不同基因型豬瘟病毒之毒力分析

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摘要

豬瘟為豬隻的重要傳染性疾病，常造成豬隻的死亡並導致養豬產業的重大損失。針對台灣分離之豬瘟病毒分析其核酸序列，可將台灣之豬瘟病毒分為不同基因亞型，其中長期存在於台灣的豬瘟病毒，稱之為本土型，歸類為 3.4 亞型；而 1994 年之後開始分離到的外來型病毒株，則歸類為 2.1 亞型。分析結果發現 1996 年之後在台灣田間豬瘟流行株已由外來型病毒完全取代本土型病毒。本研究為瞭解台灣田間過去流行的 3.4 基因亞型豬瘟病毒株以及現今主要流行的 2.1 基因亞型病毒株存在之差異性，選擇兩種基因型之主要代表病毒株，分別以細胞及動物試驗，透過體內（*in vivo*）以及體外（*in vitro*）的方式，嘗試著找出這兩型病毒株所存在之差異點。細胞試驗的結果顯示，2.1 亞型與 3.4 亞型病毒株生長曲線並無明顯差異，但 2.1 亞型細胞外/細胞內比例高於 3.4 亞型，顯示 2.1 亞型病毒的釋放更有效率。動物試驗的結果顯示，在同時感染 2.1 亞型與 3.4 亞型病毒的豬隻，2.1 亞型病毒較早偵測到且力價顯著高於 3.4 亞型，表示 2.1 亞型病毒在豬隻的增殖更有效率。這些研究成果將能更深入了解豬瘟病毒的特性，同時對於豬瘟的防疫也有實質的助益。

Competitive replication kinetics and pathogenicity in pigs co-infected with historical and newly invading classical swine fever viruses

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Abstract

Classical swine fever (CSF), also known as hog cholera, is caused by classical swine fever virus (CSFV) and is an economically important and highly contagious disease affecting pigs. Analysis of the E2 and NS5B sequences from CSFVs that were isolated from field outbreaks in Taiwan showed that the viruses could be divided into different genotypes. The historical subgroup (genotype 3.4) in Taiwan seems to have been endemic before the 1920s. The exotic subgroup (genotype 2.1) was first isolated in 1994 and further sporadic outbreaks of this subgroup has subsequently occurred. Analysis also showed that, during the these more recent outbreaks, the CSFV population has shifted from genotype 3.4-dominant to 2.1-dominant after 1996. To understand the mechanisms of viral population shifts in the field, viruses belong togenotype 2.1 and 3.4 have been analyzed in depth both *in vitro* and *in vivo* to compare viral replication rates and pathogenicity between these two genotype viruses. Inoculation of the viruses into cells (*in vivo*) demonstrated that the CSFV genotype 2.1 has a higher S/C (secreted/intracellular) ratio than genotype 3.4, indicating that genotype 2.1 is secreted efficiently into the supernatant. In pigs challenged with the CSFV genotypes 2.1 and 3.4, genotype 2.1 was detected earlier and the viral titer was higher than genotype 3.4, indicating that genotype 2.1 replicated more efficiently in pigs. These findings will be useful to further understand the characteristics of CSFV and will be helpful for the control of CSFV.