Wu, Hung-Yi

Professor
Professional specialty: Molecular Virology, Virus Pathogenesis, Coronavirus, RNA Viruses
Courses:
Undergraduate: Veterinary Pathology.
Graduate: Advanced Pathobiology, Virus Replication, Pathogenesis of Virus.
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Educational Background

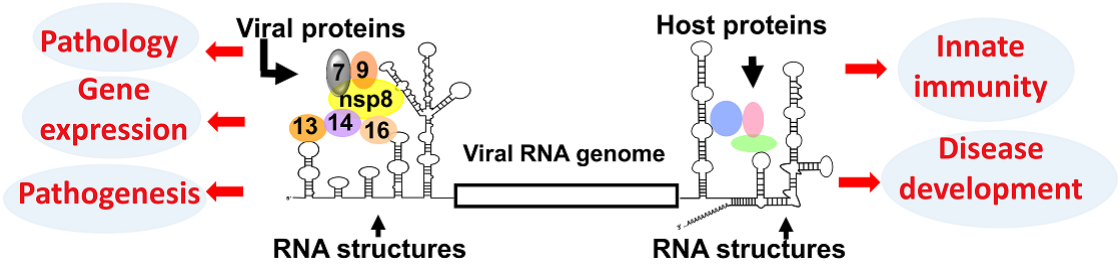
Ph.D. Department of Comparative and Experimental Medicine, University of Tennessee, (2003)
M.S. Department of Veterinary Medicine, National Chung Hsing University, (1996)
D.V.M. Department. of Veterinary Medicine, National Chung Hsing University, (1994)

Current Position and Professional Career

Professor, (2019.08-present), Graduate Institute of Veterinary Pathobiology, National Chung Hsing University,
Associate Professor, (2015.02-2019.07), Graduate Institute of Veterinary Pathobiology, National Chung Hsing University,
Assistant Professor, (2010.02-2015.01), Graduate Institute of Veterinary Pathobiology, National Chung Hsing University,
Postdoctoral Fellow, (2004.01-2010.01), Department of Pathobiology, University of Tennessee.
Research Assistant, (1999.08-2003.12), Department of Comparative and Experimental Medicine, University of Tennessee.
Research Assistant, (1996.09-1997.06), Department of Veterinary Medicine, National Chung Hsing University

Research interests

Our research interests focus on the RNA genome structures of RNA viruses (including coronavirus) and their interactions with viral or/and host proteins important for (i) pathology, (ii) gene expression including replication, transcription and translation, (iii) pathogenesis, (iv) innate immunity and (v) the development of diseases. Our aims are to identify the viral RNA structures, viral proteins or/and host proteins required for viral survival. The identified RNA structures of proteins are therefore the ideal candidates for the development of antiviral drugs or vaccine, which in turn can protect us from viral infection and prevent economic loss. We welcome people who are interested in our projects to join us.



Selected Publications

1. Lin CH, Hsieh FC, Wang M, Hsu C, Hsu HW, Yang CC, Yang CY, **Wu HY*. 2023.** Identification of subgenomic mRNAs derived from the **coronavirus** 1a/1b protein gene: Implications for coronavirus **transcription**. **Virology**, 589:109920. (SCI, 21/36 virology IF:3.7). nstc 111-2327-B-005-003.
2. Lin CH, Hsieh FC, Lai CC, Wang WC, Kuo CY, Yang CC, Hsu HW, Tam HM, Yang CY, **Wu HY*. 2023**. Identification of the protein coding capability of **coronavirus** defective viral genomes by mass spectrometry. **Virology Journal,** 7;20(1):290. (SCI, 14/36 virology IF:4.8). nstc

109-2313-B-005-013-MY3.

3. Lin CH, Hsieh FC, Chang YC, Yang CY, Hsu HW, Yang CC, Tam HM, **Wu HY***. **2023**. Targeting the conserved **coronavirus** octamer motif GGAAGAGC is a strategy for the development of coronavirus vaccine. **Virology Journal**, 15;20(1):267. (SCI, 14/36 virology IF:4.8). nstc 112-1313-B-005-041.
4. Lin CH, Tam HM, Yang CY, Hsieh FC, Wang JL, Yang CC, Hsu HW, Liu HP, **Wu HY***. **2023**. Evolution of the **coronavirus** spike protein in the full length genome and defective viral genome under diverse selection pressures. **Journal of General Virology**, 104(11). (SCI, 19/36 virology IF:3.8).nstc 110-2327-B-005-003.
5. Lin CH, Chen B, Chao DY, Hsieh FC, Lai CC, Wang WC, Kuo CY, Yang CC, Hsu HW, Tam HM, **Wu HY***. **2023**. Biological characterization of **coronavirus** noncanonical **transcripts** in vitro and in vivo. **Virology Journal**, 12;20(1):232. (SCI, 14/36 virology IF:4.8). nstc 109-2313-B-005-013-MY3.
6. Lin CH, Chen B, Chao DY, Hsieh FC, Yang CC, Hsu HW, Tam HM, **Wu HY***. **2023**. Unveiling the biology of defective viral genomes in vitro and in vivo: implications for gene expression and pathogenesis of **coronavirus**. **Virology Journal**, 6;20(1):225. (SCI, 14/36 virology IF:4.8). nstc 109-2313-B-005-013-MY3.
7. Lin CH, Yang CY, Wang ML, Ou SC, Lo CY, Tsai TL, **Wu HY* 2020**. Effects of **coronavirus** persistence on the genome structure and subsequent gene expression, pathogenicity and adaptation capability. **Cells, 2020**, 9, 2322. (SCI, 51/194, Cell Biology, IF=7.666). MOST 109-2313-B-005-013-MY3.
8. Lin CH,Yang CY, Ou SC,Wang ML,Lo CY,Tsai TL, **Wu HY***.2020.The impacts of antivirals on the **coronavirus** Genome Structure and Subsequent Pathogenicity, Virus Fitness and Antiviral Design. **Biomedicines**, 8, 376. (SCI, 121/276, Pharmacology, IF=4.757). MOST 109-2313-B-005-013-MY3.
9. Lo CY, Tsai TL, Lin CN, Lin CH, **Wu HY***. **2019**. Interaction of coronavirus nucleocapsid protein with the 5'- and 3'-ends of the **coronavirus** genome is involved in genome circularization and negative-strand RNA synthesis. **FEBS Journal**. doi: 10.1111/febs.14863.(SCI, 88/296, Biochemistry & Molecular Biology, IF: 5.622). MOST 106-2313-B-005-046-MY3.
10. Tsai TL, Lin CH, Lin CN, Lo CY, **Wu HY***. **2018**. Interplay between the poly(A) tail, poly(A)-binding protein, and coronavirus nucleocapsid protein regulates gene expression of **coronavirus** and the host cell. **Journal of Virology**, 01162-18. (SCI, 11/37, Virology, IF: 6.549). MOST 106-2313-B-005-046-MY3
11. Peng YH, Lin CH, Lin CN, Lo CY, Tsai TL, **Wu HY***. **2016**. Characterization of the Role of Hexamer AGUAAA and Poly(A) Tail in **Coronavirus** Polyadenylation. **PLoS One**, DOI:10.1371/journal.pone.0165077. (SCI, 29/73;Multidisciplinary Sciences, IF: 3.752). MOST 101-2313-B-005-010-MY3.
12. Yeh PY, **Wu HY***. **2014**. Identification of cis-acting elements on positive-strand subgenomic mRNA required for the synthesis of negative-strand counterpart in bovine **coronavirus**. **Viruses**, 6:2938-59. (SCI, 14/38=37.8%; Virology, IF: 5.818). NSC 100-2313-B-005-031.
13. Liao WY, Ke TY, **Wu HY***. **2014**. The 3'-terminal 55 nucleotides of bovine **coronavirus** defective interfering RNA harbor cis-acting elements required for both negative- and positive-strand RNA synthesis. **PLoS One**, 9: e98422. (SCI, 29/73=39.7%; Multidisciplinary Sciences, IF: 3.752).NSC 99-2313-B-005-024.
14. **Wu HY**, Guan BJ, Su YP, Fan YH, Brian DA* **2014**. Reselection of a genomic upstream open reading frame in mouse hepatitis **coronavirus** 5'-untranslated-region mutants. **Journal of Virology**, 88(2):846-58. (SCI, 11/37; Virology, IF: 6.549).
15. Ke TY, Liao WY, Wu HY*. **2013**. A Leaderless Genome Identified during Persistent Bovine **Coronavirus** Infection Is Associated with Attenuation of Gene Expression. **PLos One**, 8(12): e82176. (SCI, 29/73=39.7%; Multidisciplinary Sciences, IF: 3.752). NSC 99-2313-B-005-024.
16. **Wu HY** and Brian, DA*. **2010**. **Subgenomic messenger RNA** amplification in **coronaviruses. Proceedings of the National Academy of Sciences USA**, 107(27): 12257–12262. (SCI, 9/73; Multidisciplinary Sciences, IF: 12.779).
17. **Wu, H Y**. and Brian, D. A*. **2007.** 5'-Proximal Hotspot for an Inducible Positive-to-Negative-Strand **Template Switch** by **Coronavirus** RNA-Dependent RNA Polymerase. **Journal of Virology**, 81:3206-15. (SCI, 11/37=29.7%; Virology, IF: 6.549)
18. **Wu, H Y**., Ozdarendeli, A., and Brian, D. A *. **2006**. Bovine **coronavirus** 5'-proximal genomic acceptor hotspot for discontinuous **transcription** is 65 nucleotides wide. **Journal of Virology**, 80:2183-93. (SCI, 11/37=29.7%; Virology, IF: 6.549)