

Diverse african swine fever viruses in China

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Dear Editor,

African swine fever (ASF), caused by African swine fever virus (ASFV), has a 100-year history. It can result in the death of a large number of pigs. Especially in the past three years, ASF spread into Asia, where that is the main pig raising area in the world. Besides Africa, Europe, and Asia, ASF also re-visited the Dominican Republic and Haiti, North America in 2021, where no ASF cases occurred in the past 40 years [1].

Since August 2018, ASF spread into China and hit hard China's pig industry [2]. At the outset, ASFVs of genotype II (Georgia-07-like virus) were considered the causative agent. The virus can cause acute diseases with near 100% mortality, and has been prevalent in China for over than 3 years.

However, in some surveillance studies, diverse ASFVs were found in China. In Sun et al. study, lower virulent genotype II ASFVs with variety of mutation forms (including mutation,

deletion, insertion, or short-fragment replacement) were confirmed, compared with Pig/HLJ/2018 (HLJ/18), the earliest isolate in China. These natural mutants possessed lower virulence and high transmissibility, and caused chronic and persistent infections in pigs [3].

More incredibly, in 2021, genotype I ASFVs were reported in two main pig raising areas (Shandong and Henan) in China, and were highly similar to NH/P68 and OURT88/3, two genotype I ASFVs isolated in Portugal in the last century. Similar to natural genotype II ASFV mutants, these genotype I ASFVs show low virulence and efficient transmissibility in pigs, and cause mild onset of infection and chronic disease [4].

The emergence of diverse ASFVs (especially lower virulent natural mutants) should bring greater difficulty to the early diagnosis of ASF and create new challenges for ASF control in China.

Conflict of interests

The authors declare no conflict of interest.

Author contributions

Sheng-Nan Chen, Chun-Ling Li and Jin-Sen Lin collected the data, analyzed it, and drafted the paper for the work. Shao-Lun Zhai and Ming-Fei Sun are co-corresponding authors of this paper, they did the financial support, review, and final approval of the paper to be published. All authors read and approved the final manuscript.

Data availability statement

The data used and analyzed during the current study are available from the corresponding author on reasonable request.

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