

CHAPTER 6

CONCLUSIONS

6.1 CHAPTER 2

- Twenty-one *Salmonella* serotypes were detected in both farms and slaughterhouses.
- *Salmonella* Rissen is the highest frequency found in both farms and slaughterhouses (30.7% and 38.0%, respectively).
- Thirty-Three antimicrobial resistance patterns were demonstrated. There were including 10 common patterns isolated from pig farms and slaughterhouses.
- The highest frequency antimicrobial resistant pattern was “AMP, S, TE” (47 isolates, 15.7%) followed by “AMP, SXT, C, S, TE” (44 isolates, 14.7%) and “AMP, SXT, S, TE” (36 isolates, 12.0%).
- The highest frequency found was ampicillin (83.33%) followed by tetracycline (75.67%) and streptomycin (64%).
- There were no statistical differences in numbers of *Salmonella* found in different sources in each antimicrobial agent except cefotaxime and sulfamethoxazole-trimethoprim.
- Ciprofloxacin and norfloxacin resistant strains were not found in both farms and slaughterhouses.
- Resistance to amoxicillin- clavulanic acid was not observed in *Salmonella* strains isolated from slaughterhouse

6.2 CHAPTER 3

- The overall prevalence of class 1 integrons carrying *Salmonella* in tested samples was 13.71% (24/175).

- The prevalence in farm strains and slaughterhouse strains were 9.58% (7/73) and 16.67% (17/102), respectively.
- Only 4 serotypes carried class 1 integron genes: *Salmonella* Rissen, Typhimurium, Stanley and Agona.
- Most of the integron-carrying *Salmonella* strains were resistant to at least two antimicrobial agents.
- Most antimicrobial resistance phenotypes were not associated with related gene cassettes harbored by *Salmonella*
- Thirty *Salmonella* strains were grouped into six sequence types: ST 469, 48, 1500, 34, 19 and 29 identified by multi loci sequence typing.
- In general, ST 469 was the predominant grouped in this study, involved with 10 *Salmonella* strains, followed by ST 34 (7 strains), and ST 48 (5 strains).
- Thirteen pulsotypes could be grouped into five sequence type profiles.
- The Simpson's Diversity Index values of MLST and PFGE were 0.753 and 0.932, respectively. In addition, the Adjusted Rand coefficient was 0.253. The Wallace coefficient of PFGE to MLST was 0.769 and the Wallace coefficient of MLST to PFGE was 0.213.

6.3 CHAPTER 4

- Of the 173 *S. enterica* strains examined, 68 sequence types and 32 clonal complexes (CCs) were identified by multi loci sequence typing.
- Twenty-one strains belonged to four sequence types were represented by 4 sequence types (ST19, ST48, ST469 and ST1500) new to AEC countries.
- The discriminatory power value of Simpson's diversity index of MLST compared with serotyping was 0.959 and 0.904, respectively.
- *Salmonella* serotypes Weltevreden, *S. Typhi*, *S. Typhimurium*, *S. Enteritidis*, *S. Kentucky* and *S. Newport* were assigned to more than one sequence type.

6.3 CHAPTER 5

- Thai *Salmonella* isolates were not segregated from global strains.
- *S. Rissen* might be the major serotypes in this region.
- The contamination of *Salmonella* spp. along swine food production might be found in this study.
- *blaTEM-1*, *blaCTX-M-14*, *blaCTX-M-18*, *blaCTX-M-55*, *bla CTX-M-57*, *blatem* precursor confer extended-spectrum β -lactamases (ESBLs) were found 73.8%. Tetracycline resistance gene was found the highest prevalence with 85.7%.
- CARD is good, convenient and fastest tool for analyses antimicrobial resistance genes.
- Simpson's Index of diversity of PFGE and WGS were 0.919 and 0.993, respectively.
- Whole-genome sequencing (WGS) has become a significant and rapidly handy tool for microbial identification, pathogenesis, comparative analyses and outbreak investigation.
- Genome wide study was found 37 genes associated with survival of this pathogen such as metal uptake, antimicrobial resistance, antiseptic resistance, mobile genetic elements (integrons, transposon) stress responses induced within biofilms (Heat shock protein, sigma factor, SOS response).
- Genome wide study can be confirmed why this pathogen is persisted and very hard to eradicate in swine production chain.