

## **Publications**

1. Feraco AM, Zhou Y, **Zheng Y**, Marks LJ, Friedmann A, Weinstein HJ, Link MP, Flerlage JE. 2023. Disease site number was not prognostic in a low-risk Hodgkin lymphoma combined modality trial: revisiting PHC HOD90. *Blood Advances*. 7(21):6665-6667.
2. Zheng Z, Gorden PJ, Xia X, **Zheng Y**, Li G. 2022. Whole-genome analysis of *Klebsiella pneumoniae* from bovine mastitis milk in the U.S. *Environmental Microbiology*. 24(3):1183-1199.
3. Li G, **Zheng Y**, Wang L, Zhang Y, Shen H. 2022. Whole Genome Sequencing of Porcine Epidemic Diarrhea Virus and Porcine Deltacoronavirus. *Animal Coronaviruses*. 277-286.
4. Arruda B, Shen H, **Zheng Y**, Li G. 2021. Novel Morbillivirus as Putative Cause of Fetal Death and Encephalitis among Swine. *Emerging Infectious Diseases*. 27(7):1858-1866.
5. Hashish A, Sato Y, Li G, **Zheng Y**, Gauger PC, El-Gazzar M. 2021. Near-Complete Genome Sequence of GI-17 Lineage Infectious Bronchitis Virus, Circulating in Iowa. *Microbiology Resource Announcements*. 10(20):e01406-20
6. Shen H, Zhang J, Gauger PC, Burrough ER, Zhang J, Harmon K, Wang L, **Zheng Y**, Petznick T, Li G. 2021. Genetic characterization of porcine sapoviruses isolated from pigs during a diarrhea outbreak in iowa, 2019. *Transboundary and emerging diseases*. 69(3):1246-1255.
7. Shen H, Zhang J, Gauger P, Burrough E, Zhang J, Harmon K, Wang L, **Zheng Y**, Petznick T, Li G. 2021. Detection and genetic characterization of porcine sapovirus from pigs with diarrhea. *Transboundary and Emerging Diseases*. DOI: 10.22541/au.161321736.68129500/v1.
8. Yang C, Wang L, Schwartz K, Burrough E, Groeltz-Thrush J, Chen Q, **Zheng Y**, Shen H, Li G. 2021. Case report and genomic characterization of a novel porcine nodavirus in the united states. *Viruses*. 13:73.
9. Gall A, Burrough E, Zhang J, Magstadt D, Yim-Im W, Stevenson G, Derscheid R, Piñeyro P, **Zheng Y**, Li G, Olds J. 2020. Identification and correlation of a novel siadenovirus in a flock of budgerigars (*melopsittacus undulates*) infected with salmonella typhimurium in the united states. *Journal of Zoo and Wildlife Medicine*. 51(3):618-630.
10. Wang M, Zeng Z, Jiang F, **Zheng Y**, Shen H, Macedo N, Sun Y, Sahin O, Li G. 2020b. Role of enterotoxigenic escherichia coli (etec) prophage in spreading antibiotic resistance in a porcine-derived environment. *Environmental Microbiology*. 22(12):4974-4984.
11. Wang L, Shen H, **Zheng Y**, Schumacher L, Li G. 2020a. Astrovirus in white-tailed deer, united states, 2018. *Emerging Infectious Diseases*. 26(2):374-376.
12. Wang A, Zhang J, Shen H, **Zheng Y**, Feng Q, Yim-Im W, Gauger P, Harmon K, Zhu S, An T-Q, Li G. 2019. Genetic diversity of porcine reproductive and respiratory syndrome virus 1 in the united states of america from 2010 to 2018. *Veterinary Microbiology*. 239:108486.

13. Cook S, Li G, **Zheng Y**, Willand Z, Issel CJ, Cook F. 2019. Molecular characterization of the major open reading frames (orfs) and enhancer elements from four geographically distinct north american equine infectious anemia virus (eiv) isolates. *Journal of Equine Veterinary Science*. 85:102852.
14. Nam B, Mekuria Z, Carossino M, Li G, **Zheng Y**, Zhang J, Cook F, Shuck K, Juliana R, Squires E, Troedsson M, Timoney P, Balasuriya U. 2019. Intra-host selection pressure drives equine arteritis virus evolution during persistent infection in the stallion reproductive tract. *Journal of Virology*. 93(12):e00045-19.
15. Jiang F, Wu Z, **Zheng Y**, Frana T, Sahin O, Zhang Q, Li G. 2019. Genotypes and antimicrobial susceptibility profiles of hemolytic escherichia coli from diarrheic piglets. *Foodborne Pathogens and Disease*. 16(2):94-103.
16. Gerber P, Shen H, **Zheng Y**, Li G, Lobato Z, Opriessnig T. 2019. Genomic sequence of a megrivirus strain identified in laying hens in brazil. *Microbiology Resource Announcements*. 8(4):e01438-18.
17. Chen Q, Wang L, Yang C, **Zheng Y**, Gauger P, Anderson T, Harmon K, Zhang J, Yoon K-J, Main R, Li G. 2018a. The emergence of novel sparrow deltacoronaviruses in the united states more closely related to porcine deltacoronaviruses than sparrow deltacoronavirus hku17. *Emerging Microbes & Infections*. 7(1):105.
18. Yang C, Wang L, Shen H, **Zheng Y**, Gauger P, Chen Q, Zhang J, Yoon K-J, Harmon K, Main R, Li G. 2018b. Detection and genomic characterization of new avian-like hepatitis e virus in a sparrow in the united states. *Archives of Virology*. 163(10):2861-2864.
19. Chen Q, Wang L, **Zheng Y**, Zhang J, Guo B, Yoon K-J, Gauger P, Harmon K, Main R, Li G. 2018c. Metagenomic analysis of the rna fraction of the fecal virome indicates high diversity in pigs infected by porcine endemic diarrhea virus in the united states. *Virology Journal*. 15(1):95.
20. Yang C, Wang L, Shen H, **Zheng Y**, Bade S, Gauger P, Chen Q, Zhang J, Guo B, Yoon K-J, Harmon K, Main R, Li G. 2018a. Detection and genetic characterization of porcine pegivirus in pigs in the united states. *Transboundary and emerging diseases*. 65(3):618-626.
21. Guo B, Kim H, **Zheng Y**, Shen H, Pogranichniy R, Schwartz K, Li G, Yoon K-J. 2018. Genomic sequence of a swine pasivirus type 1 strain identified in u.S. Swine. *Genome Announcements*. 6:e01569-01517.
22. Zhang J, Yim-Im W, Chen Q, **Zheng Y**, Schumacher L, Huang H, Gauger P, Harmon K, Li G. 2018. Identification of porcine epidemic diarrhea virus variant with a large spike gene deletion from a clinical swine sample in the united states. *Virus Genes*. 54:1-5.
23. Arruda B, Arruda P, Hensch M, Chen q, **Zheng Y**, Yang C, Gatto IR, Matias Ferreyra F, Gauger P, Schwartz K, Bradner L, Harmon K, Hause B, Li G. 2017a. Porcine astrovirus type 3 in central nervous system of swine with polioencephalomyelitis. *Emerging Infectious Diseases*. 23(12):2097-2100.

24. Cullen J, Lithio A, Seetharam AS, **Zheng Y**, Li G, Nettleton D, O'Connor A. 2017. Microbial community sequencing analysis of the calf eye microbiota and relationship to infectious bovine keratoconjunctivitis. *Veterinary Microbiology*. 207:267-279.
25. Zhang J\*, **Zheng Y\***, Xia X-Q, Chen q, Bade S, Yoon K-J, Harmon K, Gauger P, Main R, Li G. 2017. High-throughput whole genome sequencing of porcine reproductive and respiratory syndrome virus from cell culture materials and clinical specimens using next-generation sequencing technology. *Journal of Veterinary Diagnostic Investigation*. 29:41-50. **\*These authors contributed equally to this work.**
26. Chen Q, **Zheng Y**, Guo B, Zhang J, Yoon K-J, Harmon K, Main R, Li G. 2016c. Complete genome sequence of porcine sapelovirus strain USA/ia33375/2015 identified in the united states. *Genome Announcements*. 4:e01055-01016.
27. Guo B, Piñeyro P, Rademacher C, **Zheng Y**, Li G, Yuan J, Hoang H, Gauger P, Madson D, Schwartz K, Canning P, Arruda B, Cooper V, Baum D, Linhares D, Main R, Yoon K-J. 2016. Novel senecavirus a in swine with vesicular disease, united states, july 2015. *Emerging Infectious Diseases*. 22(7):1325-7.
28. Chen Q, Thomas J, Gimenez Lirola L, Hardham J, Gao Q, Gerber P, Opriessnig T, **Zheng Y**, Li G, Gauger P, Madson D, Magstadt D, Zhang J. 2016b. Evaluation of serological cross-reactivity and cross-neutralization between the united states porcine epidemic diarrhea virus prototype and s-indel-variant strains. *BMC Veterinary Research*. 12:70.
29. Chen Q, Gauger P, Stafne M, Thomas J, Madson D, Huang H, **Zheng Y**, Li G, Zhang J. 2016a. Pathogenesis comparison between the united states porcine epidemic diarrhea virus prototype and s-indel-variant strains in conventional neonatal piglets. *The Journal of general virology*. 97(5):1107-1121.
30. Zhang J, Piñeyro P, Chen q, **Zheng Y**, Li G, Rademacher C, Derscheid R, Guo B, Yoon K-J, Madson D, Gauger P, Schwartz K, Harmon K, Linhares D, Main R. 2015. Full-length genome sequences of senecavirus a from recent idiopathic vesicular disease outbreaks in u.S. Swine. *Genome Announcements*. 3:e01270-01215.
31. Nam B, Li G, **Zheng Y**, Zhang J, Shuck K, Timoney P, Balasuriya U, Km S, Pj T, Balasuriya. 2015. Complete genome sequence of noncytopathic bovine viral diarrhea virus 1 contaminating a high-passaged rk-13 cell line. *Genome Announcements*. 3:e01115-01115.
32. Huang Y\*, **Zheng Y\***, Su Z, Gu X. 2009. Differences in duplication age distributions between human GPCRs and their downstream genes from a network prospective. *BMC Genomics* 10 Suppl 1:S14. **\*These authors contributed equally to this work.**
33. **Zheng Y**, Xu D, Gu X. 2007. Functional divergence after gene duplication and sequence-structure relationship: a case study of G-protein alpha subunits. *J Exp Zool B Mol Dev Evol* 308:85-96.
34. Gu X, **Zheng Y**, Huang Y, Xu D. 2007. Using ancestral sequence inference to determine the trend of functional divergence after gene duplication. *Ancestral Sequence Reconstruction* pp. 117-128 (Ed. Liberles D, Oxford University Press, New York, 2007).

35. Meng X, Ruan D, Kang L, Zhu D, She J, Luo L, **Zheng Y**, Li X. 2003. Age-related morphological impairments in the rat hippocampus following developmental lead exposure: An MRI, LM and EM study. *Environ Toxicol Pharmacol* 13:187-197.
36. Wang L, **Zheng Y**, Zhang X. 2002. Isolation and characterization of a porin-like outer membrane protein from *Xanthomonas campestris* pv. *campestris*. *IUBMB Life* 54:13-18.