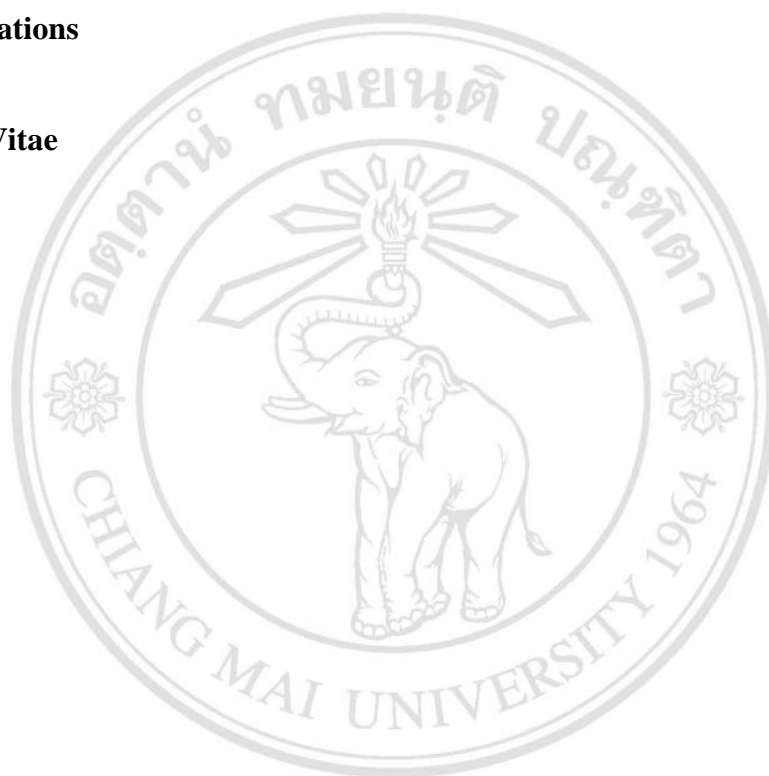


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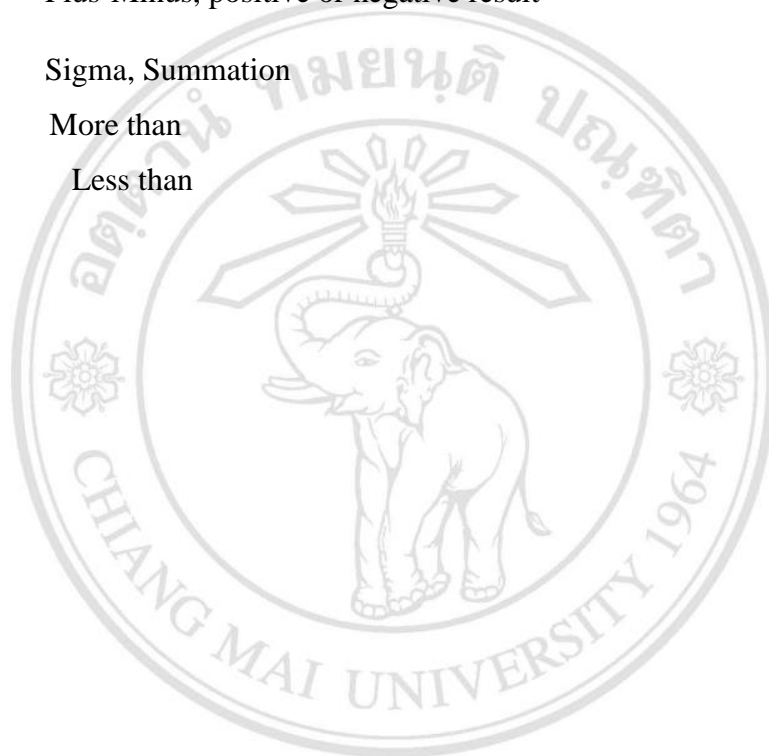
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LIST OF ABBREVIATIONS

| | | |
|------|---|----------------------------------|
| AMP | = | Ampicillin |
| AUG | = | Amoxicillin-clavulanic acid |
| bp | = | base pair |
| C | = | Chloramphenicol |
| CIP | = | Ciprofloxacin |
| CTX | = | Cefotaxime |
| D | = | Simpson diversity index |
| G | = | Genotype |
| GWAS | = | Genome wide association study |
| MDR | = | Multidrug resistance |
| MLST | = | Multi locus sequence typing |
| NA | = | Nalidixic acid |
| NOR | = | Norfloxacin |
| P | = | Phenotype |
| PFGE | = | Pulsed-field gel electrophoresis |
| S | = | Streptomycin |
| ST | = | Sequence type |
| SXT | = | Sulfamethoxazole-Trimethoprim |
| TE | = | Tetracycline |
| SLH | = | Slaughterhouse |
| WGS | = | Whole genome sequencing |

LIST OF SYMBOLS

| | |
|----------|---|
| β | Beta |
| - | Minus, negative results |
| + | Plus, positive results |
| \pm | Plus-Minus, positive or negative result |
| Σ | Sigma, Summation |
| $>$ | More than |
| $<$ | Less than |



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STATEMENT OF ORIGINALITY

1. This study focused on molecular epidemiology of *Salmonella* spp. isolated from swine industries in Chiang Mai and Lamphun Provinces. The tools used in this study included serotyping, Multi Locus Sequence Typing and Whole genome sequencing. To protect, surveillance the spreading of this organism through consumers protection.
2. In addition, antimicrobial resistance *Salmonella* spp. was also determined by antimicrobial susceptibility test, Presence of class 1 integrons responsible for several multidrug resistance trait and whole genome sequencing which was used to predict antimicrobial resistance ability of the isolates. This information used in selection suitable and effective antimicrobial treatment.
3. Finally, the mechanism for survival of this organism in swine industries environment was determined by genome wide association study. This may help in developing a more effective cleaning and disinfection program in swine industries.

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ข้อความแห่งการริเริ่ม

- 1) วิทยานิพนธ์นี้ได้มุ่งเน้นเกี่ยวกับบอณูระบาดวิทยาของเชื้อซัลโมเนลลาที่เพาะแยกได้จากอุตสาหกรรมการผลิตสุกร ในจังหวัดเชียงใหม่ และลำพูน โดยใช้เทคนิคต่างๆ ได้แก่ การหาซีโรไทป์ Multi Locus Sequence Typing และ Whole genome sequencing เพื่อนำข้อมูลไปใช้ในการป้องกันและเฝ้าระวังการแพร่กระจายของเชื้อสู่ผู้บริโภค
- 2) นอกจากนี้ ยังมีศึกษาเกี่ยวกับการดื้อยาปฏิชีวนะของเชื้อซัลโมเนลลา โดยการศึกษาจากการทดสอบความไวของยาปฏิชีวนะของเชื้อ การหายีนอินทริกอนชนิดที่ 1 ซึ่งก่อให้เกิดการดื้อต่อยาปฏิชีวนะได้หลายชนิด และการหายีนดื้อยาปฏิชีวนะของเชื้อโดยวิธีการ Whole genome sequencing เพื่อทำนายการดื้อต่อยาปฏิชีวนะของเชื้อ ซึ่งข้อมูลนี้ในการเลือกใช้ยาปฏิชีวนะในการรักษาการติดเชื้อได้อย่างมีประสิทธิภาพ
- 3) สุดท้ายนี้ ได้ทำการศึกษาความสัมพันธ์แนวกว้างตลอดจีโนม (Genome wide association study) ของเชื้อซัลโมเนลลา เพื่อวิเคราะห์หากลไกที่ทำให้เชื้อทนและอยู่รอดในสิ่งแวดล้อมในอุตสาหกรรมการผลิตสุกร เพื่อเป็นแนวทางในการพัฒนาและปรับปรุงระบบสุขาภิบาลและการเลือกใช้น้ำยามาเชื้อต่อไปได้

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