

# 豬流行性下痢病例報告

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## 摘要

去年冬季，台灣中南部陸續傳出哺乳小豬出現下痢及死亡疫情。本(103)年1月21日，本所收到來自屏東、雲林等地之疑似小豬下痢檢體。由於引發小豬下痢疫情之病毒性病原有傳染性胃腸炎、豬流行性下痢及輪狀病毒症等，這些病原引起的臨床症狀是非常相似的。經以病毒分離及RT-PCR檢測檢體病原之核酸等方式，初步診斷為豬病毒性下痢感染。隨後經電子顯微鏡及核酸定序等方式，確認本次造成仔豬下痢疫情之病原為豬流行性下痢病毒。而該病毒核酸M基因部分序列經與基因庫中豬流行性下痢病毒發表之基因進行比對後發現，本次引發流行之病毒株與美國2013年引發流行之病毒株序列相似度達100%。而與過去流行之標準病毒株CV-777相似度為98.1%。截至目前為止，本病之疫情已漸趨緩。全國送檢感染陽性率為75.61%(31/41)，計有9個縣市、31場豬隻確認感染。

# **Case Report: Porcine Epidemic Diarrhea**

Ming-Chung Deng

## **Abstract**

In January 2014, the suckling piglets exhibited severe diarrhea and death in pig farms in Pingtung and Yunlin County, Taiwan. The specimens were submitted to Animal Health Research Institute on January 21. It's very difficult to differentiate transmissible gastroenteritis (TGE), porcine epidemic diarrhea (PED) and porcine rotavirus infection by clinical syndromes. According to virus isolation and RT-PCR, the preliminary diagnosis was PED infection. The PED was confirmed by transmission electron microscope (TEM) examination and gene sequencing. Furthermore, the partial M gene of isolated PEDV was compared with other PEDV sequence in Genbank. The isolated PEDV was 100% identity with US strain isolated in 2013, and 98.1% identity with classical strain CV-777. Until now, the outbreak of PED has gradually slowed down. The positive rate of PEDV was 75.61% (31/41), including 31 pig farms distributed in 9 counties.