

# 豬隻砂尼卡病毒分子流行病學與致病性研究

新興傳染病組

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## 摘要

砂尼卡病毒 (*Senecavirus A*, SVA) 為一種新興的豬隻水疱性疾病病原，臨床症狀與口蹄疫及豬水疱病等其他水疱性病毒感染相似，難以單憑外觀進行鑑別診斷。本研究針對 7 株臺灣 SVA 分離株進行全長序列與親緣分析，結果顯示這些病毒株與美國近年流行株具有高度相似性，且於親緣關係樹歸屬於相同分支。進一步透過口鼻途徑將選定之 SVA 分離株接種於 24 週齡豬隻，透過臨床監測與樣本採集，評估其致病性與免疫反應。試驗期間定期採集口腔與直腸拭子、血清樣本，分別以即時反轉錄聚合酶連鎖反應與病毒中和試驗進行檢測，並分析病毒於犧牲豬隻組織中分布情形。結果發現，所有攻毒組豬隻均出現水疱病變，且感染後第 28 天仍可由口腔拭子中檢出病毒核酸，而血清中和抗體至感染後第 56 天仍維持高度力價，病毒核酸則廣泛存在於多種組織中。綜上，本研究整合分子流行病學與動物感染模式，系統性分析 SVA 感染豬隻於感染初期至後期的病毒動態與免疫反應歷程，可作為後續致病機轉、傳播途徑與防控措施等深入性研究提供重要基礎。

# **Molecular epidemiology and pathogenicity study of**

## ***Senecavirus A in swine***

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### **Abstract**

*Senecavirus A* (SVA) is an emerging vesicular disease pathogen in swine, with clinical signs that closely resemble those caused by other vesicular viruses such as foot and mouth disease virus (FMDV) and swine vesicular disease virus (SVDV), making differential diagnosis based on clinical appearance challenging. In this study, we analyzed the full-length genome sequences and phylogenetic relationships of seven SVA isolates in Taiwan. The results revealed that these strains shared high sequence identity with contemporary strains from the United States and clustered within the same lineage in the phylogenetic tree. One of the SVA isolate from this study was further inoculated into 24-week-old pigs via oral-nasal route to evaluate its pathogenicity and immunological responses through clinical monitoring and sampling. During the experiment, oral and rectal swabs as well as serum samples were collected at regular intervals. All samples were tested using real-time reverse transcription PCR (RRT-PCR) and virus neutralization tests (VNT), respectively. Additionally, tissues from challenged sacrificed pigs were examined for viral distribution. All pigs in the group developed typical vesicular lesions, with viral RNA detectable in oral swabs up to 28 days post-infection (dpi). Neutralizing antibodies were maintained at high level through 56 dpi, and viral RNAs were widely distributed across various tissues. Overall, this study integrated molecular epidemiology and experimental infection models to systematically characterize the viral dynamics and host immune responses during the early and late phases of SVA infection in pigs. The findings provide a valuable foundation for future studies on SVA pathogenesis, transmission routes, and control strategies.