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**Genetic Mapping: Insights into Antibiotic Resistance Disparity between Porcine and Human ESBL *Salmonella* ST34 in Thailand through Genomic Analysis.**

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**Abstract:**

**Background/Objective:** Antibiotics have been vital in human and livestock health over the years. However, their overuse and misuse have precipitated a crisis of bacterial resistance, posing a significant threat to global health. *Salmonella* causing gastroenteritis, has increasingly become resistant to multiple antibiotics due to the emergence of Extended-Spectrum Beta-Lactamases (ESBLs). Reports of ESBL-producing *Salmonella*, notably the ST34 strain, are on the rise in Thailand, raising concerns about potential transmission to humans through food products originating from livestock. This study aims to elucidate the genomic epidemiology and antimicrobial resistance profiles of ESBL-producing *Salmonella* ST34 isolated from Thai slaughterhouses and other sources.

**Methods:** DNA from 5 *Salmonella* strains obtained from 570 samples of two slaughterhouses were sequenced using whole-genome analysis. Integrating our sequences with existing databases provided comprehensive insights into the genetic profiles of these strains. Subsequent bioinformatic analyses revealed crucial genetic linkages and resistance patterns.

**Results:** Our findings revealed a high prevalence of genes conferring resistance to multiple antibiotics, including third generation cephalosporins, quinolones, sulfamethoxazole, and tetracycline. Moreover, results identified the co-localization of ESBL (*bla*CTX-M-55) and quinolone resistance genes (*qnrS1*) within the same plasmid, suggesting the potential for simultaneous acquisition of multiple antibiotic resistances. Phylogenetic analysis unveiled significant epidemiological connections within slaughterhouses, indicating intra-facility transmission of *Salmonella* during processing. Furthermore, genetic links between *Salmonella* strains from humans, pigs, and slaughterhouses underscored the risk of zoonotic and cross-transmission.

**Conclusion:** Our study highlights the importance of continuous monitoring, stringent biosecurity measures, and responsible antibiotic use in both human and animal medicine. Furthermore, targeted intervention strategies informed by genomic epidemiology are crucial for effectively managing antibiotic resistance. These findings underscore the imperative of proactive measures to combat the growing threat of antibiotic-resistant bacteria, safeguarding public health for future generations.

**Keywords:** ESBL, pig, *Salmonella* spp.*,* slaughterhouse, Whole genome sequencing