

MOLECULAR EPIDEMIOLOGY AND ANTIBIOGRAM OF *SALMONELLA* ISOLATES FROM HUMANS, SWINE AND PORK

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Abstract. The objectives of this study were to determine prevalence, antimicrobial resistance pattern and molecular epidemiology by pulsed-field gel electrophoresis (PFGE) of *Salmonella* isolated from humans, swine and pork. Three hundred and thirteen samples (84 humans, 84 swine and 145 pork) were collected from farms, slaughterhouses and retail markets in Nong Bua Lum Phu Province, northeastern Thailand from April 2012 to September 2013. Highest prevalence of *Salmonella* isolated from humans (43%) and swine (52%) were found at markets, followed by farms (28% and 32%, respectively) and slaughterhouses (24% and 26%, respectively). At farms, the most frequently identified serovar from humans was *S. Stanley* but from swine *S. Rissen*, the latter also being the most frequent from humans and pork samples at slaughterhouses and markets. All *S. Rissen* isolates were resistant to ampicillin, sulfamethoxazole/trimethoprim and tetracycline, and showed multidrug resistance patterns. PFGE of *Xba*I-digested chromosomal DNA performed on 36 *S. Rissen* isolates demonstrated five clusters: cluster A and B containing 1 pulsotype each from 1 isolate, cluster C contained 3 pulsotypes from 10 isolates, cluster D contained 2 pulsotypes from 19 isolates, and cluster E contained 1 pulsotype from 5 isolates. Serovars, antimicrobial resistance profiles and PFGE patterns were similar among *Salmonella* isolates from the three sources surveyed suggesting that swine is the major reservoir of salmonellosis and poor hygienic slaughterhouse procedures could promote contamination of pork and infection in humans.

Keywords: *Salmonella*, antimicrobial resistance, humans, pork, swine

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