

Analysis of Phenotypic Antimicrobial Resistance Patterns of *Salmonella* in Meat Using Hierarchical Clustering in Western Thailand, 2022–2024

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Abstract

Background: Antimicrobial resistance (AMR) in *Salmonella* is a major global concern, especially through contaminated meat. Multidrug-resistant (MDR) strains, defined as resistance to three or more antimicrobial classes, are increasingly detected in livestock and threaten both food safety and treatment success. Although Thailand applies a “One Health” surveillance framework, phenotypic resistance data in food-producing animals remain limited. Strengthening this area is crucial because resistant strains from livestock can enter humans via the food chain. This study used hierarchical clustering to group isolates by similarity in resistance profiles, revealing resistance clusters, MDR patterns, and emerging trends that enhance traditional analyses.

Objective: To characterize phenotypic AMR patterns of *Salmonella* isolates from pork and poultry meat in western Thailand (2022–2024) using hierarchical clustering, and to assess epidemiological differences in MDR contamination.

Methods: A total of 446 *Salmonella* isolates were cultured and identified from pork and poultry meat samples collected in western Thailand between 2022 and 2024. The dataset used in this study was secondary data, derived from routine surveillance activities and subsequently analyzed for research purposes. Antimicrobial susceptibility testing was performed against 11 agents following Clinical and Laboratory Standards Institute (CLSI) guidelines. Minimum inhibitory concentration (MIC) values were converted into ordinal scales and then normalized to place all variables on a comparable 0–1 range, ensuring equal contribution to distance calculations. The processed data were analyzed using agglomerative hierarchical clustering, employing Euclidean distance and Ward’s linkage in Orange Data Mining (version 3.36). Epidemiological differences in multidrug resistance (MDR) contamination were assessed using odds ratios (OR) with 95% confidence intervals and the chi square test.

Results: Five distinct resistance clusters were identified (average Silhouette coefficient = 0.16, consistent with the expected heterogeneity of phenotypic AMR data). Cluster 1 ($n = 183$) exhibited minimal resistance (<6%). Cluster 2 ($n = 64$) showed extensive MDR, with AMP (100%), CHL, GEN, and TET (>95%), and CTX (>92%). Cluster 3 ($n = 82$) displayed moderate resistance to AMP (78%) and TET (76%) but remained susceptible to cephalosporins. Cluster 4 ($n = 37$) demonstrated high resistance to older antimicrobials (AMP 100%, CHL 95%, TET 89%, and SXT 86%) but full susceptibility to CTX, CAZ, CST, GEN, and MEM. Cluster 5 ($n = 80$) showed a resistance profile similar to Cluster 3 but with markedly higher resistance to AMP (95%) and TET (96%). Epidemiological analysis revealed that only pork had a significantly higher risk of MDR contamination than poultry meat (OR 2.16, 95% CI 1.47–3.19, $p < 0.001$), while no difference was observed between slaughterhouses and retail markets.

Conclusion: This study revealed substantial heterogeneity in phenotypic antimicrobial resistance among *Salmonella* isolates from pork and poultry meat in western Thailand, resulting in five distinct resistance clusters ranging from fully susceptible to extensively multidrug-resistant profiles. The identification of clusters with high resistance to older antimicrobials (AMP, CHL, TET, SXT) and the presence of a strongly MDR group underscore the ongoing selective pressure within the food production system. Pork was identified as a significantly higher-risk source of MDR contamination than poultry meat, highlighting a critical control point for targeted interventions. Overall, the findings emphasize the need to strengthen AMR surveillance within the One Health framework and to implement evidence-based strategies to mitigate the spread of resistant *Salmonella* through the food chain.

Keywords: *Salmonella*, Antimicrobial resistance, Multidrug resistance, Hierarchical clustering, Western Thailand

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