

Genomic Analysis of *Salmonella* Isolates from Broilers and Swine in Upper Northern Thailand Using Long-read Whole Genome Sequencing

Orawan Boonma¹, Arphaphorn Dokphut¹, Kamonrat Krutharote¹ and Nattinee Kittiwat^{1,*}

Abstract

Background: *Salmonella* spp. is an important foodborne pathogen affecting public health and livestock production. The increasing prevalence of antimicrobial resistance (AMR), particularly multidrug resistance (MDR), poses a critical challenge to effective treatment and control. Recent advances in whole genome sequencing (WGS), especially long-read technologies, enable high-resolution and comprehensive genome analysis, facilitating precise characterization of genetic diversity, transmission dynamics, and resistance profiles.

Objectives: To comprehensively characterize and analyze the genomic features, antimicrobial resistance profiles, and phylogenetic relationships of *Salmonella* isolates from broilers and swine in Upper Northern Thailand using long-read WGS, and to evaluate the concordance between phenotypic and genotypic antimicrobial resistance.

Methods: A total of 20 *Salmonella* isolates obtained from cecal and meat samples of broilers and swine collected from slaughterhouses and retail meat shops across six provinces in Upper Northern Thailand in 2023 were analyzed using long-read WGS. The assembled genomes were subjected to bioinformatic analyses for comprehensive genomic characterization, including serotype determination and sequence type (ST) assignment based on multilocus sequence typing (MLST). Pangenome and phylogenetic analyses were conducted to characterize gene diversity and assess genetic relationships among isolates. Antimicrobial resistance genes (ARGs) and plasmid profiles were identified to characterize resistance determinants. Phenotypic susceptibility to nine antimicrobial agents was determined by broth microdilution test, and concordance between phenotypic and genotypic resistance was assessed using Cohen's kappa.

Results: All 20 isolates were successfully sequenced and assembled into high-quality genomes. Nine serotypes and nine sequence types (STs) were identified, with ST29 (Stanley) and ST469 (Rissen) predominating. Several STs (ST29, ST462, ST469, and ST1543) were distributed across multiple provinces and hosts, suggesting potential cross-host transmission and regional dissemination. Pangenome analysis identified 8,956 genes, including 41.4% core genes, which exhibited phylogenomic clustering that strictly aligned with ST classifications. A total of 25 ARGs across 10 antimicrobial classes were detected, including clinically important *bla*_{CTX-M-55}, *qnrS1* and *mcr-1.1*. MDR was observed in most STs (7/9 STs). Plasmids were detected in 60% of isolates, predominantly Col and Inc types. Phenotypic–genotypic AMR concordance ranged from moderate to substantial agreement ($\kappa = 0.53$ – 0.70).

Conclusion: *Salmonella* isolates from Upper Northern Thailand exhibited substantial genetic diversity, widespread MDR, and clinically important resistance determinants. These findings, enabled by long-read WGS, highlight the need for strengthened genomic surveillance in livestock production and the food chain to inform targeted control strategies and mitigate antimicrobial resistance risks within a One Health framework.

Keywords: *Salmonella*, Whole genome sequencing, Antimicrobial resistance, Livestock, Northern Thailand

¹ Veterinary Research and Development Center (Upper Northern Region), Lampang, Thailand

* Corresponding author; E-mail: nattinee.k@dld.go.th