triggers the 2024 winter epidemic peak

Lu Kang, Fang Huang, Yi-Mo Deng, Geng Hu, Yiting Wang, Aihua Li, Hui Xie, Xiaofeng Wei, Yuling Han, Ming Luo, Ian G. Barr, George F. Gao, Liang Wang, Quanyi Wang
Virol. Sin. 2026 Jan.; 41(1):48–57.
<https://doi.org/10.1016/j.virs.2026.01.006>

Integrated multiplex PCR and metatranscriptomics reveal upper-lower airway microbial landscapes in pediatric respiratory infections

Peilan Wei, Lu Zhang, Qingtao Hu, Airu Zhu, Zhen Zhuang, 1 10 23 35 48 58 Zhaoyong Zhang, Shengnan Zhang, Jiantao Chen, Xinyi Xiong, Bin Qu, Yuanyuan Zhang, Lei Chen, Zhiwei Xu, Zhao Chen, Qier Zhong, Xindan Xing, Xinxin Li, Jingjing Gao, Yifang He, Guifei Xie, Juan Shang, Xiaoke Guo, Jiaxin Jiang, Yongxia Shi, Jingxian Zhao, Yanqun Wang, Jincun Zhao, Yingkang Jin
Virol. Sin. 2026 Jan.; 41(1):58–69.
<https://doi.org/10.1016/j.virs.2026.02.001>

Evidence of human exposure to tick-borne viruses based on viromes of ticks and presence of specific antibodies among patients in Hainan Island, Southern China

You Zhang, Yuan Bai, Jun Ni, Junming Shi, Yanfang Zhang, Lesley Bell-Sakyi, Xiaoli Wu, Changhua He, Fei Deng, Feifei Yin, Shu Shen, Yaohui Fang
Virol. Sin. 2026 Jan.; 41(1):70–83.
<https://doi.org/10.1016/j.virs.2026.02.008>

Characteristics of humoral and T-cell immune responses in people living with HIV after breakthrough SARS-CoV-2 Omicron variant infection during December 2022 to January 2023

Hai-Bo Ding, Hong Sun, Yong-Hui Feng, Qing-Hai Hu, Qi Wang, Nan Li, Qing-Qing Ma, Wen Tian, Yan-Chun Peng, Jia-Qi Chen, Jin-Li Song, Hua-Lu Cui, Hai-Long Li, Wen-Qing Geng, Tao Dong, Xiao-Xu Han, Hong Shang

Virol. Sin. 2026 Jan.; 41(1):84–96.

<https://doi.org/10.1016/j.virs.2026.01.003>

Genomic assembly, rescue, and characterization of a functional pseudorabies virus

Hengrui Hu, Xiquan Ke, Han Xiao, Xianfei Shang, Qiran Yin, Jiang Li, Xiangmin Li, Zhihong Hu, Ping Qian, Manli Wang

Virol. Sin. 2026 Jan.; 41(1):97–106.

<https://doi.org/10.1016/j.virs.2025.11.010>

Development of the reverse genetics system for viral hemorrhagic septicemia virus genotype IVa and its application in antiviral compound screening

Hao Huang, Xiaobing Lu, Tianlai Hong, Yihong Chen, Meisheng Yi, Kuntong Jia

Virol. Sin. 2026 Jan.; 41(1):107–118.

<https://doi.org/10.1016/j.virs.2025.12.010>

Enhancing the stability of influenza a reporter viruses by recoding the *gfp* gene

Jing Hu, Jianchao Li, Qifeng Li, Shengqiang Jiang, Ziqian Cao, Hongying Chen

Virol. Sin. 2025 Oct.; 40(6): 119–131.

<https://doi.org/10.1016/j.virs.2026.01.005>

Pseudorabies virus TK protein antagonizes alpha interferon response by interfering with the JAK1-STAT1 interaction

Jingjing Song, Rulan Bai, Dongyue Xing, Chuang Li, Xuan Chen, Feiyang Zheng, Mingyi Lei, Yujin Wang, Yuxin Liu, Jun Tang, Pinghuang Liu, Changyong Cheng, Jin Yuan, Rui Zhang

Virol. Sin. 2026 Jan.; 41(1):132–143.

<https://doi.org/10.1016/j.virs.2026.01.004>

Nuclear translocation of Sp100A suppresses multiple DNA viruses and limits HSV-1 lytic replication *in vivo*

Yilei Ma, Weidong Li, Jialing Li, Xiao Zhang, Xiuyan Guo, Zhu Li, Yunsheng Xu, Pei Xu

Virol. Sin. 2026 Jan.; 41(1):144–156.

<https://doi.org/10.1016/j.virs.2026.02.003>

Single-cell transcriptomic analyses of HSV-1 reactivation from latently infected tree shrew and mouse trigeminal ganglia reveal differing molecular and cellular processes

Yunshuang Ye, Erlin Wang, Mengqiu Yin, Shiqing Zou, Guijun Chen, Liping Yang, Nigel W. Fraser, Xia Cao, Xinglou Yang, Jumin Zhou

Virol. Sin. 2026 Jan.; 41(1):157–171.

<https://doi.org/10.1016/j.virs.2026.02.009>

Desmoglein 2 (DSG2)-knockout human respiratory epithelial cell model to study species B adenovirus receptor usage

Nora Bahlmann, Montaha Alshawabkeh, Raphael Tsoukas, Katrin Schröer, Sebastian Schellhorn, Mareike Sieler, Thomas Dittmar, Eric Ehrke-Schulz, Anja Ehrhardt, Wenli Zhang

Virol. Sin. 2026 Jan.; 41(1):172–181.

<https://doi.org/10.1016/j.virs.2026.02.007>

Multivalent display of envelope protein domain III with Mi3 nanoparticles induces protective immunity against lethal Zika virus infection in mice

Xikui Sun, Huadong Jiang, Wenqiang Yu, Nana Wang, Zhengfeng Li, Junnan Lu, Xiaolu Xie, Liqiang Feng

Virol. Sin. 2026 Jan.; 41(1):182–195.

<https://doi.org/10.1016/j.virs.2025.12.012>

Systematic evaluation of HSV-1 Δ 34.5 Δ 47 as a dual-function platform for attenuated HSV-1 vaccine and heterologous antigen delivery

Ziyu Wen, Haohang Wang, Yu Liao, Shunran Li, Minjuan Shi, Mingting Cui, Jun Qian, Caijun Sun

Virol. Sin. 2026 Jan.; 41(1):196–207.

<https://doi.org/10.1016/j.virs.2026.01.002>

Phloretin targeting the 3CLpro Cys144 exhibits broad-spectrum antiviral activity against swine enteric coronavirus

Jiawei Xiao, Donghua Guo, Xiaoxu Xing, Limin Jiang, Shanshan Qi, Jun Wang, Wenfei Bai, Shiping Yu, Fanbo Shen, Xingyang Guo, Xinglin Wang, Wei Zhou, Hansong Li, Feiyu Zhao, Li Feng, Jialin Zhang, Yaru Xu, Dan Yang, Haixin Liu, Dongbo Sun

Virol. Sin. 2026 Jan.; 41(1):208–226.

<https://doi.org/10.1016/j.virs.2026.02.011>

Letters

Emergence and molecular characterization of bovine papular stomatitis virus in Chinese cattle

Yue Sun, Wenyan Gu, Yiman Xue, Zhuoya Li, Changchun Tu, Liqian Zhu

Virol. Sin. 2026 Jan.; 41(1):227–230.

<https://doi.org/10.1016/j.virs.2025.12.011>

GP38 is a structural component of Crimean-Congo hemorrhagic fever virus particles

Heya Na, Guibo Rao, Lu Peng, Jiang Li, Manli Wang, Zhihong Hu, Sheng Cao, Xi Wang

Virol. Sin. 2026 Jan.; 41(1):231–235.

<https://doi.org/10.1016/j.virs.2026.02.006>

Development of a stable replicon system of a pangolin merbecovirus for antiviral screening

Chun-Guang Wu, Jian-Hua Wang, Bo Zhu, Jing Chen

Virol. Sin. 2026 Jan.; 41(1):236–239.

<https://doi.org/10.1016/j.virs.2026.02.004>

News and Views

GlycoRNAs: Biological functions and novel antiviral targets

Yue Kang, Jian-jian Ji, Peng Cao

Virol. Sin. 2026 Jan.; 41(1):240–245.

<https://doi.org/10.1016/j.virs.2026.02.010>

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Dear Dr. Gralinski, Lisa E,

We are delighted to share with you the [latest issue of Virologica Sinica](#). Kindly find the articles listed below. Your comments and suggestions are appreciated.

Zika virus (ZIKV), with the remarkable ability to breach multiple blood-tissue barriers, leads to severe consequences such as fetal microcephaly, Guillain-Barré syndrome, testicular damage, and ocular lesions. In this issue, Hui et al. systematically reviewed the molecular mechanisms, commonalities, and tissue-specific features of ZIKV penetration across multiple barriers, as well as the pathological significance of barrier breakdown. The cover depicts a medieval siege fortress as a metaphor for the body's frontline defensive blood-tissue barriers—the blood-brain barrier (BBB), blood-testis barrier (BTB), blood-placenta barrier (BPB), and blood-retina barrier (BRB). ZIKV (red particles) attacks from different directions via diverse strategies: transcytosis, disruption of tight junctions, immune cell “Trojan horse” entry, and inflammation-induced barrier leakage. Four impaired organs behind the fortress represent typical pathological damages caused by ZIKV infection (Kindly designed and provided by Prof. Ying Wu and Dr. Lixia Hui). See page 247–260 for details.

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Reviews

Breaking barriers and beyond: Mechanisms and pathological implications of Zika virus traversal across blood-tissue interfaces

Lixia Hui, Danyu Qian, Yulei Guo, Zhengjun Yi, Tao Guo, Aixin Li, Ying Wu

Structural vaccinology expedites rational design of next-generation vaccines for influenza and respiratory syncytial virus

Lei Deng, Jia-Ye Liu, Ya-Xuan Peng

Research Articles

Metatranscriptomics uncovers host immune and microbiome signatures specific to and shared between human metapneumovirus and respiratory syncytial virus infections in children

Hongwei Zhao, Ju Yin, Yingdong Dong, Qianyu Feng, Huifang Liu, Shuaibing Han, Zhengde Xie, Lili Xu

The expression of CD39 on NK cells relates to poor HIV-1 suppression in treatment-naïve HIV-1-infected individuals: Association with elevated IL-10 secretion and TIGIT co-expression

Xin Zhang, Qianqian Xu, Junyan Jin, Hongxia Yan, Xiaofan Lu, Zhen Li, Zhiying Liu, Rui Wang, Lin Yuan, Zhenglai Ma, Tong Zhang, Hao Wu, Bin Su

ZNF219 inhibits porcine epidemic diarrhea virus by degrading viral S2 protein

Wenli Zhao, Ning Kong, Daoliang Lan, Yu Zhang, Hailong Liu, Chunyun Liu, Wenzhen Qin, Xinyu Yang, Tian Liu, Wu Tong, Hai Yu, Hao Zheng, Guangzhi Tong, Shengsong Xie, Guangxu Xing, Tongling Shan

EBV nuclear antigen 1 hijacks DDX5/BZLF1 axis to facilitate viral lytic replication

Li Yang, Shuyu Xin, Shen Li, Pengfei Cao, Zeyu Sun, Mingjuan Jiang, Yujie Xin, Xiaoling Su, Jing Yang, Jianhong Lu

Two orthobunyaviruses: OYAV and EBIV co-opt the AhR-CYP1A1 axis to suppress type I interferon responses

Qianyun Hu, Fei Wang, Xiaoyu Wang, Xiaokui Li, Zhiming Yuan, Maohua Zhong, Han Xia

Establishment of severe in vitro and in vivo infection models for coxsackievirus B4 and their application in identifying viral virulence determinants

Haoyi Liu, Xianglin Xuan, Bizhen Tang, Huan Wang, Li Zhang, Shuyan Qiu, Chuncong Mo, Xiao Li, Xingui Tian, Rong Zhou, Qian Liu, Wenkuan Liu

STING1 negatively regulates translation and replication of foot-and-mouth disease virus independently of interferon and is antagonized by the viral proteins 3C and 2B

Wenhua Shao, Wei Zhang, Zhitong Chen, Tingting Zhou, Xiaoyi Zhao, Hongyi Liu, Chuangwei Chen, Xingyan Dong, Weijun Cao, Zongsheng Zhao, Fan Yang, Zixiang Zhu, Haixue Zheng

Unveiling the cryptic diversity and distribution of elements related to virophage mavirus through deep mining of pPolB proteins

Yutong Wei, Qiyang Liu, Zhen Gong, Guan-Zhu Han

Genomic-epidemiological analysis of 15 million SARS-CoV-2 genomes reveals accelerated fitness gain of JN.1 lineage

Zhong-yi Lei, Qian-tong Jin, Xiao-min Zhang, Xiao-chen Bo, Zi-lin Ren, Yi-gang Tong, Ming Ni

Cepharanthine hydrochloride alleviates herpesvirus encephalitis by inhibiting Nrf2 degradation

Qiongzhen Zeng, Weixiangmin Zou, Jiaqi Wu, Menghe Li, Zexu Wang, Caiwenjie La, Cuifang Ye, Zhe Ren, Yifei Wang, Kai Zheng

Development and characterization of neutralizing monoclonal antibodies against clinically relevant human adenovirus subgroup B serotypes

Yuelin Wang, Wei Dou, Yingying Chen, Ke Liu, Mengjun Li, Tyuji Hoshino, Yushan Jiang, Vladislav Victorovich Khrustalev, Alexey V. Churov, Alexander N. Orekhov, Wei Zhao, Ling Li, Yang Yang, Chenguang Shen

Nanobody targeting glycan cap confers broad orthoebolavirus neutralization

Xinhui Zhang, Yi Liao, Xiuying Liu, Jingya Zhou, Peixiang Gao, Xuemeng Dong, Shengnan Pan, Huarui Duan, Junyu Liu, Xiaojing Chi, Wei Yang

A semi-replicating VSV (srVSV)-based platform for developing broad-spectrum mucosal vaccines against influenza A viruses

Xianmiao Ye, Junnan Lu, Zirong Han, Zhishan Fan, Xinru Hu, Lichuang Jiao, Lisha Deng, Wenming Liu, Junqi Liu, Weiqi Pan, Ling Chen, Liqiang Feng, Caijun Sun

Generation of G9 genotype porcine rotavirus using reverse genetics system and its application for antiviral screen and vaccine development

Nan Han, Ran Tao, Xi Cheng, Hui Deng, Jianxin Wang, Xianyu Bian, Jinzhu Zhou, Xuejiao Zhu, Min Sun, Xuehan Zhang, Mi Hu, Rongli Guo, Wei Wang, Siyuan Ding, Bin Li

HVT-based multiepitope vaccine administered subcutaneously or in ovo boosts protection of inactivated H9N2 vaccine against heterologous virus

Zimin Xie, Yingyi Chen, Shanyao Du, Xiumei Huang, Yuhuan Shao, Jiangwu Huang, Ming Liao, Manman Dai

Letters

Emergence of a novel H4N6 avian influenza virus with mammalian adaptation isolated from migratory birds in Zhejiang Province, China, 2024

Yongchun Yang, Han Liu, Yaling Li, Lin Liu, Tiantian Chen, Jiahao Zhang

Identification of a novel HIV-1 circulating recombinant form (CRF161_0107) from CRF01_AE-C5 lineage among men who have sex with men in southwestern China

Min Chen, Huichao Chen, Yanling Ma, Manhong Jia, Wenfei Ding

Identification and characterization of a novel ulcerative enteritis-associated adenovirus of quail causing cross-species infection in chickens

Hui Tang, Yin Shi, Qing Zhang, Fei Zhu, Jia-Yao Hou, Jing-Ying Liao, Yi-Shuai Zhang, Chang-Xin Jing, Xin-Qi Liu, Chao-Ting Xiao

Development of an HSV-1 F strain BAC system using the synthetic platform

Qiran Yin, Han Xiao, Hengrui Hu, Jiang Li, Manli Wang, Zhihong Hu

Feline calicivirus VP1-based mRNA vaccine protects cats against FCV challenge

Dan Zang, Wuchang Heng, Ruiyu Li, Chenxi Wei, Ruibin Qi, Getachew Mulatu Dilba, Jiasen Liu, Qian Jiang, Honglin Jia, Hongtao Kang

A natural five-amino-acid insert at the S2' cleavage site of MERS-CoV spike enhances viral membrane fusion

Guimin Dai, Wenjie Chen, Wenying Cao, Guigen Zhang

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A collection of our featured articles are listed below for your review.

Current status of dengue fever epidemics and vaccine development

Shiqi He, Dongying Fan, Yuqing Guo, Yuheng Guan, Ziyang Sheng, Na Gao, Jing An

Antiviral agents for dengue virus

Yinghan Jiang, Yanran Wang, Yaqun Xu, Yuxin Tian, Mengyuan Zhao, Chenguang Shen, Yang Yang, Minghui Ye

Zika virus transmission in *Aedes aegypti*: A systematic study on the ability of mosquitoes to transmit the virus horizontally and vertically

Xugang Wang, Chaonan Qian, Chenxi Zhang, Siyun Hu, Muhammad Asad, Chengjie Yang, Bingrui Liao, Xiaotao Guo, Chen Zhang, Quanzhi Li, Xinyao Li, Qiuying Huang, Youhui Si, Bibo Zhu, Shengbo Cao, Jing Ye

Eltrombopag, an FDA-approved drug, inhibits dengue virus type 2 by targeting NS2B-NS3 protease

Xuerui Zhu, Xiao Gao, Yan Wu, Jia Lu, Xinlan Chen, Chenshu Zhao, Haoyu Li, Zhongfa Zhang, Shuwen Liu, Gen Xiao, Xiaoyan Pan

Establishment and application of a surrogate model for human Ebola virus disease in BSL-2 laboratory

Wanying Yang, Wujian Li, Wujie Zhou, Shen Wang, Weiqi Wang, Zhenshan Wang, Na Feng, Tiecheng Wang, Y Xie, Yongkun Zhao, Feihu Yan, Xianzhu Xia

Nanobody targeting glycan cap confers broad orthoebolavirus neutralization

Xinhui Zhang, Yi Liao, Xiuying Liu, Jingya Zhou, Peixiang Gao, Xuemeng Dong, Shengnan Pan, Huarui Duan, Jun Liu, Xiaojing Chi, Wei Yang

Ebola virus VP35 perturbs type I interferon signaling to facilitate viral replication

Zengguo Cao, Chenchen Liu, Cheng Peng, Yong Ran, Yulin Yao, Gengfu Xiao, Entao Li, Zixi Chen, Xia Chuai, Sa Chiu

Cross-species transmission and host range genes in poxviruses

Chen-Hui Yang, A-Ling Song, Ye Qiu, Xing-Yi Ge

The unique immune evasion mechanisms of the mpox virus and their implication for developing new vaccines and immunotherapies

Dong Fang, Yan Liu, Dou Dou, Bin Su

Current antiviral therapies and promising drug candidates against respiratory syncytial virus infection

Ziheng Feng, Zhengde Xie, Lili Xu

The coronavirus 3CL protease: Unveiling its complex host interactions and central role in viral pathogenesis

Yecheng Zhang, Xinlei Ji, Dan Huang, Gen Lu, Xinwen Chen

Insights into recent advancements in human and animal rotavirus vaccines: Exploring new frontiers

Ahmed H. Ghonaim, Sherin R. Rouby, Wedad M. Nageeb, Ashraf Ahmed Elgendy, Rong Xu, Changsheng Jiang
Noha H. Ghonaim, Qigai He, Wentao Li

HBV and host metabolic crosstalk: Reprogramming pathways for viral replication and pathogenesis

YanYing Yan, Zhiqiang Wei, Min Zheng, Mengji Lu, Xueyu Wang

Crimean-Congo hemorrhagic fever: An emerging threat in Europe

Mohammad Fereidouni (محمدفریدونی), Jens H. Kuhn, David B. Pecor, Dmitry A. Apanaskevich (Апанаскевич Дмитрий Александрович), Kurtesh Sherifi, Jelena Protić (Јелена Протић), Teodora Karevska (Теодора Каревска), Golubinka Boshevska (Голубинка Бошевска), María Paz Sánchez-Seco, Anna Papa (Άννα Παπά), Maryam Keshtkar-Jahromi (مریم کشتکار جهرمی)

HIF-1 α promotes virus replication and cytokine storm in H1N1 virus-induced severe pneumonia through cellular metabolic reprogramming

Xiaoxiao Meng, Yong Zhu, Wenyu Yang, Jiaxiang Zhang, Wei Jin, Rui Tian, Zhengfeng Yang, Ruilan Wang

Pyogenic Acid A, a Small-Molecule PD-1/SHP-2 Inhibitor, Enhances Efficacy of Therapeutic Melanoma Vaccines and Prophylactic Influenza Vaccines

Yan Yan, Yitong Li, Wenyi Mei, Yixin Li, Qian Wang, Honglin Li, Lu Lu, Shibo Jiang

The role of T cells in influenza infection and vaccination

Yuxuan Li, Chenxi Zhu, Yi Wang, Heather Miller, Kamel Benlagha, Maria G. Byazrova, Alexander Filatov, Lu Yang, Chaohong Liu

Antibacterial activity evaluation of a novel K3-specific phage against *Acinetobacter baumannii* and evidence for receptor-binding domain transfer across morphologies

Xiangkuan Zheng, Meihan Liu, Pei Li, Sixiang Xu, Long Chen, Guoxin Xu, Xiaoxiao Pang, Hong Du, Yishan zhen, Xiang Huo, Zhongming Tan, Juan Li, Zhirong Li, Wei Zhang

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Hepatitis B virus (HBV) contributes to the progression of hepatocellular carcinoma (HCC), in part through regulation of the tumor suppressor PTEN. Although the transcriptional control of PTEN by HBV has been well characterized, its post-transcriptional regulation remains largely unclear. In this issue, Lin et al. identify that the m⁵C methyltransferase NSUN2 catalyzes m⁵C modification of PTEN mRNA at chr10:89717756, while the reader protein YBX1 recognizes and binds to the modified transcript, thereby enhancing its stability. Further evidence indicates that viral proteins HBsAg and HBx suppress the expression of NSUN2 and YBX1, leading to reduced m⁵C modification, decreased PTEN mRNA stability, and diminished PTEN protein levels, ultimately promoting HBV-associated HCC progression. The cover image depicts an HBV “army” attacking “Liver City.” The m⁵C modification acts as a protective “shield” for the PTEN “soldiers”. Once this protective shield is pierced by viral invaders, PTEN function is markedly impaired, leaving the entire “Liver City” in peril. (Cover art kindly designed and provided by Prof. Xu Lin, Dr. Shuxiang Wu, and Dr. Mengxian Lin.). See page 547–565 for details.

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Reviews

Crimean-Congo hemorrhagic fever: An emerging threat in Europe

Mohammad Fereidouni, Jens H. Kuhn, David B. Pecor, Dmitry A. Apanaskevich, Kurtesh Sherifi, Jelena Protić, Teodora Karevska, Golubinka Boshevska, María Paz Sánchez-Seco, Anna Papa, Maryam Keshtkar-Jahromi

Research Articles

The epidemiology and disease burden of enterovirus infections among hospitalized children in China: An 8-year national cross-sectional study

Yi Wang, Fei Li, Hui Xu, Yiliang Fu, Guoshuang Feng, Hanwen Zhang, Juan Huang, Zhengde Xie, Xiangpeng Chen

Metagenomic and serological evidence of emerging tick-borne viruses in livestock, humans, and rats in Pakistan

Muhammad Ammar, Yaohui Fang, Muhammad Saqib, Jian Xiao, Awais-Ur-Rahman Sial, Qiaoli Wu, Muhammad Khalid Mansoor, Xiaoli Wu, Muhammad Moaaz, Muhammad Usama Butt, Rehman Hafeez, Kashif Iqbal, Ali Zohaib, Shu Shen, Fei Deng

A comprehensive RNA virome from molluscan transcriptomes reveals extensive diversity and modular genome evolution

Jiaxiang Li, Kewei Chen, Xin Chen, Kaiyang Zheng, Shujuan Sun, Hao Yu, Yue Dong, Ziyue Wang, Yixuan Xu, Andrew McMinn, Yeong Yik Sung, Wen Jye Mok, Li Lian Wong, Yantao Liang, Min Wang

Hepatitis B virus promotes hepatocellular carcinoma progression by disrupting NSUN2/YBX1-mediated m⁵C modification of *PTEN* mRNA

Mengxian Lin, Kunqi Chen, Hang Li, Xinjian Lin, Shuxiang Wu, Xu Lin

Immune profile and mitochondrial alterations driven by age and HIV infection: Associations with T-cell senescence in people with HIV receiving suppressive antiretroviral therapy

Junyan Jin, Xin Zhang, Qianqian Xu, Wei Xia, Hongxia Yan, Hao Wu, Christiane Moog, Tong Zhang, Bin Su

Age-related pharyngeal microbiome and host transcriptomic signatures underlying fever responses in RSV bronchiolitis

Ying Li, Jingyuan Zhang, Haizhou Liu, Muhammad Noman, Muhammad Arif Rizwan, Ismaila Damilare Isiaka, Hebin Chen, Wenqing Li, Nan Zhao, Yan Li, Yamin Sun, Xiaoxia Lu, Di Liu, Yi Yan

Induction of mitochondrial fission and mtDNA leakage via the Smad3/Drp1 axis by PEDV infection activates the TLR9/NF- κ B/IL-1 β inflammatory pathway

Hangao Xie, Jinlian Guan, Fengjie Tian, Ting Xiong, Haixia Feng, Fei Xu, Ziqing Zhou, Dongsheng He, Dingxiang Liu, Ruiai Chen

ASFV pA137R protein triggers inflammatory response by inducing NF- κ B signaling pathway and facilitating NLRP3 inflammasome assembly

Yi Zeng, Xiaohong Liu, Siqi Dong, Hanyu Wu, Li Huang, Changjiang Weng

RNF26 bridges ER stress and autophagy in the clearance of MERS envelope protein

Ziyue Li, Yang Wang, Jingbo Qie, Shuangqu Li, Zhaobing Gao, Hin Chu, Bingqing Xia

Dominant HA motif 131/132-NT shapes the phenotype of avian H9N2 influenza virus by modulating agglutination property, receptor specificity and infectivity in animals

Xue Chen, Jinze Dong, Chuankuo Zhao, Linlin Wang, Xinyang Gao, Zhixin Li, Honglei Sun, Yipeng Sun, Jinhua Liu, Rui Zhang, Juan Pu

Degradation of ACSL3 by influenza A virus shifts unfolded protein response from antiviral defense to viral evasion

Shuoxuan Zhao, Yichao Chen, Tianxin Zhang, Yaoyao Gao, Jing Wu, Fangji Yang, Yongxiang Liu, Xuesong Liu, Nan Qi

EV-A71 induces GSDME-dependent T-cell pyroptosis: A novel mechanism and MeCbl therapeutic potential

Chong Wang, Bingyu Guo, Yilin Li, Xi Zhou, Zongqiang Cui, Yujie Ren

Antiviral activity of Saponin C from *Liriope muscari* against influenza A virus and SARS-CoV-2

Yuhan Gong, Junwen Liu, Wenxuan Ding, Yuxing Yan, Xue Hu, Gary Wong, Huaijie Jia, Zhengxiang Wang, Xin Li, Jiayi Chen, Xin Zhang, Chao Shan, Shuai Xu, Xiaoxia Wang

Therapeutic efficacy of a K1-specific bacteriophage against hypervirulent *Klebsiella pneumoniae* in a mouse infection model

Xiaona Yan, Mengmeng Su, Sixiang Xu, Xiangkuan Zheng, Xiaoyue Li, Peifan Liu, Yilin Fang, Libin Tan, Long Chen, Hong Du, Panpan Tong, Yuxia Zhang, Qinghai Ren, Wei Zhang

A C-type single-domain antibody with protective efficacy against H1N1 via respiratory administration

Bihao Wu, Haiwei Zhang, Xiangxing He, Zhe Zhang, Xiaohui Liu, Rui Gong

Bruton's tyrosine kinase inhibitor BTKi-2 inhibits mpox virus and vaccinia virus infection

Chen Yang, Runchu Zhao, Shuting Huo, Yaqing Zhang, Jingxi Feng, Mingli Gong, Lin Zhu, Conggang Zhang, Linqi Zhang, Jing Xue, Rong Zhang, Qihui Wang, Qiang Ding

Letters

Identification and geographic evolutionary analysis of human pegivirus infection based on metatranscriptomic sequencing

Shan Lu, Pei-Yu Zhen, Cai Bian, Ming-Zhu Zhang, Nan-Nan Yao, Xiao-Ling Su, Yu-Tong Huang, Chen Shan, Jia-Yi Pan, Lin Zhao, Yuan-Chun Zheng, Jia-Fu Jiang, Xiao-Min Zheng, Run-Ze Ye, Wu-Chun Cao

The guanosine nucleotide analog bemnifosbuvir inhibits hepatitis E virus infection in cell and organoid models

Kuan Liu, Yang Wang, Xincheng Li, Yilan Zhao, Luc J.W. van der Laan, Pengfei Li, Qiuwei Pan

A ferritin nanoparticle-displayed spike protein-based ELISA for serological surveillance and immune evaluation of porcine deltacoronavirus

Rui Geng, Hanqin Shen, Duan Li, Shengjin Liu, Siying Zeng, Feng Chen, Hao Zhang, Yongchang Cao

Development of a replicon cell line-based high throughput antiviral assay for screening inhibitors of Mayaro virus

First complete genomic sequencing of recent canine rabies viruses in Sierra Leone suggests cross-border transmission of Africa 2H subclade

Sheng Sun, Abdul Gudush Jalloh, Jinxia Zhang, Shuo Yu, Xiankai Liu, Weidi Xu, Yan Liu, Changchun Tu, Ye Feng

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To present at the 7th International Symposium on Emergin Viral Diseases Oct 19-21, 2016 and the Nature Conference on Viral Infection and Immune Response October 21-23, 2016, both in Wuhan, China							
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If more than one account, give the account # in the far right column for each expense.				25210	49000	463501	CHOSR 5105100 1

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Date	Amount	Converted Amount	Reason	Car,Taxi, Train, Boat, etc.			Acct #
10/5/2016	19.19		Uber to airport				
10/5/2016	1,160.36		fly to China	plane			
10/18/2016	361 RMB		train to Wuhan	train			
10/19/2016	20 RMB		taxi to hotel				
10/21/2016	27 RMB		taxi to 2nd hotel				
10/23/2016	860 RMB		fly to Beijing				
10/23/2016	113 RMB		taxi to hotel				
10/25/2016	99 RMB		taxi to airport				
10/25/2016	34.14		Uber home				

Per Diem-List breakfast, lunch & dinner separately (only if in-state or out of state)

Date	Amount		Country/State				Acct #
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10/18/2016		dinner	Zhangjiajie, China				
10/18/2016		dinner	Wuhan, China				
10/19/2016		breakfast	Wuhan, China				
10/19/2016		lunch	Wuhan, China				
10/20/2016		breakfast	Wuhan, China				
10/21/2016		breakfast	Wuhan, China				
10/22/2016		dinner	Wuhan, China				
10/23/2016		dinner	Wuhan, China				
10/25/2016		breakfast	Beijing, China				
10/25/2016		lunch	Beijing, China				
10/25/2016		dinner	Beijing, China				
10/25/2016		dinner	Detroit, MI				
			two dinners because of the time change coming back to the US!				

361 RMB	361
20 RMB	20
27 RMB	27
860 RMB	860
113 RMB	113
99 RMB	99
700.02 RMB	700.02
700.02 RMB	700.02
578.88 RMB	578.88
1800 RMB	1800
5 RMB	5
	5263.92 RMB

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10/18/2016	171.95		Wuhan, China				
10/19/2016	171.95		Wuhan, China				
10/20/2016	171.95		Wuhan, China				
10/21/2016	700.02 RMB		Wuhan, China				
10/22/2016	700.02 RMB		Wuhan, China				
10/23/2016	578.88 RMB		Beijing, China				

Date	Other Expense	Converted	Description			Acct #
8/10/2016	1800 RMB		Nature Conference registration fee			
8/30/2016	258.00		Chinese Visa w/ processing			
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Cell Host Response to Infection with Novel Human Coronavirus EMC Predicts Potential Antivirals and Important Differences with SARS Coronavirus

Laurence Josset, Vineet D. Menachery, Lisa E. Gralinski, et al.

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RESEARCH ARTICLE

Cell Host Response to Infection with Novel Human Coronavirus EMC Predicts Potential Antivirals and Important Differences with SARS Coronavirus

Laurence Josset,^a Vineet D. Menachery,^{b,c} Lisa E. Gralinski,^{b,c} Sudhakar Agnihothram,^{b,c} Pavel Sova,^a Victoria S. Carter,^a Boyd L. Yount,^{b,c} Rachel L. Graham,^{b,c} Ralph S. Baric,^{b,c} Michael G. Katze^a

Department of Microbiology, School of Medicine, University of Washington, Seattle, Washington, USA^a; Department of Epidemiology^b and Department of Microbiology and Immunology,^c University of North Carolina at Chapel Hill, Chapel Hill, North Carolina, USA

L.J. and V.D.M. contributed equally to this work.

ABSTRACT A novel human coronavirus (HCoV-EMC) was recently identified in the Middle East as the causative agent of a severe acute respiratory syndrome (SARS) resembling the illness caused by SARS coronavirus (SARS-CoV). Although derived from the CoV family, the two viruses are genetically distinct and do not use the same receptor. Here, we investigated whether HCoV-EMC and SARS-CoV induce similar or distinct host responses after infection of a human lung epithelial cell line. HCoV-EMC was able to replicate as efficiently as SARS-CoV in Calu-3 cells and similarly induced minimal transcriptomic changes before 12 h postinfection. Later in infection, HCoV-EMC induced a massive dysregulation of the host transcriptome, to a much greater extent than SARS-CoV. Both viruses induced a similar activation of pattern recognition receptors and the interleukin 17 (IL-17) pathway, but HCoV-EMC specifically down-regulated the expression of several genes within the antigen presentation pathway, including both type I and II major histocompatibility complex (MHC) genes. This could have an important impact on the ability of the host to mount an adaptive host response. A unique set of 207 genes was dysregulated early and permanently throughout infection with HCoV-EMC, and was used in a computational screen to predict potential antiviral compounds, including kinase inhibitors and glucocorticoids. Overall, HCoV-EMC and SARS-CoV elicit distinct host gene expression responses, which might impact *in vivo* pathogenesis and could orient therapeutic strategies against that emergent virus.

IMPORTANCE Identification of a novel coronavirus causing fatal respiratory infection in humans raises concerns about a possible widespread outbreak of severe respiratory infection similar to the one caused by SARS-CoV. Using a human lung epithelial cell line and global transcriptomic profiling, we identified differences in the host response between HCoV-EMC and SARS-CoV. This enables rapid assessment of viral properties and the ability to anticipate possible differences in human clinical responses to HCoV-EMC and SARS-CoV. We used this information to predict potential effective drugs against HCoV-EMC, a method that could be more generally used to identify candidate therapeutics in future disease outbreaks. These data will help to generate hypotheses and make rapid advancements in characterizing this new virus.

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Invited Editor Michael Buchmeier, University of California, Irvine **Editor** Michael Buchmeier, University of California, Irvine

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Address correspondence to Michael G. Katze, honey@u.washington.edu.

In September 2012, a novel human coronavirus, HCoV-EMC, was reported to health authorities from two cases of acute respiratory syndrome with renal failure (1–4). The most recent update by the WHO identified a total of 17 confirmed cases of human infection, including 11 deaths, suggesting a mortality rate of ~65% (5). All of these individuals had a history of recent travel to the Middle East. Identification of clusters of coronavirus cases indicates that HCoV-EMC can be transmitted from human to human (6) and raises concern about a possible outbreak of this virus, similar to the one caused by a related virus, the severe acute respiratory syndrome-related coronavirus (SARS-CoV), in 2002–2003. SARS-CoV, originating in China, spread throughout Asia and to other continents and affected more than 8,000 people (7, 8). The overall mortality during the outbreak was estimated at 9.6% (7).

While the mortality rate of HCoV-EMC cannot be assessed with certainty, it could be more pathogenic than SARS-CoV.

HCoV-EMC belongs to the genus betacoronavirus, as does SARS-CoV. However, HCoV-EMC is more closely related to the bat coronaviruses HKU4 and HKU5 (lineage 2C) than it is to SARS-CoV (lineage 2B) (2, 9). Less than 50% amino acid sequence identity is conserved in the replicase domains between SARS-CoV and HCoV-EMC. Another important difference between the two viruses is that they do not use the same host cell receptor for infection (10). Indeed, it was clearly shown that human angiotensin-converting receptor 2 (hACE2), used by SARS-CoV, is not the HCoV-EMC receptor (10). Dipeptidyl peptidase 4 was recently identified as the HCoV-EMC receptor (11). This receptor is conserved among different species such as bats and humans,

partially explaining the large host range of HCoV-EMC. This was somewhat surprising, as coronaviruses generally show strict host specificity.

While recent identification of the crystal structure of HCoV-EMC protease suggests that a wide-spectrum CoV protease inhibitor could block the catalytic site (12), there is currently no proven antiviral treatment for HCoV-EMC. Viruses rely on host factors to replicate and often hijack cellular processes initiated in response to infection to ensure efficient replication (13). Targeting cellular responses has been shown to inhibit viral replication (13, 14). Furthermore, immunomodulatory drugs that reduce the excessive host inflammatory response to respiratory viruses, as seen with influenza virus infections, have therapeutic benefit (reviewed in reference 15). Several genome-based drug repurposing strategies successfully identified known drugs that could be reused to treat lung cancer, inflammatory bowel disease (16), and influenza virus infection (14). Such an approach has the advantage of accelerating treatment availability, which could be crucial in case of an outbreak of an emerging pathogen.

Overall, differences in viral sequences, host cell receptor, and host range indicate that HCoV-EMC and SARS-CoV may have distinct strategies for interacting with their hosts. This fact could impact treatment strategies. To begin to assess this question, we compared the host response of human cells to HCoV-EMC and SARS-CoV infection using global transcriptomic profiling. Our goal was to gain a rapid and comprehensive assessment of the host response to HCoV-EMC infection that could guide research on this emerging virus. Importantly, we used this information to computationally predict antiviral treatment and identified a broad down-regulation of the antigen presentation pathway that may be important *in vivo* for the development of an adaptive immune response.

RESULTS

SARS-CoV and HCoV-EMC have similar replication kinetics but different cytopathic effects in a human epithelial cell line.

To characterize HCoV-EMC, we sought a cell line that mimics the human airway. Calu-3 cells, derived from epithelial cells lining the human conducting airway, can be differentiated into polarized ciliated cells and permit robust replication of several respiratory viruses, including SARS-CoV, influenza A virus, and respiratory syncytial virus (RSV) (17–20). Therefore, Calu-3 cells were infected with HCoV-EMC using a multiplicity of infection (MOI) of 5, and results were compared with those for Calu-3 cells infected with SARS-CoV Urbani at the same MOI. The viruses replicated to similar levels, with both peaking at $>10^7$ PFU at 24 h postinfection (hpi) (Fig. 1). While SARS-CoV has been previously shown to maintain steady replication and cell viability to 72 hpi (19), HCoV-EMC induced substantial cytopathic effect at 18 to 24 hpi, with significant cell rounding and detaching. Together, these data suggest that although HCoV-EMC and SARS-CoV exhibit similar replication kinetics, they elicit different host responses in lung epithelial cells.

HCoV-EMC induces earlier and different transcriptional changes than SARS-CoV. To assess the global host transcriptional response following infection with HCoV-EMC, samples of infected Calu-3 cells were collected throughout a 24-h time course postinfection. Genes that were differentially expressed (DE) compared to time-matched mock-infected controls were determined using the statistical cutoff of a *q* value of <0.01 and an absolute

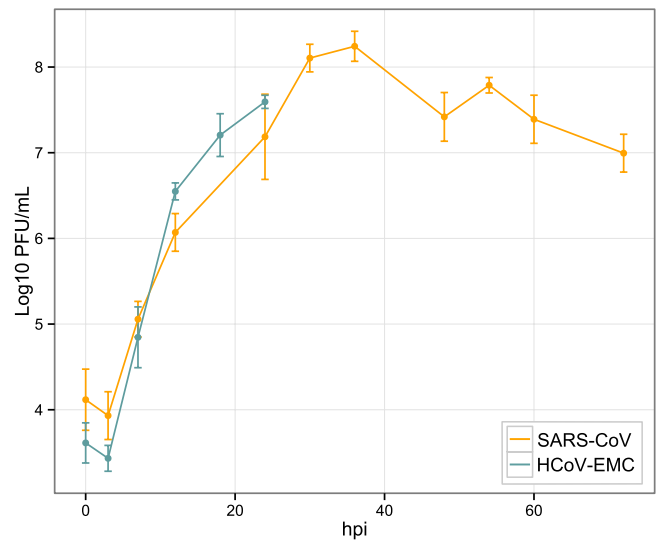


FIG 1 HCoV-EMC replicates at a level similar to that of SARS-CoV in human epithelial cells. Triplicate wells of Calu-3 2B4 cells were infected with HCoV-EMC (MOI, 5). Medium from each well was collected and analyzed by plaque assay for viral growth kinetics in VeroE6 cells. The corresponding cells were harvested for transcriptomic analysis. SARS-CoV titers after infection of Calu-3 2B4 cells at an MOI of 5 were determined using the same method (19). The error bars represent the standard deviations among triplicate cell samples.

$\log_2(\text{FC})$ of >1 . These genes were compared to DE genes from Calu-3 cells infected with SARS-CoV across a 72-h time course using the same statistical cutoff (Fig. 2).

As previously observed (19), SARS-CoV is able to replicate actively with a surprisingly small number of significant transcriptional changes before 24 hpi (from 5 DE genes at 0 hpi to 47 genes at 12 hpi) (Fig. 2A). Similarly, HCoV-EMC induced fewer transcriptional changes before 12 hpi than after. However, HCoV-EMC replication at early times postinfection induced more changes than SARS-CoV, with the number of DE genes ranging from 28 at 0 hpi to 206 genes at 12 hpi (Fig. 2A). At later times postinfection, a massive host response was observed during HCoV-EMC infection, with 6,532 DE genes at 18 hpi and 11,664 genes at 24 hpi, while SARS-CoV induced changes of only 792 genes at 24 hpi with maximum changes at 48 and 54 hpi of 6,496 and 6,498 genes, respectively.

To evaluate the similarity of transcriptional dysregulation between HCoV-EMC and SARS-CoV, we determined the percentage of overlap among DE genes changing in the *same* direction at each time point (Fig. 2B). The intersection between up- or down-regulated DE genes for each condition was calculated separately and then averaged to determine the percentage of intersecting genes (Fig. 2B). The overlap between signatures at late times postinfection for a single virus was very high; for example, 89% of the genes DE by HCoV-EMC at 18 hpi were also DE at 24 hpi, and on average 77% of the DE genes at 24 hpi with SARS-CoV were also DE at later times postinfection. However, the overlap between SARS-CoV and HCoV-EMC at the same time point was low; for example, only 3% of the DE genes in response to HCoV-EMC at 24 hpi were also DE by SARS-CoV at this time point. Of note, the intersection of DE genes between the two infections was higher when later times postinfection for SARS-CoV were compared with earlier time points for HCoV-EMC. On average 22% of the

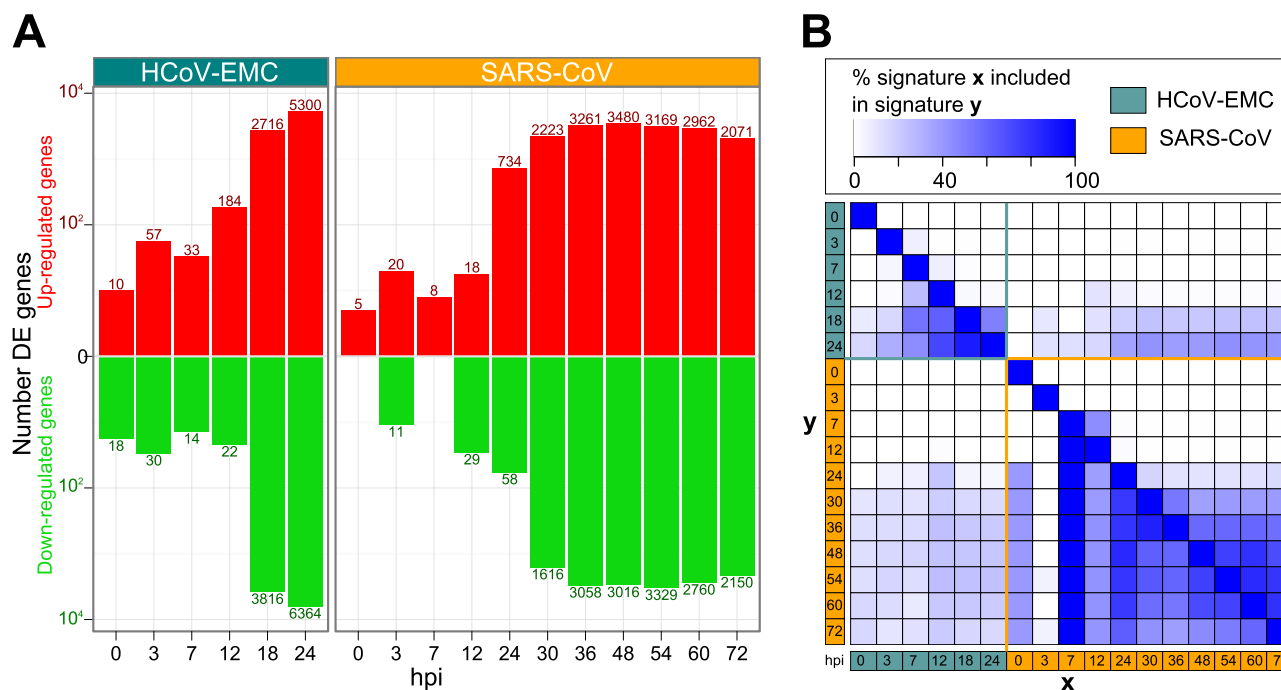


FIG 2 HCoV-EMC induces more and different transcriptional changes than SARS-CoV at similar times postinfection. (A) Number of up-regulated (red) and down-regulated (green) differentially expressed (DE) genes after infection with HCoV-EMC and SARS-CoV compared to time-matched mock-infected controls. The criterion used for differential expression analysis is a q value of <0.01 as determined by Limma's empirical Bayes moderated t test and a $|\log_2 \text{FC}|$ of >1 . (B) Percentage of DE genes under the condition shown on the x axis that intersect with DE genes under the condition shown on the y axis. To identify overlap among genes changing in the same direction, up- and down-regulated signatures are intersected separately, and the average of the two percentages is shown by a white-to-blue gradient (0% to 100%).

HCoV-EMC signatures from 12 to 24 hpi overlapped the signatures of SARS-CoV from 36 to 72 hpi. Together, these results indicate that HCoV-EMC induced both a more robust and a largely different host response compared to that induced by SARS-CoV at similar times postinfection. However, changes induced from 12 to 24 hpi after HCoV-EMC were more similar to changes induced late after SARS-CoV infection (24 to 72 hpi).

HCoV-EMC massively dysregulates the host transcriptome at late times postinfection. At late times postinfection, HCoV-EMC induced drastic changes in the host transcriptome with 12,392 DE genes at 18 hpi and/or 24 hpi. To characterize this late signature, we compared the $\log_2$ fold change ($\log_2 \text{FC}$) expression values of these 12,392 genes after infection with SARS-CoV or HCoV-EMC (Fig. 3 and www.systemsvirology.org). There were 3,474 genes (28%) expressed similarly to those in SARS-CoV-infected samples at the same or later times postinfection and 8,918 genes (72%) expressed differently than during SARS-CoV infection. These genes were further clustered according to their expression pattern in HCoV-EMC infected cells (clusters I and III contain genes up-regulated after HCoV-EMC infection at 18 to 24 hpi; clusters II and IV contain down-regulated genes). Enrichment in canonical pathways for each of this cluster was performed and is shown Fig. 3B.

Genes that were up-regulated by both HCoV-EMC and SARS-CoV (cluster I), though later by SARS-CoV than by HCoV-EMC, were primarily related to viral recognition and the activation of innate immune pathways: the IL-17-related pathway and activation of interferon regulatory factor (IRF) by cytosolic pattern recognition receptors. Genes down-regulated by both viruses (cluster II) were related to metabolism.

Genes specifically up-regulated by HCoV-EMC were statistically enriched in only 2 pathways: cAMP-mediated signaling and protein ubiquitination. Because ubiquitination is involved in the innate immune antiviral response (21), this could represent an interesting mechanism to explore further. Finally, genes specifically down-regulated after HCoV-EMC infection were largely related to the antigen presentation pathway. In addition, the other identified canonical pathways are strongly related to lymphocyte signaling processes. Together, these data suggest that HCoV-EMC may quickly move to interfere with elements of the adaptive immune response, in contrast to SARS-CoV.

The antigen presentation pathway is broadly down-regulated after HCoV-EMC infection. As down-regulation of the antigen presentation pathway may have important implications for the development of the adaptive response, we more closely examined changes in this pathway after infection with HCoV-EMC (Fig. 4). Twenty-two genes related to major histocompatibility complex (MHC) class I, MHC class II, or antigen presentation were found to be down-regulated after HCoV-EMC infection (Fig. 4A), while in contrast, the vast majority of these genes were up-regulated by SARS-CoV infection after 36 hpi (Fig. 4B). Interestingly, transcriptional regulators of MHC class I (*NLR5*) and MHC class II (*CIITA*) were transiently up-regulated early after HCoV-EMC infection (at 12 and 0 hpi, respectively). Other genes were down-regulated starting at 12 hpi. Importantly, both MHC class I genes (*HLA-A*, *-B*, *-C*, *-E*, and *-G*) and class II genes (*HLA-DMB*, *-DPA1*, *-DPB1*, *-DQA1*, *-DRA*, *-DRB1*, *-DRB3*, *-DRB4*, and *-DRB5*) had decreased expression values after infection. Several genes from the MHC I pathway, including proteasome genes (*PSMB8* and *PSMB9*), genes from the peptide-loading complex

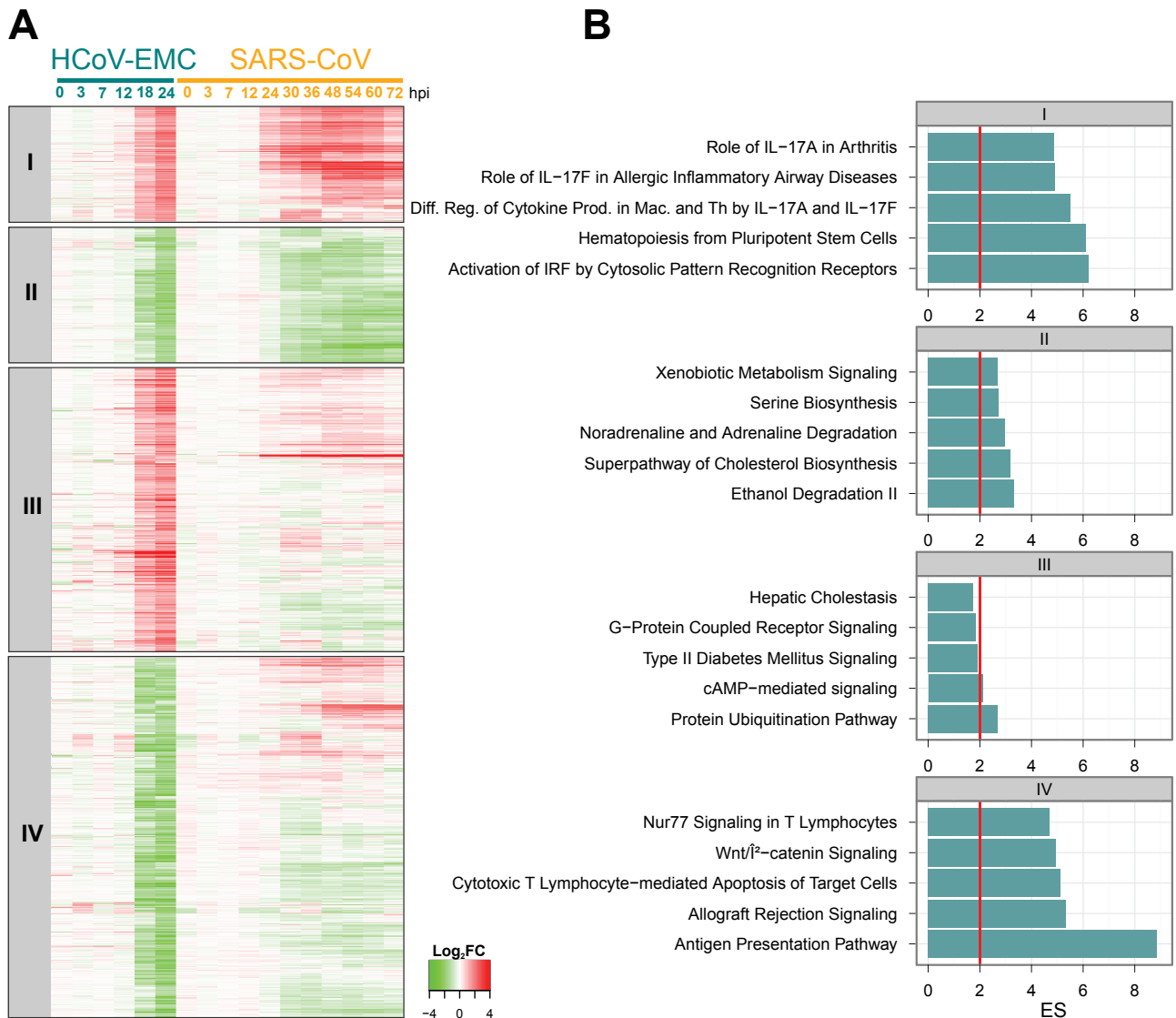


FIG 3 HCoV-EMC massively dysregulates the host transcriptome at late times postinfection and triggers both similar and unique pathways compared to those induced by SARS-CoV. (A) Heatmap depicting the expression values of 12,392 genes DE after infection with HCoV-EMC at late times postinfection (union of DE genes at 18 and 24 hpi). Genes were clustered into four main sets: set I includes 1,599 genes that are significantly up-regulated after infection with both HCoV-EMC and SARS-CoV; set II includes 1,875 genes that are significantly down-regulated after infection with both HCoV-EMC and SARS-CoV; set III includes 3,922 genes that are significantly up-regulated after infection with HCoV-EMC but not DE with SARS-CoV; and set IV includes 4,996 genes that are significantly down-regulated after infection with HCoV-EMC but not DE with SARS-CoV. (B) For each of the four clusters, the top 5 enriched canonical pathways are reported. Enrichment score (ES) was defined as $-\log_{10}(P \text{ value})$ of enrichment. Red lines depict the limit of significance ($P < 0.01$).

(*PDIA3* and *TAPBP*), and *B2M*, were down-regulated, as well as the gene for the invariant chain (*CD74*), which belongs to the MHC II pathway. Down-regulation of genes within MHC I and II pathways was confirmed by quantitative reverse transcription-PCR (RT-PCR), with all 9 genes tested having significantly decreased expression in HCoV-EMC samples (Fig. 4C). Together, the data show that HCoV-EMC and SARS-CoV induce opposite regulation of the entire antigen presentation pathway.

Early and sustained transcriptional changes may be reverted by kinase inhibitors and glucocorticoids. With the goal of identifying possible drugs that will modulate the host response throughout infection and from early times postinfection, we focused on characterizing the early transcriptional changes induced

by HCoV-EMC that remained stable throughout the infection. Among the 348 genes DE early after infection (at 0, 3, 7, and/or 12 hpi), 207 (59%) remained dysregulated, with the same pattern at later times postinfection. We chose to focus on this 207-gene signature to avoid transient events that were specific to one time postinfection and to exclude genes with inconsistent expression patterns across the course of infection. Expression values for these genes are displayed in Fig. 5A and are available at www.systems.virology.org. This early signature was enriched in genes related to the inflammatory response with IL-17, tumor necrosis factor 2 (TNFR2)-related pathways, and predicted activation of chemotaxis of leukocytes (see Table S1 in the supplemental material). None of the 207 genes were DE early after SARS-CoV infection;

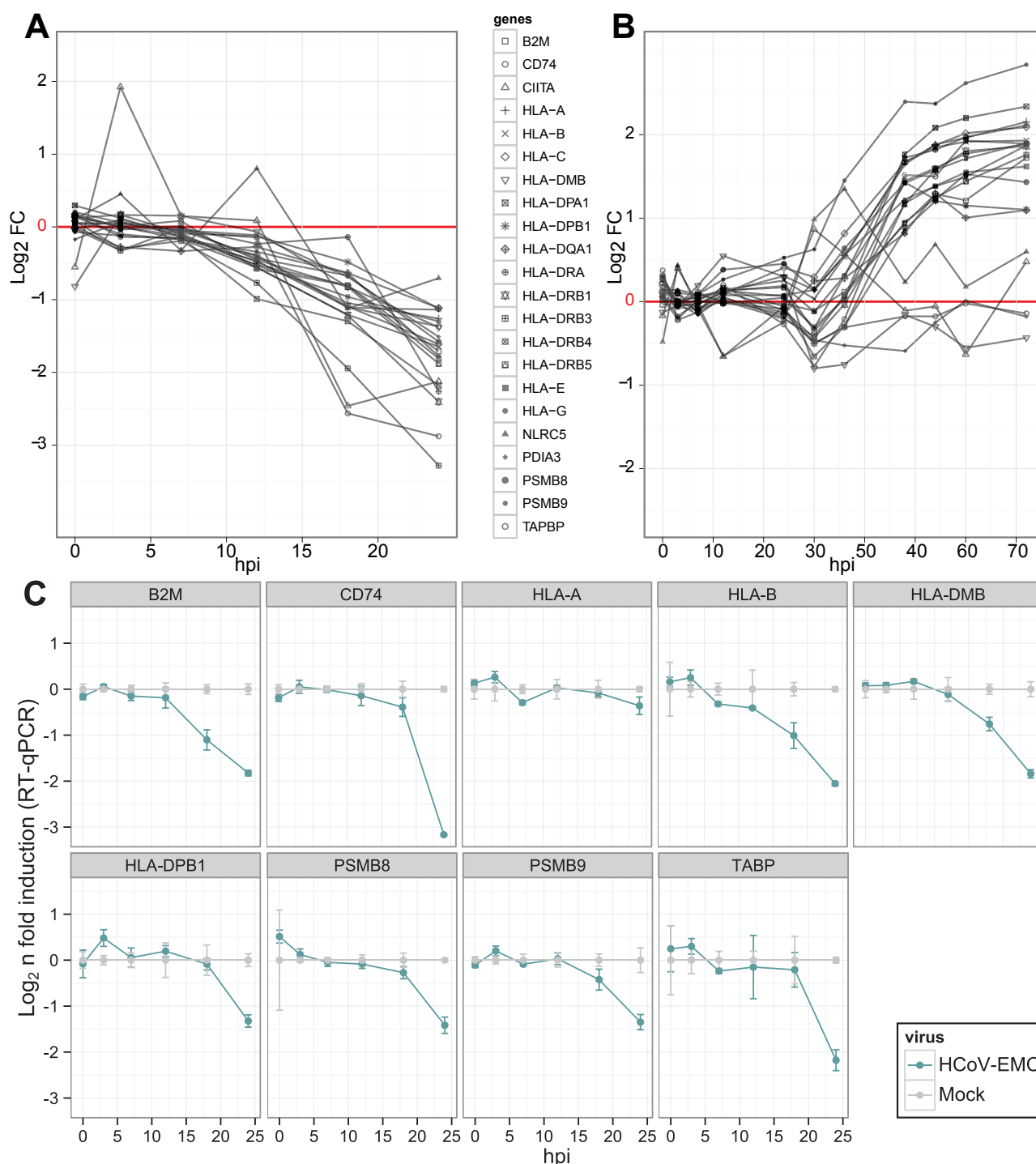


FIG 4 The antigen presentation pathway is specifically down-regulated after infection with HCoV-EMC. (A) Temporal gene expression changes of the 22 genes belonging to the antigen presentation pathway specifically down-regulated after HCoV-EMC infection. (B) Temporal changes for the same set of genes after SARS-CoV infection. Note that the time scale and log₂ FC ranges are not the same in panels A and B. (C) Quantitative RT-qPCR measurement of the antigen presentation pathway genes expression following HCoV-EMC infection.

however, expression of 51 genes (24.5%) was changed after 24 hpi. This subset of 51 genes was enriched in cell viability molecules, glucocorticoid receptor signaling, and IL-17-related pathways.

In an effort to identify potential drugs that could block the host response to HCoV-EMC, we used the early 207-gene signature

and IPA (Ingenuity pathway analysis) upstream regulator analysis (see Materials and Methods) to identify the upstream regulators that may be responsible for gene expression changes observed early after infection. Upstream regulators are defined as any molecule that can affect the expression of another molecule, including

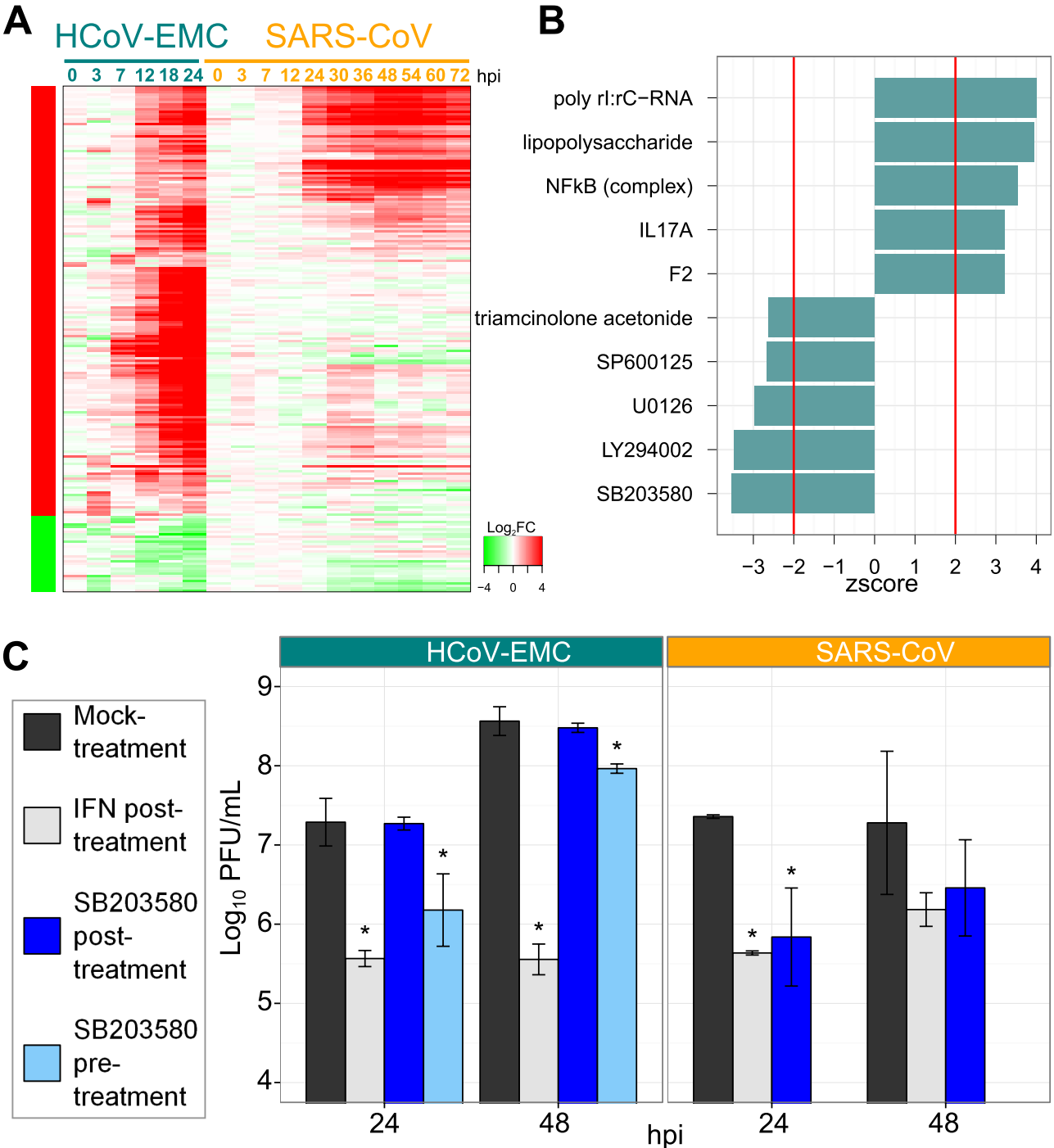


FIG 5 Expression values and major upstream regulators for the 207 genes dysregulated early and constantly after infection with HCoV-EMC. (A) Heatmap depicting the expression values of 207 genes whose expression changed early after infection with HCoV-EMC (at 0, 3, 7, and/or 12 hpi) and remained up- or down-regulated later in infection (18 and 24 hpi). The color key on the left indicates the direction of changes across infection, with red depicting genes significantly up-regulated at at least one time postinfection and green showing genes significantly down-regulated. Genes were clustered based on their expression values across samples using Pearson correlation and complete linkage function. (B) Top 5 activated upstream regulators and top 5 inhibited upstream regulators of the early signature. The prediction of activation state is based on the global direction of changes of the 207 genes throughout infection with HCoV-EMC. Red lines depict the limit of significance ($|z\text{ score}| > 2$). (C) Analysis of HCoV-EMC and SARS-CoV replication following SB203580 pre- or posttreatment (5 μM). IFN- α posttreatment was used as a reference. *, $P < 0.01$ (Student's t test).

transcription factors, cytokines, micro-RNAs and drugs. The activation state for each regulator was predicted based on global direction of changes throughout infection for previously pub-

lished targets of this regulator. The predicted top five activated and top five down-regulated regulators are shown in Fig. 5B. The top five activated upstream regulators included genes and mole-

cules that are known to induce the activation of inflammatory genes that were also found up-regulated in the early signature. The top predicted inhibited regulators included four kinase inhibitors (SB203580, LY294002, U0126, and SP600125) and one corticosteroid (triamcinolone acetonide). These molecules are known to down-regulate the same genes that were up-regulated early and across HCoV-EMC infection. In addition, several kinase inhibitors (including SB203580, LY294002, and U0126) and a glucocorticoid (dexamethasone) were also predicted to be negative regulators of genes changed similarly after SARS-CoV and HCoV-EMC infection at late times postinfection (see Table S2 in the supplemental material). Therefore, we hypothesize that treating cells with these drugs might partially revert CoV signatures and inhibit deleterious host responses and/or viral replication in the case of both SARS-CoV and HCoV-EMC.

In silico and in vitro evidence for kinase inhibitors as potential anti-CoV. To test these hypotheses, we first analyzed whether cells treated with identified kinase inhibitors have gene expression profiles opposite to the one induced after viral infection. To this end, we used Connectivity Map (cmap), which is a database of more than 1,309 drug transcriptional signatures in several cell lines (22). This data-driven tool allows the identification of molecules that induce similar or opposite transcriptional changes relative to the query signature, based on their connectivity scores. The connectivity score is a value between +1 and -1, where a high positive score indicates that the drug induces changes similar to those induced by viral infection, while a high negative score indicates that the drug reverses the expression of the HCoV-EMC signature. Cmap includes transcriptional profiles of several kinase inhibitors, including two compounds that were predicted to be potential negative regulators of viral response in IPA upstream regulator analysis (SB203580 and LY294002). SB203580 had a connectivity score of -0.733 in MCF7 cells (Data set S1 in the supplemental material), and LY294002 had negative scores in 4 of the 5 cell lines tested in cmap (-0.281 in HL60, -0.146 in MCF7, -0.252 in PC3, and -0.811 in SKMEL5), indicating that these two drugs reversed the expression profile of HCoV-EMC signature. Other related kinase inhibitors present in cmap are U0125 (a derivative of U0126) and SB202190, which both had negative scores in PC3 cells (-0.649 and -0.406, respectively).

To further validate the potential effectiveness of identified kinase inhibitors, we evaluated the ability of the top predicted negative upstream regulator, SB203580, to interfere with viral replication (Fig. 5C). Importantly, this kinase inhibitor was predicted to regulate genes that were DE similarly by SARS-CoV and HCoV-EMC at late times postinfection (see Table S2 in the supplemental material) and could therefore inhibit both viruses' replication. Treating cells with 5 μ M SB203580 following SARS-CoV infection resulted in a significant decrease of 20% in the $\log_{10}$ viral titer at 24 hpi ($P < 0.01$); these replication levels are similar to those in interferon (IFN)-treated cells. SB203580 was less effective against EMC-CoV, showing no efficacy with posttreatment; however, pretreatment of infection resulted in significant decreases of 15% and 7% of the $\log_{10}$ viral titer, at 24 and 48 hpi, respectively ($P < 0.01$). Efficacy against SARS-CoV can be explained by the fact that all genes that were DE after SARS-CoV infection were predicted to be regulated by kinase inhibitors (cluster I and II genes [Fig. 3] and additional genes specific to SARS-CoV [data not shown]), while the 8,918 genes specific to HCoV-EMC (clusters III and IV [Fig. 3]) did not include any kinase inhibitor in their upstream

negative regulators (see Table S2). In addition, host response dynamics to SARS-CoV and HCoV-EMC were different, with a delayed and more limited response to SARS-CoV allowing SB203580 posttreatment to be effective. In contrast, EMC-CoV rapidly induced host expression changes and thus required SB203580 pretreatment for measurable effect. As genes specific to HCoV-EMC were predicted to be negatively regulated by other classes of molecules (like gemfibrozil, which targets PPAR α ; $z = 2.96$), it will be important to determine whether using such molecules in combination with kinase inhibitors like SB203580 could provide a better inhibition of viral replication. Together, these data demonstrate the efficacy of SB203580 against two unique CoVs and validate *in silico* approaches to predict effective drug treatment for emergent viruses.

DISCUSSION

HCoV-EMC was isolated from a patient who died from an acute respiratory disease similar to that caused by SARS-CoV. However, there are several indicators that the host responses to these two viruses may be significantly different. Several cases of HCoV-EMC infection have resulted in renal failure, which has rarely been observed in SARS-CoV infection. In addition, SARS-CoV and HCoV-EMC do not use the same cell receptor, and there are important differences in their genomic sequences. This study adds strength to the assertion that "HCoV-EMC is not the same as SARS-CoV" (23). Indeed, even though we identified specific characteristics of the SARS-CoV response in the HCoV-EMC signatures, HCoV-EMC induced robust and specific transcriptional responses that were distinct from those induced by SARS-CoV, including the broad down-regulation of MHC molecules.

This study is the first global transcriptomic analysis of the cellular response to HCoV-EMC infection. Kindler et al. performed RNA-Seq on human airway epithelium (HAE) cells infected with HCoV-EMC (24). However, their analysis was focused on viral sequences and did not include a genome-wide analysis of the host response. They did, however, use RT-qPCR (quantitative PCR) to compare expression levels of a set of 15 genes, including IFN, RNA sensor molecules, and IFN-stimulated genes (ISGs), following infection with HCoV-EMC, SARS-CoV, or HCoV-229E (MOI 0.1). In our study, we confirm that SARS-CoV and HCoV-EMC induce a similar up-regulation of RNA sensor molecules, such as *RIGI*, *MDA5*, and two of three genes of ISGF3 (*IRF9* and *STAT1*) (genes in cluster I [Fig. 3]). Of note, HCoV-EMC titers were up to 10^2 -fold higher than those of SARS-CoV in HAE cells (24), whereas we observed similar viral replication of the two CoVs in Calu-3 cells. Lower replication of SARS-CoV in HAE cells might be explained by the mixed cell population in these primary cultures, with likely nonuniform expression of SARS-CoV receptor (*ACE2*). In contrast, Calu-3 2B4 cells used in our study are a clonal population of Calu-3 cells sorted for *ACE2* expression which support high replication of SARS-CoV. In addition, while Kindler et al. noted the absence of induction of *IFN- β* at 3, 6, and 12 hpi (24), we found a specific up-regulation of *IFN- α 5* and *IFN- β 1* by HCoV-EMC at 18 and 24 hpi (genes in cluster III) and an up-regulation of *IFN- α 21* by both SARS-CoV and HCoV-EMC at 24 hpi (cluster I) (expression values for all DE genes are available at <http://www.systemsvirology.org>). These data illustrate that HCoV-EMC and SARS-CoV both trigger the activation of pattern recognition receptors but may subsequently induce different levels of IFN. Moreover, there were stark differences in global downstream ISG

expression following infection with SARS-CoV or HCoV-EMC; this analysis is discussed in detail elsewhere (V. D. Menachery et al., submitted for publication).

Activation of similar innate viral-sensing pathways by HCoV-EMC and SARS-CoV is not surprising given the conservation of this mechanism to detect foreign RNA and familial relationships of the viruses. We also found that both viruses induced proinflammatory cytokines related to IL-17 pathways. It has previously been shown that IL-17A-related gene expression exacerbates severe respiratory syncytial virus (RSV) or influenza virus infection (25, 26). IL-17A was predicted to be activated throughout infection with HCoV-EMC and may induce immune-mediated pathology that possibly contributes to a high mortality rate. IL-17A is known to be produced by T-helper cells, but its expression in Calu3 cells was increased up to 2-fold at 24 hpi after HCoV-EMC infection. Interestingly, IL-17C and IL-17F, which can be produced by epithelial cells under certain inflammatory conditions and which activate pathways similar to IL-17A-mediated responses (27), were increased earlier and to a greater extent following HCoV-EMC infection (up to 3-fold at 18 hpi for IL-17C and 4-fold at 7 hpi for IL-17F). Therefore, further study of the IL-17 response may provide interesting targets to limit lung injury (26).

A main difference between responses to HCoV-EMC and SARS-CoV was the specific down-regulation of the antigen presentation pathway after HCoV-EMC infection. In contrast, these genes were found to be up-regulated after SARS-CoV infection. Several viruses have evolved mechanisms to inhibit both the MHC class I (reviewed in references 28 and 29) and class II (reviewed in reference 30) pathways. While expression of MHC class II is usually limited to professional antigen-presenting cells, human lung epithelial cells constitutively express this complex (31). Our data demonstrated down-regulation of the MHC class II transactivator (*CIITA*) after HCoV-EMC infection, a finding that possibly explains decreases in MHC class II molecule expression; this is a common viral strategy used to block that pathway (30). MHC class II inhibition can prevent class II-mediated presentation of endogenous viral antigens produced within infected cells and impair the adaptive immune response. Similarly, MHC class I genes were also down-regulated after HCoV-EMC infection; decreasing expression of MHC class I can attenuate CD8 T-cell-mediated recognition of infected cells and could allow immune evasion by HCoV-EMC. Finally, *PSMB8* and *PSMB9*, parts of the immunoproteasome, were also down-regulated by HCoV-EMC; these components replace portions of the standard proteasome and enhance production of MHC class I binding peptides (32). In their absence, proteins targeted for degradation may not generate peptides that robustly bind MHC class I, thus limiting their presentation. Down-regulation of *PSMB8* and *PSMB9* could counteract the host response to viral infection, including up-regulation of ubiquitins and ubiquitin ligases observed during HCoV-EMC infection (Fig. 3B) that may ineffectively target viral protein for degradation. Together, the inhibition of MHC class I and II as well as immunoproteasome construction may have an important impact on the *in vivo* adaptive immune response against HCoV-EMC.

While there is no proven effective antiviral therapy against SARS-CoV (33), several molecules have *in vitro* antiviral activity, including ribavirin, lopinavir, and type I IFN, but their benefits for patients are unclear (33). IFN- α pretreatment of cells has been shown to inhibit HCoV-EMC replication (24), but no direct antiviral therapies have been reported. Targeting host factors impor-

tant for the virus, instead of the virus itself, has been investigated for HIV (34) and influenza virus (13). For example, **inhibiting upstream regulators (such as NF- κ B) that control the host response to influenza virus infection has been shown to reduce virus replication *in vitro* and in mice** (35). Inhibition of immunophilins that interact with the viral nonstructural protein 1 (Nsp1) resulted in potent inhibition of SARS-CoV replication (36, 37). In this study, we characterized upstream regulators predicted to be activated (e.g., NF- κ B and IL-17, which could be targeted with specific inhibitors) and upstream regulators predicted to be inhibited.

The top five inhibited regulators included one glucocorticoid and four kinase inhibitors; these drugs may be able to directly block part of the host response and impact viral replication/pathogenesis. Among them, LY294002, a potent inhibitor of phosphatidylinositol 3 kinase (PI3K), has known antiviral activity, inhibiting the replication of influenza virus (38), vaccinia virus (39), and HCMV (40). SB203580, an inhibitor of p38 MAPK, is also an effective antiviral against the encephalomyocarditis virus (41), RSV (42), and HIV (43). LY294002 and SB203580 were also identified in Connectivity Map, a database of drug-associated gene expression profiles (22), as molecules reversing components of the HCoV-EMC gene expression signature. Finally, SB203580 showed promising antiviral results against both HCoV-EMC and SARS-CoV in our *in vitro* assay (Fig. 4C). Further extensive studies, including dose-response tests and tests of other kinase inhibitors, are ongoing. Nonetheless, these results validate our genome-based drug prediction, which allows rapid identification of effective antivirals. Despite central roles of PI3K and MAPK pathways in regulating multiple cellular processes, many kinase inhibitors targeting these pathways have been shown to be safe and well tolerated *in vivo* (reviewed in references 44 and 45). It has been hypothesized that mitogenic MAPK and survival PI3K/Akt pathways may be of major importance only during early development of an organism and may be dispensable in adult tissues (13). Several drugs targeting JNK, PI3K, and MEK have shown promising therapeutic potential in humans against a variety of diseases, including cancer and inflammatory disorder (44, 45). p38 MAPK inhibitors have also been evaluated in humans, but the first generation of molecules, including SB203580, has a high *in vivo* toxicity (liver and/or central nervous system). However, development of novel nontoxic inhibitors (e.g., ML3403) (46), more selective molecules (e.g., AS1940477) (47), and administration via inhalation (48) are promising strategies for use of this class of inhibitor for treatment of pulmonary disease. Overall, these results indicate that kinase inhibitors could be used as broad anti-CoV agents which might be combined with other host-targeting molecules, like peroxisome proliferator-activated receptor α (PPAR α) agonists, to better inhibit HCoV-EMC replication.

In conclusion, using global gene expression profiling, we have shown that HCoV-EMC induces a dramatic host transcriptional response, most of which does not overlap the response induced by SARS-CoV. This study highlights the advantages of high-throughput “-omics” to globally and efficiently characterize emerging pathogens. The robust host gene expression analysis of HCoV-EMC infection provides a plethora of data to mine for further hypotheses and understanding. Host response profiles can also be used to quickly identify possible treatment strategies, and we anticipate that host transcriptional profiling will become a gen-

eral strategy for the rapid characterization of future emerging viruses.

MATERIALS AND METHODS

Cells and virus. Calu-3 2B4 cells, a clonal population of Calu-3 cells sorted for ACE2 expression, were grown in minimum essential media (MEM; Gibco) supplemented with 20% fetal bovine serum (HyClone) and 1% antibiotic antimycotic (Gibco). Viral titrations and propagation HCoV-EMC were performed in VeroE6 cells using standard methods. Human coronavirus EMC 2012 (HCoV-EMC) was received from Bart L. Haagmans (Erasmus Medical Center, Rotterdam, Netherlands) via MTA. Experiments with SARS-CoV were previously performed under the same conditions using the same cells (19).

Calu-3 cell infections. All work was performed in a biosafety level 3 (BSL3) facility supported by redundant exhaust fans, and personnel protective equipment was worn, including Tyvek suits, hoods, and HEPA-filtered powered air-purifying respirators as previously described (49). Cells were washed with phosphate-buffered saline (PBS) and inoculated with virus at an MOI of 5 or mock diluted in PBS for 40 min at 37°C. Following inoculation, cells were washed 3 times, and fresh medium was added to signify time zero. Triplicate samples of mock-infected and virus-infected Calu-3 2B4 cells were harvested between 0 and 72 hpi.

RNA isolation and microarray processing. RNA isolation from Calu-3 2B4 cells, subsequent hybridization to Agilent 4×44K human HG arrays, and processing of raw data were performed as previously described (18). We analyzed triplicates for each time postinfection except for 12 hpi, for which one replicate did not pass RNA quality control and was therefore excluded. For direct comparison with SARS-CoV-infected cells, raw data from HCoV-EMC experiments were quantile normalized together with the SARS-CoV data set (GEO series accession number GSE33267). All probes were required to meet Agilent Feature Extraction QC criteria for all replicates at at least one infection time point (33,773 probes passed QC filtering). For each sample, a log₂ fold change (log₂ FC) value was calculated as the difference between log₂ normalized data for this sample and the average of log₂ normalized data for time- and data set-matched mock-infected samples.

Statistical analysis. Differential expression was determined by comparing SARS-CoV- or HCoV-EMC-infected replicates to time- and data set-matched mock-infected controls, based on a linear model fit for each probe using the R package Limma (50). Criteria for differential expression were an absolute log₂ FC of 1 and a *q* value of <0.01 calculated using a moderated *t* test with subsequent Benjamini-Hochberg correction. Differentially expressed (DE) genes after HCoV-EMC infection at early times postinfection were defined as all genes DE at 0, 3, 7, or 12 hpi, and genes DE at late times postinfection were defined as all genes DE at 18 or 24 hpi. To identify genes with similar patterns of variation at early and late times postinfection, early and late signatures were intersected considering up-regulated and down-regulated genes separately and then combined to define the signature of 207 stable genes. To cluster the genes DE at late times postinfection following HCoV-EMC infection, differential expression was also calculated directly between SARS-CoV- and HCoV-EMC-infected samples using the same criteria. A comparison of similar times postinfection was performed, except for HCoV-EMC-infected samples at 18 hpi, which were compared to SARS-CoV samples at 24 hpi. HCoV-EMC samples at 24 hpi were compared with SARS samples at 24 hpi and later times postinfection (30, 36, 48, 54, 60, and 72 hpi). Genes similarly changed between HCoV-EMC and SARS-CoV (cluster I and II) were defined as genes DE by both viruses compared to their time-matched mocks and that were also not differentially changed between HCoV-EMC and SARS-CoV in at least one of the previously listed comparisons. Genes of cluster III and IV were genes DE at late times postinfection following HCoV-EMC infection that were not similarly changed between HCoV-EMC and SARS-CoV. To further cluster the genes based on their expression value after HCoV-EMC infection, log₂ FC values at 18 and 24 hpi were averaged, and clusters I and III were genes with average log₂ FC

values of >0, while cluster II and IV genes had average log₂ FC values of <0.

Functional enrichment and upstream regulator analysis. Functional analysis of statistically significant gene expression changes was performed using Ingenuity Pathways Knowledge Base (IPA; Ingenuity Systems). For all gene set enrichment analyses, a right-tailed Fisher's exact test was used to calculate a *P* value determining the probability that each biological function assigned to that data set was due to chance alone. All enrichment scores were calculated in IPA using the probes that passed our QC filter as the background data set.

Upstream regulator analysis, which was used to predict regulators and infer their activation state, is based on prior knowledge of expected effects between regulators and their known target genes according to the IPA database. A *z* score is calculated and determines whether gene expression changes for known targets of each regulator are consistent with what is expected from the literature (*z* > 2, regulator predicted to be activated) or are anti-correlated with the literature (*z* < 2, regulator predicted to be inhibited).

Quantitative reverse transcription PCR (RT-PCR). RNA was reverse transcribed using the QuantiTect reverse transcription kit (Qiagen). The resulting cDNA samples were diluted 50×. Primer sets for SYBR green quantitative RT-PCR were designed using Primer3 (51). Primer sequences are available in Table S3 in the supplemental material. Relative gene expression in infected samples compared to that in mock-infected cells was calculated using the 2^{−ΔΔCT} method (52), using the *MYL6* gene as a calibrator, as the expression of *MYL6* did not significantly change in HCoV-EMC-infected cells in the microarray data.

Connectivity map. To determine whether some drugs can reverse the HCoV-EMC infection signature, we used the publicly available Connectivity Map (cmap) database (build 02) (22). Cmap is a collection of genome-wide transcriptional data from cultured human cells treated with 1,309 different compounds. We used the list of 207 DE genes that are stable after infection with HCoV-EMC. Agilent probes were mapped to Affymetrix U133A probe sets using the BioMart ID converter tool (53) in order to query the cmap database. Results were filtered based on their negative connectivity enrichment score.

Antiviral *in vitro* assay. For *in vitro* evaluation of the p38 MAPK inhibitor SB203580 (Sigma), VeroE6 cells were incubated for 4 h with the drug at 5 μM prior infection with HCoV-EMC at an MOI of 0.01 (pretreatment condition), medium was replaced during the 40-min infection, and medium containing SB203580 was added back following inoculation (54). For the posttreatment condition, cells were treated with SB203580 at 5 μM or type I IFN (100 U/ml; PBL Interferon Source) at 0 hpi following the infection inoculation.

Publicly available data. Normalized matrixes and expression values can be found at <https://www.systemsvirology.org/project/home/Data%20%26%20Resources/Experimental%20Metadata/HCoV-EMC%20infection%20in%20Calu-3%20cells/begin.view?>. The other data set utilized was Calu-3 cells infected with SARS-CoV at MOI 5 (GSE33267).

Microarray data accession numbers. Raw microarray data have been deposited in NCBI's Gene Expression Omnibus under accession number GSE45042.

SUPPLEMENTAL MATERIAL

Supplemental material for this article may be found at <http://mbio.asm.org/lookup/suppl/doi:10.1128/mBio.00165-13/-DCSupplemental>.

Table S1, DOCX file, 0.1 MB.

Table S2, DOCX file, 0.1 MB.

Table S3, DOCX file, 0.1 MB.

Data set S1, XLS file, 0.5 MB.

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