

Abstract

(Study 1)The emergence of ciprofloxacin-resistant *Salmonella enterica* serovar *Choleraesuis* in recent years has become an important public health issue in Taiwan. The resistant strains for human infections are considered to be from pigs. In this study, we characterized 157 swine and 42 human *S. 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 (GA and GB) were identified. Isolates in cluster GA were from both human and swine origins, while those in cluster GB were from only pigs. Among the various genotypes identified, gt-1a was the most prevalent, which was found in 71% (30/42) and 48% (76/157) 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 and 34% of swine isolates were resistant to three fluoroquinolones (ciprofloxacin, enrofloxacin and norfloxacin). Our findings indicated that a clonal group of *S. Choleraesuis* may have been circulating in human and swine populations in Taiwan for years, and the fluoroquinolone-resistant *S. Choleraesuis* was most likely evolved from a gt-1a clone, emerged in 2000, and then caused infections widely in humans and pigs. Nevertheless, it is still debatable as to 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 found in human isolates than in pig isolates.

(Study 2)Fifteen foodborne disease outbreaks were identified in Central Taiwan during the period of 1997-2003. Of the outbreaks, 7 caused by *S. Typhimurium*, 4 by *S. Bareilly*, 3 by *S. Enteritidis*, and 1 by *S. Cairo*. All the *Typhimurium* outbreaks were associated with eating raw beef and raw pork and *Enteritidis* outbreaks were associated with consuming chicken meal or egg products. The salmonellae isolates recovered from the outbreaks were subjected to PFGE analysis. PFGE patterns were compared with those in the *Salmonella* DNA fingerprint database, which contained PFGE patterns and host information of more than 3,000 salmonellae isolates of various serotypes. PFGE pattern comparison revealed that genetic relatedness among those *Typhimurium* isolates originated from beef was higher than those originated from pork. The comparison also found that *Typhimurium* isolates of beef origin had high genetic relatedness with a large group of isolates collected in 1998-2002, implying that most *Typhimurium* infections could result from consuming beef. PFGE genotyping also confirmed that the *Bareilly* isolates from the four outbreaks had common source of contamination. The PFGE genotypes of the isolates from the

two Enteritidis outbreaks were the major types for the Enteritidis isolates of year 2004, suggesting that the genetic strains had been circulating in Taiwan for years. Tracking contamination source is the most decisive means for control of salmonellae infections. PFGE genotyping of outbreak-originated and sporadic isolates can help to trace source of contamination.

Keywords : Salmonella ; drug resistance ; molecular epidemiology ; pulsed-field gel electrophoresis ; plasmid profile analysis