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Multidrug-resistant *Salmonella typhimurium* and *Salmonella enteritidis* Identified by Multiplex PCR in Korea

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Antibiotic resistance in *Salmonella enteritidis* and *Salmonella typhimurium*, one of the most frequent etiologic pathogens of food-borne bacterial gastroenteritidis in human, is a serious health problem worldwide. Fifteen and 22 each of *S. enteritidis* and *S. typhimurium* were isolated from 1983 to 1999 in Korea and tested for their antibiotic resistance patterns and phage types. *S. enteritidis* isolates were highly resistant to sulfonamides (86.7%) and four isolates (26.7%) showed multiple antibiotic resistance. The most frequent phage type (PT) of *S. enteritids* was PT1 (33.3%) and none of the PT1 isolates had multiple antibiotic resistance. *S. typhimurium* isolates were highly resistant to streptomycin, sulfonamides, and tetracycline, 100%, 95.5%, and 86.4%, respectively. The incidence of multiple antibiotic resistance of *S. typhimurium* isolates was extremely high (100%) comparing to *S. enteritidis* isolates (26.7%). Two of the five ACSSuT type *S. typhimurium* isolates, resistant to ampicillin, chloramphenicol, streptomycin, sulfonamides, and tetracycline, were phage type DT104. All *S. typhimurium* isolates were sensitive to florfenicol.

For the rapid detection of multiple antibiotic resistant *S. enteritidis* and *S. typhimurium* isolates, particularly ACSSuT type *S. typhimurium* DT104, antibiotic resistance genes and *Salmonella* spp. specific gene, *cmlA/tetR*, *PSE-1*, and *TEM*, and *SipB/C*, were amplified using four pairs of primers in hot-started multiplex polymerase chain reaction (PCR). In the multiplex PCR, the two Korea isolates of *S. typhimurium* DT104 showed *TEM* amplicons instead of *PSE-1* for the ampicillin resistance. The multiplex PCR used in this study was useful in rapid detection of ACSSuT type *S. typhimurium* and identification of β-lactamase gene distribution among *Salmonella* isolates.