

**Ciprofloxacin-resistant *Salmonella enterica*  
Typhimurium and Choleraesuis from pig's to humans,  
Taiwan.**

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摘要

**Abstract**

We evaluated the disk susceptibility data of 671 nontyphoid *Salmonella* isolates collected from different parts of Taiwan from March 2001 to August 2001 and 1,261 nontyphoid *Salmonella* isolates from the National Taiwan University Hospital from 1996 to 2001. Overall, ciprofloxacin resistance was found in 2.7% (18/671) of all nontyphoid *Salmonella* isolates, in 1.4% (5/347) of *Salmonella enterica* serotype Typhimurium and in 7.5% (8/107) in *S. enterica* serotype Choleraesuis nationwide. MICs of six newer fluoroquinolones were determined for the following isolates: 37 isolates of ciprofloxacin-resistant (human) *S. Typhimurium* (N = 26) and Choleraesuis (N = 11), 10 isolates of ciprofloxacin-susceptible (MIC <1 mg/mL) (human) isolates of these two serotypes, and 15 swine isolates from *S. Choleraesuis* (N = 13) and Typhimurium (N = 2) with reduced susceptibility to ciprofloxacin (MIC >0.12 microg/mL). Sequence analysis of the *gyrA*, *gyrB*, *parC*, *parE*, and *acrR* genes, ciprofloxacin accumulation, and genotypes generated by pulsed-field gel electrophoresis with three restriction enzymes (*SpeI*, *XbaI*, and *BlnI*) were performed. All 26 *S. Typhimurium* isolates from humans and pigs belonged to genotype I. For *S. Choleraesuis* isolates, 91% (10/11) of human isolates and 54% (7/13) of swine isolates belonged to genotype B. These two genotypes isolates from humans all exhibited a high-level of resistance to ciprofloxacin (MIC 16-64 mg/mL). They had two-base substitutions in the *gyrA* gene at codons 83 (Ser83Phe) and 87 (Asp87Gly or Asp87Asn) and in the *parC* gene at codon 80 (Ser80Arg, Ser80Ile, or Ser84Lys). Our investigation documented that not only did these two *S. enterica* isolates have a high

prevalence of ciprofloxacin resistance nationwide but also that some closely related ciprofloxacin-resistant strains are disseminated from pigs to humans

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