

Full name: Yu-Liang Huang



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## Biography

Since 2007, Dr. Huang involved in the studies of swine viral diseases, including the porcine circovirus type 2, porcine reproductive and respiratory syndrome virus, classical swine fever virus (CSFV), and porcine epidemic diarrhea virus in Veterinary Research Institute (VRI). Regarding the CSFV studies and diagnosis, his lab is focus on the items of pathogenesis, immune regulation, vaccine, disease control and national CSFV surveillance programs after 2008. His laboratory has developed several CSFV technologies, including reverse transcription multiplex real-time PCR, for the detection and genotyping of CSFV and continues to work on the molecular pathogenesis and immune regulation of CSFV *in vitro* and *in vivo* studies. Dr. Huang has published over 20 papers in peer-reviewed journals.

## **Current employment**

Veterinary Research Institute, 2007-present
 WOAH Expert for Classical swine fever virus, 2022-present
 Education

 2005-2012
 PhD., Graduate Institute of Veterinary Medicine, School of Veterinary Medicine, National Taiwan University,
 2003-2005
 Master, Graduate Institute of Veterinary Medicine, Nation Pingtung University of Science and Technology
 2001-2003
 DVM, Department of Veterinary Medicine, Nation Pingtung University of Science and Technology



1994-2001 DVM, Department of Veterinary Medicine, National Chiayi University

## **Research Articles**

- Chen WT, Liu HM, Chang CY, Deng MC, <u>Huang YL</u>, Chang YC, Chang HW. Cross-reactivities and cross-neutralization of different envelope glycoproteins E2 antibodies against different genotypes of classical swine fever virus. Front Vet Sci. 2023 Apr 27;10:1169766.
- Chang CY, Tsai KJ, Deng MC, Wang FI, Liu HM, Tsai SH, Tu YC, Lin NN, <u>Huang YL</u>. Transmission of Classical Swine Fever Virus in Cohabitating Piglets with Various Immune Statuses Following Attenuated Live Vaccine. Animals (Basel). 2023 Jan 21;13(3):368.
- Tsai KJ, Tu YC, Wu CH, Huang CW, Ting LJ, <u>Huang YL</u>, Pan CH, Chang CY, Deng MC, Lee F. First detection and phylogenetic analysis of lumpy skin disease virus from Kinmen Island, Taiwan in 2020. J Vet Med Sci. 2022.
- Huang YL, Meyer D, Postel A, Tsai KJ, Liu HM, Yang CH, Huang YC, Berkley N, Deng MC, Wang FI, Becher P, Crooke H, Chang CY. Identification of a common conformational epitope on the glycoprotein E2 of classical swine fever virus and border disease virus. Viruses. 13:1655, 2021.
- Huang YL, Tsai KJ, Deng MC, Liu HM, Huang CC, Wang FI, Chang CY. In Vivo Demonstration of the Superior Replication and Infectivity of Genotype 2.1 with Respect to Genotype 3.4 of Classical Swine Fever Virus by Dual Infections. Pathogens 9:261, 2020.
- Tsai KJ, Deng MC, Wang FI, Tsai SH, Chang C, Chang CY, <u>Huang</u> <u>YL.</u> Deletion in the S1 Region of Porcine Epidemic Diarrhea Virus Reduces the Virulence and Influences the Virus-Neutralizing Activity of the Antibody Induced. Viruses 12:1378, 2020
- Chang CY, Cheng IC, Chang YC, Tsai PS, Lai SY, <u>Huang YL</u>, Jeng CR, Pang VF, Chang HW. Identification of neutralizing monoclonal antibodies targeting novel conformational epitopes of the porcine epidemic diarrhoea virus spike protein. Sci Rep. 9:2529, 2019.



- 8. <u>**Huang YL**</u>, Deng MC, Tsai KJ, Liu HM, Huang CC, Wang FI, Chang CY. Competitive replication kinetics and pathogenicity in pigs co-infected with historical and newly invading classical swine fever viruses. Virus Res. 228:39-45. 2017.
- Chiou HY, <u>Huang YL</u>, Deng MC, Chang CY, Jeng CR, Tsai PS, Yang C, Pang VF, Chang HW. Phylogenetic Analysis of the Spike (S) Gene of the New Variants of Porcine Epidemic Diarrhoea Virus in Taiwan. Transbound Emerg Dis. 64(1):157-166, 2017.
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- Sung MH, Deng MC, Chung YH, <u>Huang YL</u>, Chang CY, Lan YC, Chou HL, Chao DY. Evolutionary characterization of the emerging porcine epidemic diarrhea virus worldwide and 2014 epidemic in Taiwan. Infect Genet Evol. 36: 108-15, 2015.
- Wang FI, Deng MC, <u>Huang YL</u>, Chang CY. Structures and Functions of Pestivirus Glycoproteins: Not Simply Surface Matters. Viruses. 7:3506-29, 2015.
- Deng MC, Chang CY, Huang TS, Kuo ST, Tsai HJ, Chang C, <u>Huang</u> <u>YL</u>. The outbreak of porcine epidemic diarrhea in Taiwan. Taiwan Veterinary Journal, 140: 115-121, 2014.
- Chang CY, Deng MC, Wang FI, Tsai HJ, Yang CH, Chang C, <u>Huang YL</u>. The application of a duplex reverse transcription realtime PCR for the surveillance of porcine reproductive and respiratory syndrome virus and porcine circovirus type 2. J Virol Methods. 201:13-9, 2014.
- Huang YL, Pang VF, Deng MC, Chang CY, Jeng CR. Porcine circovirus type 2 decreases the infection and replication of attenuated classical swine fever virus in porcine alveolar macrophages Res Vet Sci. 96:187-95, 2014
- Huang YL, Deng MC, Wang FI, Huang CC, Chang CY. The challenges of classical swine fever control: modified live and E2 subunit vaccines. Virus Res. 22: 1-11, 2014
- 17. Wang C, Pang VF, Lee F, Liao PC, <u>**Huang YL**</u>, Lin YL, Lai SS, Jeng CR. Development and evaluation of a loop-mediated isothermal amplification method for rapid detection and differentiation of two



genotypes of porcine circovirus type 2. J Microbiol Immunol Infect. 8, 2013.

- Lin CM, Jeng CR, Liu JP, Lin EC, Chang CC, <u>Huang YL</u>, Tsai YC, Chia MY, Wan CH, Pang VF. Immune gene expression profiles in swine inguinal lymph nodes with different viral loads of porcine circovirus type 2. Vet Microbiol. 162:519-29, 2013.
- Chang CY, Huang CC, Deng MC, <u>Huang YL</u>, Lin YJ, Liu HM, Lin YL, Wang FI. Identification of conformational epitopes and antigenspecific residues at the D/A domains and the extra membrane Cterminal region of E2 glycoprotein of classical swine fever virus. Virus Res. 168: 56-63, 2012.
- 20. <u>Huang YL</u>, Pang VF, Deng MC, Chang CY, Shih CN, Wan CH, Jeng CR. Reduction of classical swine fever virus-specific cell proliferative response of porcine peripheral blood mononuclear cells by porcine circovirus type 2. Taiwan Vet J 38: 164-176, 2012
- Huang YL, Pang VF, Lin CM, Tsai YC, Chia MY, Deng MC, Chang CY, Jeng CR. Porcine circovirus type 2 (PCV2) infection decreases the efficacy of an attenuated classical swine fever virus (CSFV) vaccine. Vet Res. 42:115, 2011.
- Chen TH, Pan CH, Jong MH, Lin HM, <u>Huang YL</u>, Hsiung KP, Chao PH, Lee F. Development of a chromatographic strip assay for detection of porcine antibodies to 3ABC non-structural protein of foot-and-mouth disease virus serotype O. J Vet Med Sci.71:703-8, 2009.
- Huang YL, Pang VF, Pan CH, Chen TH, Jong MH, Huang TS, Jeng CR. Development of a reverse transcription multiplex real-time PCR for the detection and genotyping of classical swine fever virus. J Virol Methods. 160:111-8, 2009.
- 24. Pan CH, Jong MH, <u>Huang YL</u>, Huang TS, Chao PH, Lai SS. Rapid detection and differentiation of wild-type and three attenuated lapinized vaccine strains of classical swine fever virus by reverse transcription polymerase chain reaction. J Vet Diagn Invest. 20:448-56, 2008.
- 25. Lin CM, Jeng CR, Chang HW, Guo IC, <u>Huang YL</u>, Tsai YC, Chia MY, Pang VF. Characterization of porcine circovirus type 2 (PCV2) infection in swine lymphocytes using mitogen-stimulated peripheral



blood lymphocytes from healthy PCV2-carrier pigs. Vet Immunol Immunopathol. 124:355-66, 2008.

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