

國內豬生殖與呼吸綜合症之分子流行病學分析

新興傳染病組

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摘要

豬生殖與呼吸綜合症病毒（PRRSV）自 1991 首次被分離以來，一直廣泛存在台灣各豬場，並造成豬場嚴重的經濟損失。本試驗將藉由分子流行病學之方式進行台灣 PRRSV 基因序列之分析，以了解此病毒於台灣的演化情況，此試驗收集本所自 2014 至 2024 年之檢體與病毒株，並進行 NSP2、ORF5、ORF7 與全長基因序列之解析與比對，結果發現，現行國內主要以北美基因型為主，舊有的 L5 基因型已消失，而是以 L3 基因型病毒株流行為主，但此 L3 基因型病毒株也會隨著時間逐漸演化出新的基因亞型，另外，也發現自 2018 年起有 L1 基因型病毒株入侵，並於 2020 年起陸續有發現國內 L3 基因型與且入侵的 L1 基因型病毒株進行重組。綜合以上，顯示國內 PRRSV 有多種病毒株交叉流行之情況。

The Molecular Epidemiology of Porcine Reproductive and Respiratory Syndrome Virus in Taiwan

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Abstract

Since the first isolation of Porcine Reproductive and Respiratory Syndrome Virus (PRRSV) in 1991, it has been widely present in pig farms across Taiwan, causing significant economic losses. This study aims to analyze the genetic sequences of PRRSV in Taiwan by molecular epidemiology method to understand the evolution of this virus in the country. The samples and virus strains collected by our institute from 2014 to 2024 were analyzed and compared, focusing on the NSP2, ORF5, ORF7, and full-length gene sequences. The results revealed that the prevailing genotype of PRRSV in Taiwan is the North American genotype, with the previously common L5 genotype now disappeared. The L3 genotype is currently dominant, but this genotype also evolves over time, leading to new genetic subtypes. Additionally, since 2018, L1 genotype virus strains have emerged, and starting from 2020, recombinant strains of both the domestic L3 genotype and the invading L1 genotype have been detected. In conclusion, the study shows that multiple PRRSV strains are co-circulating in pig farms in Taiwan.