

台灣地區豬第二型環狀病毒基因型之探討與分析

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摘要

豬第二型環狀病毒(Porcine circovirus type 2; PCV2)在國內之養豬場為引起豬離乳後多發性消耗綜合症(postweaning multisystemic wasting syndrome; PMWS)之主要病原。本次研究主要是收集 2001 年至 2011 年 571 株台灣 PCV2 病毒株，經分析各病毒株之基因體全長(complete genome)序列後發現，台灣 PCV2 病毒株主要以 PCV2a 及 PCV2b 二種基因型為主，其中 PCV2a 之流行率為 22.9%，PCV2b 之流行率為 77.1%。在 2001 年時台灣 PCV2 病毒株之基因型主要以 PCV2a 為主，至 2003 年時台灣 PCV2 病毒株則以 PCV2b 取代 PCV2a 成為主要之基因型。不同病毒株之間 complete genome 之相似性為 89.6–100%，而第二開讀窗(open reading frame 2; ORF2)所轉譯的結構蛋白衣之胺基酸相似性則為 86.9–100%。分析 571 株台灣 PCV2 病毒株之 complete genome、第一開讀窗(ORF1)及 ORF2 非同義與同義核苷酸多型性比例(non-synonymous/synonymous; dN/dS)後，其結果顯示台灣 PCV2 病毒株之基因序列呈現負向選擇(negative selection)，但是部分 ORF2 胺基酸，包括第 47、53、57–60、63、68、72、75–77、80、121、131、134、136、169、190、191 以及 232 胺基酸呈現較高度變異以及呈現正向選擇(positive selection)。本次研究分析 2001 年至 2011 年之間台灣 PCV2 病毒株基因序列後發現台灣 PCV2 病毒株之 ORF2 基因呈現較高度變異以及基因漂變(genetic shift)的現象。

Analysis of genotypes of porcine circovirus type 2 in Taiwan

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Abstract

Porcine circovirus type 2 (PCV2) is the major causative agent of postweaning multisystemic wasting syndrome (PMWS) in Taiwanese pig farms. We analyzed the complete genomes of 571 PCV2 isolates in Taiwan from 2001 to 2011 and divided the isolates into two distinct genotypes, PCV2a and PCV2b. Of the 571 Taiwanese PCV2 isolates, 22.9% (131/571) belonged to PCV2a and 77.1% (440/571) to PCV2b. In this study, PCV2a isolates were the most common in 2001, and then PCV2b isolates became the most common and widely distributed isolates beginning 2003. Sequence comparisons between the 571 isolates indicated 89.6–100% nucleotide identity between the complete genomes and 86.9–100% identity between the amino acid sequences of open reading frame (ORF) 2 of the putative capsid protein. Analysis of non-synonymous/synonymous (dN/dS) ratios of complete genome, ORF1 and ORF2 between 571 Taiwanese PCV2 isolates suggested that Taiwanese PCV2 genes evolved under a negative selection, but some residues of ORF2, including residues 47, 53, 57–60, 63, 68, 72, 75–77, 80, 121, 131, 134, 136, 169, 190, 191, and 232 were more variable and under positive selection pressure. These results suggest a higher of genetic variation and a shift in ORF2 among the Taiwanese PCV2 isolates collected in this study from 2001 to 2011.