

Lianyu Huang

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RESEARCH INTEREST

Virology; Epidemiology; Host-pathogen interactions; Virus gene evolution and host adaptation.

EDUCATION BACKGROUND

Harbin Veterinary Research Institute, CAAS

Harbin, China

M.Sc.(Ag.) in Veterinary Medicine GPA: 3.8/4.0 Average score: 91/100

Jun.2020-present

Advisor: Prof. Dongming Zhao and Dr. Encheng Sun

Sichuan Agricultural University ("Project 211" University)

Chengdu, China

B.Sc.(Ag.) in Veterinary Medicine GPA: 3.5/5.0 Average score: 85/100

Sep.2015-Jun.2019

PUBLICATIONS AND MANUSCRIPTS

- Encheng Sun*, Lianyu Huang*, *et al.* 2021. Genotype I African Swine Fever Viruses Emerged in Domestic Pigs in China and Caused Chronic Infection. *Emerging Microbes & Infections* 10(1):2183–93. doi: 10.1080/22221751.2021.1999779. (JCR Q1, IF=19.568)
- Encheng Sun*, Zhenjiang Zhang*, Zilong Wang*, Xijun He*, Xianfeng Zhang, Lulu Wang, Wenqing Wang, Lianyu Huang, *et al.* 2021. Emergence and Prevalence of Naturally Occurring Lower Virulent African Swine Fever Viruses in Domestic Pigs in China in 2020. *Science China Life Sciences* 64(5):752–65. doi: 10.1007/s11427-021-1904-4. (JCR Q1, IF= 10.372)
- Dongming Zhao*, Encheng Sun*, Lianyu Huang*, *et al.* Highly lethal genotype I and II hybrid African swine fever viruses detected in pigs in China. 2022. (*Nature Communications*, under publish)

RESEARCH EXPERIENCE

Research on Epidemiological surveillance and pathogenicity analysis of African swine fever virus in northeastern provinces of China from 2020 to 2022

May 2021-Present

Master Dissertation Research

- Surveilled African swine fever virus (ASFV) in northeastern provinces of China by using qPCR to identify positive samples.
- Identified biological characteristics of respective ASFVs through cell culture, virus isolation, HAD assay, immunofluorescence assay, and electron microscopy.
- Sequenced 3 individual genes and the whole genomes of ASFVs utilizing molecular cloning technology (including PCR, quantitative PCR, and TA cloning), sanger sequencing, and third-generation sequencing technology (TGS). And processed data utilizing DNASTar and SnapGene.
- Visualized genome alignment by using MAFFT, IQ-tree, MEGA 11, BRIG, iTOL, GraphPad Prism, and Adobe Illustrator to demonstrate the evolution of ASFV in China.
- Designed and conducted animal experiments in vivo under the supervision of supervisors to characterize the pathogenicity of representative ASFV.
- Detected IgG against the ASFV p72 protein by collecting serum samples and applying ELISA.

Identification of effective compounds inhibiting African Swine Fever virus infection from FDA-approved and plant-sourced compound libraries

Nov.2020-Feb.2021

Project member

- Detected protein expression and interaction by using Western Blot.
- Counted cells by applying Flowcytometry under the guidance of a senior student.
- Cultured HEK293T to be infected by ASFV to test Tissue Culture Infectious Dose Assays (TCID₅₀).

Drug resistance analysis of some oral-derived bacteria in giant pandas

Apr.2018-Jan.2019

Bachelor Dissertation Research

- Resuscitated and re-cultured 72 bacteria strains, carried out antimicrobial susceptibility test of all bacteria by using the K-B method, and 8 relevant drug resistance genes of all bacteria were amplified by PCR.
- Processed and analyzed experimental data in Excel.

PROJECT EXPERIENCE

Research on the pathogenic ecology and genetic evolution of African swine fever virus

May 2021-Dec.2022

(National key R&D projects of China, Subproject, Project approval No: 2021YFD1800101-3)

This project selects 10 important or highly variable genes for sequencing of the positive samples which come from some farms, slaughterhouses, harmless treatment plants, and markets. 30 important strains are sequenced to analyze the genetic mutants. According to the sequencing results, the genetic variation characteristics are analyzed, and a diagnosis method for variant strains is established.

Contribution:

- Written the initial materials of this project and was responsible for sample testing and statistics.
- Prepared peripheral blood mononuclear cells (PBMCs), culture porcine alveolar macrophages (PAMs), and HEK293T.
- Tested 1068 samples, sequenced genes of isolates, and aligned the sequence fragments and genome.
- Organized the experimental data and write two parts of an article, including the introduction and the method, under the guidance of my supervisor.

Study on the Infection and Pathogenic Mechanism of African Swine Fever

Jul.2019-Jun.2022

(National Natural Science Foundation of China, Project approval No: 31941002)

This project further studies and discusses the epidemiological situation and pathogenesis of African swine fever virus by using methods of molecular biology and cell biology. Through the study, further study the host-pathogen interactions.

Contribution:

- Tested and sequenced 902 samples which were from farms, slaughterhouses, and markets.
- Organized and analyzed the sequence data and write the periodic report on this project.

HONORS AND AWARDS

National Scholarship for Postgraduates in 2021

Dec.2021

(Certificate No: SSY2020135105, Scholarship amount: RMB20,000)

Excellence in Course Learning of CAAS

Oct.2021

Social activities Excellence Award of CAAS

Oct.2021

First-class academic scholarship for master's degree students

Sep.2021

(Scholarship amount: RMB9,000)

“Muyuan” Scholarship of CAAS (Scholarship amount: RMB5,000)

Aug.2021

SKILLS & OTHERS

Language: English (IELTS: Total score-6.5, Reading-6.5, Writing-6.5, Listening-6.0, Speaking-6.0).

Experimental skills: cell culture, isolation and culture of viruses, ELISA, ELISpot, PCR, RT-PCR, qPCR, TA cloning, primer design, construct plasmids, SDS-PAGE, recombinant protein expression and purification, Western Blot, Flowcytometry, Third generation sequencing technology (TGS), etc.

Software skills: SnapGene, MAFFT, IQ-tree, MEGA 11, GraphPad Prism, DNASTar, Oligo 7, Adobe Illustrator, Adobe Photoshop, BLAST Ring Image Generator (BRIG), etc.

Hobbies: Playing harmonica and swimming.