本土型與外來型豬瘟病毒同時感染豬隻之比較試驗

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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，進行不同攻毒代數兩種基因型豬瘟病毒同時感染豬隻試驗。豬隻攻毒試驗的結果顯示，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，同時感染第二代豬隻之 2.1 亞型與 3.4 亞型病毒量差異更加明顯、2.1 亞型病毒比第一代更早偵測到、 3.4 亞型病毒比第一代更晚偵測到，顯示 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。

Competition between historical and newly invading classical swine fever viruses in co-infected pigs

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Abstract

Classical swine fever (CSF), which is caused by the classical swine fever virus (CSFV), is an economically important and highly contagious disease infecting domestic and wild pigs. In Taiwan, CSFVs identified in field outbreaks have been found to belong to two distinct genotypes. Since 1996, the CSFV population has shifted from the historical sub-genotype, 3.4, to a newly invading sub-genotype, 2.1. This study analyzed the competition between these two sub-genotype viruses in co-infected pigs to simulate natural situations in the field. In pigs inoculated with the same dose of each virus sub-genotype, results demonstrate that the sub-genotype 2.1 strain, consistently replicates more efficiently than the sub-genotype 3.4 strain.. In the second passage of co-infection in pigs, the replication efficiency of the sub-genotype 2.1 strain was even higher than during the first passage. Comparisons between the first and second passages of co-infection, demonstrated that the genotype 2.1 strain could be detected earlier in co-infected P2 pigs than in co-infectedP1 pigs. Moreover, the sub-genotype 3.4 strain was detected later in co-infected P2 pigs than in co-infected P1 pigs. This study thus demonstrates a possible explanation for the observed CSFV population shifts in the field, whereby the newly invading sub-genotype 2.1 replicated and dispersed more efficiently than sub-genotype 3.4 did, leading to the predominance of 2.1 viruses in the field. These findings will be useful for the further understanding of CSFV biology and therefore, helpful for the control of CSFV.