

**Epidemiologic relationship between
fluoroquinolone-resistant *Salmonella enterica*
serovar Choleraesuis strains isolated from
humans and pigs in Taiwan (1997 to 2002)**

葉光勝

**Chang CC;Lin YH;Chang CF;Yeh KS;Chiu CH;Chu
C;Chien MS;Hsu YM;Tsai LS;Chiou CS**

摘要

Abstract

The emergence of ciprofloxacin-resistant *Salmonella enterica* serovar Choleraesuis in recent years has become an important public health issue in Taiwan. The resistant strains that cause human infections are considered to be from pigs. In this study, we characterized 157 swine and 42 human *Salmonella* serovar Choleraesuis isolates by pulsed-field gel electrophoresis (PFGE) and drug susceptibility testing to investigate the epidemiologic relationship among the isolates. By PFGE analyses, two major clusters (clusters GA and GB) were identified. Isolates in cluster GA were of both human and swine origins, while those in cluster GB were from pigs only. Among the various genotypes identified, genotype gt-1a was the most prevalent, which was found in 71% (30 of 42) and 48% (76 of 157) of human and swine isolates, respectively. The susceptibility tests for the 106 gt-1a isolates identified 44 susceptibility profiles and showed that 73% of human isolates and 34% of swine isolates were resistant to three fluoroquinolones (ciprofloxacin, enrofloxacin, and norfloxacin). Our findings indicate that a clonal group of *Salmonella* serovar Choleraesuis may have been circulating in human and swine populations in Taiwan for years and that the fluoroquinolone-resistant *Salmonella* serovar Choleraesuis strains most likely evolved from a gt-1a clone that emerged in 2000 and that then caused widespread infections in humans and pigs. Nevertheless, it is still debatable whether those *Salmonella* infections in humans are caused by isolates derived from pigs, on the basis of the higher fluoroquinolone and other antimicrobial resistance percentages in human isolates than in pig isolates.