

## 中文摘要

豬霍亂沙門氏菌 (*Salmonella Choleraesuis*)是豬常見之致病菌,此感染症在人類也會造成嚴重的系統性感染。過去在臨床上使用抗生素治療此疾病有相當好的效果。然而,也由於抗生素的使用,近年來多重抗藥性的 *S. Choleraesuis* 感染也越來越常見。為了瞭解豬和人之間交互感染 *S. Choleraesuis* 之相關性,並找出其中可能持續循環的特殊基因型,本研究利用臨床上採集於 1997 至 2002 年間 54 株人之分離株和 158 株豬之分離株,使用 *Xba* I 進行限制? 切割其染色體 DNA,再以脈衝式電場電泳 (pulsed-field gel electrophoresis, PFGE)方法進行基因分型分析。結果於豬和人分離株各別找出五種與十一種基因型別。而且在 55%豬分離株中之 PFGE 分型結果,具有高度關性,此叢集型別定義為基因型 1 型 (gt 1)。與此 gt 1 相似的基因型同樣可在 69%的人類分離株中發現。抗藥性測試結果顯示,豬分離株與人類分離株中分別有 96%與 88%具有 5 種或 5 種以上抗生素之抗藥性。進一步由各年之分布結果來看,gt 1 型仍為人類及動物分離株最常見的基因型別。此研究結果充分顯示,相同基因型且具有多重抗藥性的 *S. Choleraesuis* 持續在台灣的動物和人之間傳遞。

## ABSTRACT

*Salmonella* Choleraesuis is a common pathogen in swine population, which also causes serious systematic infection in humans. Antimicrobial treatment was useful in clinical management. However, in recent years, multi-drug-resistance *S. Choleraesuis* is frequently seen in clinical settings. In order to trace the relationship and find the circulating *S. Choleraesuis* stains between pigs and humans, chromosomal DNA from 158 pig isolates and 54 human isolates were subjected to molecular analysis by pulsed-field gel electrophoresis (PFGE) with *XbaI* digestion. In this study, we successfully identified five and nine PFGE genotypes in swine and human isolates, respectively. In the swine isolates, 55% of them were with closely related PFGE patterns, designated as genotype 1 (gt 1). The similar genotype was also identified in 69% of the human isolates. By antimicrobial susceptibility test, 96% and 88% of the swine and human *S. Choleraesuis* isolates were multi-drug-resistance strains, which were resistant to at least 5 different antibiotics tested. Further stratified by different collection years, *S. Choleaesuis* with gt1 type was still the most prevalent one in pigs and humans. These observations strongly suggested that multi-drug resistance *S. Choleraesuis* with unique genotype be circulating between pigs and humans in Taiwan.