

Dear Editor,

We would like to submit the attached manuscript entitled "**Molecular epidemiology and biological characteristics of swine pseudorabies virus in Henan province of China during 2012 to 2019**", which we wish to be considered for publication in *Transboundary and Emerging Diseases*.

All authors will have a significant intellectual contribution to the work and concur with the submission. The article is original and has not been published elsewhere, either completely, in part, or in another form. The manuscript has not been submitted to another journal and will not be published elsewhere. The authors have no conflicts of interest to declare.

Since late 2011, pseudorabies virus (PRV) infection was re-emerged in vaccinated pig farms in China, and widely spread in many provinces of China, which caused tremendous economic losses in the swine industry. To further understand the epidemic and biological characteristics of the virus, a total of 1,174 tissue samples were collected from Bartha-K61-immunized swine farms in Henan province of China from 2012 to 2019, and PRV strains were isolated and the complete length of gE and gC genes were sequenced and analyzed. The results showed that the detection rate of PRV was 15.25% (179/1174), which varied from 6.61% to 25.00% during 2012-2019. The 16 PRV isolates were obtained, and could cause clinical symptoms and death in mice. The phylogenetic trees based on the sequences of gE and gC genes showed that all the 16 PRV strains in this study clustered to a relatively independent branch altogether with other Chinese variant PRV strains (after 2012). Moreover, the

sequence analysis of the isolates revealed that gE and gC both contained amino acid insertions, substitutions or deletions compared with European-American PRV strains and early Chinese PRV strains (before 2012). In addition, it was first reported that Chinese variants isolated in this study had a unique amino acid substitution at site 280 (F to L) of gC gene. In the protection assay, the emulsion containing inactivated PRV NY isolate could provide complete protection against variant NY, and the titer of neutralizing antibodies was 1:82. This study might enrich our understanding of the evolution of variant PRVs as well as pave the way for finding a model virus to develop a novel vaccine based on PRV variants.

Thank you very much for your considering our manuscript for potential publication. I'm looking forward to hearing from you soon.

Sincerely yours,

Hong-Ying Chen