



การนำเสนอผลงาน

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

Supaporn Meeboon, Kittiya Paiboonkunkon, Trakarnsak Paethaisong



นางสาวสุภาพร มีบุญ

นักวิทยาศาสตร์การแพทย์ชำนาญการพิเศษ



ศวพ.ภาคตะวันตก จ.ราชบุรี

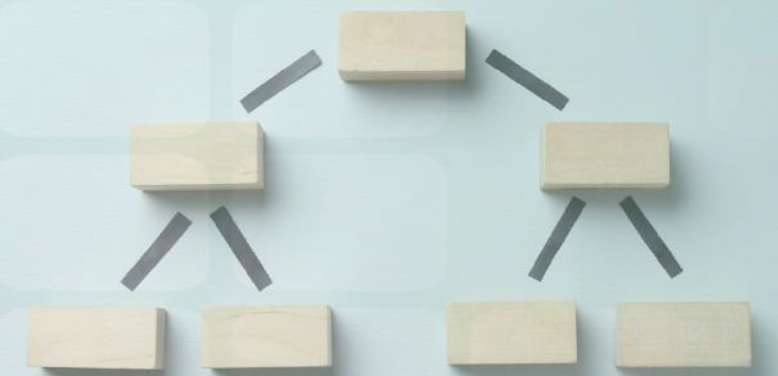


Background

- Antimicrobial resistance (AMR) in *Salmonella* is a global public health concern, particularly due to contamination in meat products.
- Multidrug-resistant (MDR) strains—defined as resistance to three or more antimicrobial classes—pose serious threats to food safety and treatment outcomes in humans.
- Strengthened surveillance under the “One Health framework” is essential, as resistant strains originating from livestock can be transmitted to humans through the food chain.

Research Objectives

- To classify the isolates based on similarity of AMR patterns using hierarchical clustering techniques.
- To investigate the antimicrobial resistance (AMR) patterns of *Salmonella* isolated from pork and poultry meat.
- To evaluate epidemiological differences and the risk of MDR occurrence in meat products.



Materials and Methods

- A total of 446 *Salmonella* isolates were used, collected between 2022 and 2024.
- Antimicrobial susceptibility testing for 11 agents was performed following CLSI guidelines to determine minimum inhibitory concentrations (MICs).
- AMP, AMC, CTX, CAZ, CIP, NAL, TET, CHL, GEN, STR, SXT



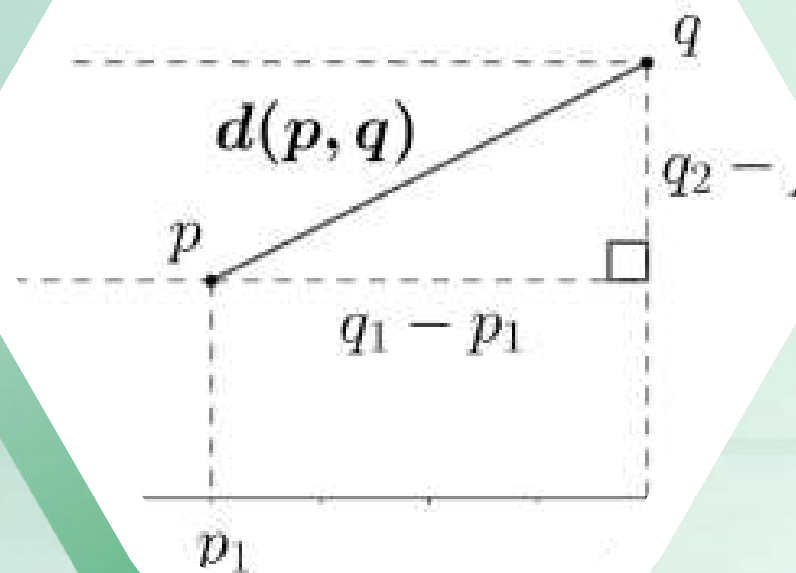
Data analysis using Data Mining (Orange)

- **Open-source data mining tool** – Orange is an open-source platform for data mining, machine learning, and visual workflow analysis.
- **Interactive analytics platform** – It provides drag-and-drop widgets for preprocessing, modeling, and visualization.
- **Developed in Slovenia** – 1996; Orange Data Mining (v 3.36).



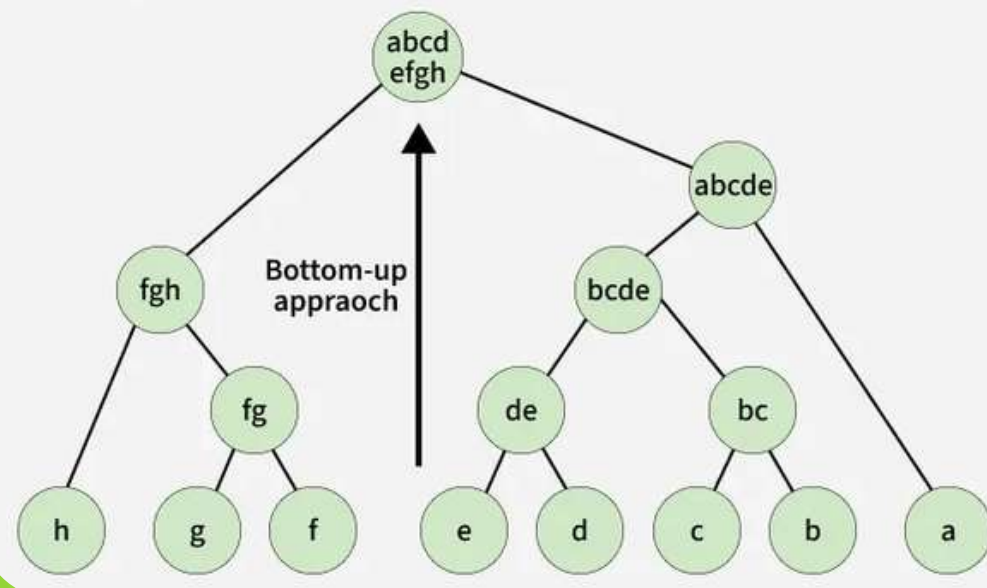
Data analysis using Data Mining (Orange)

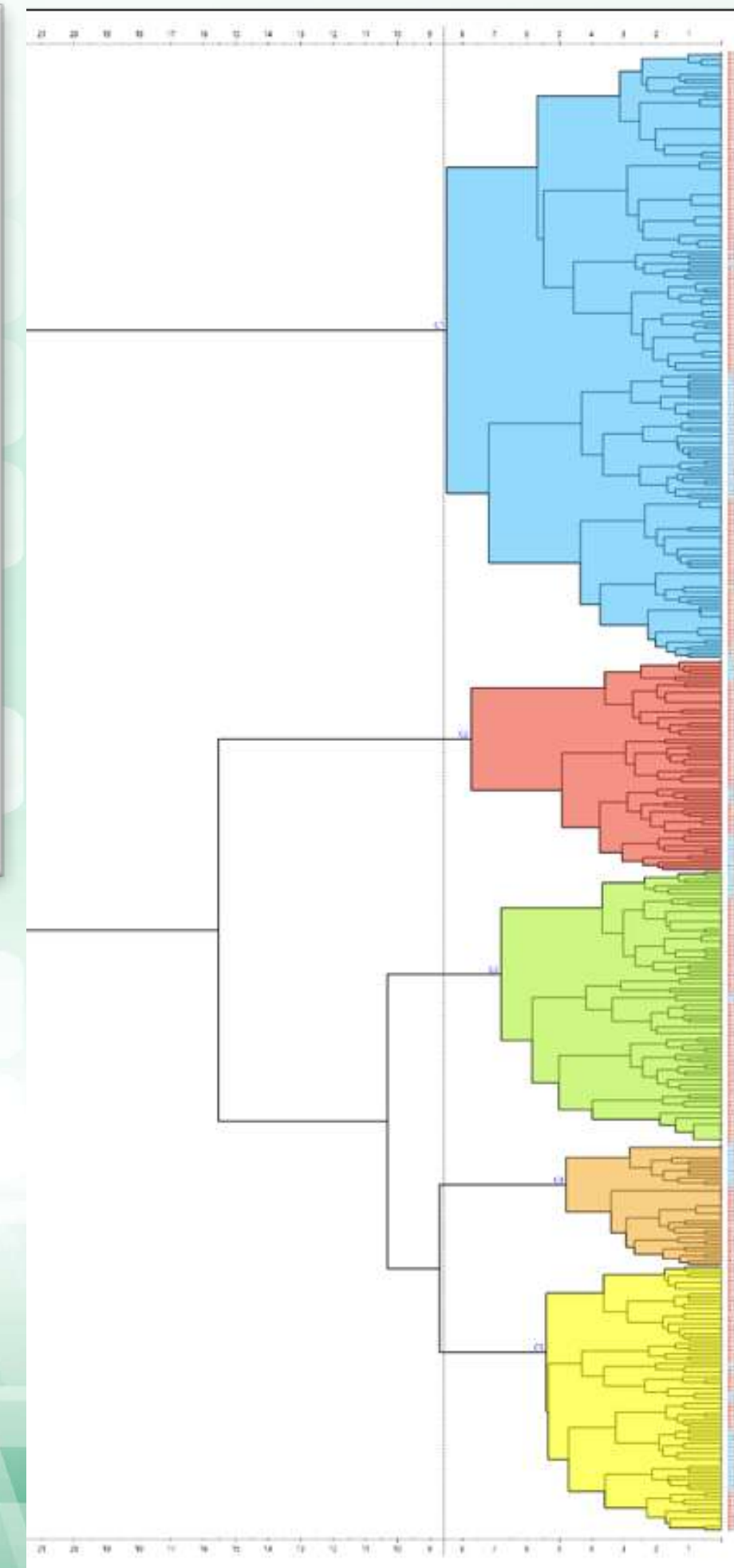
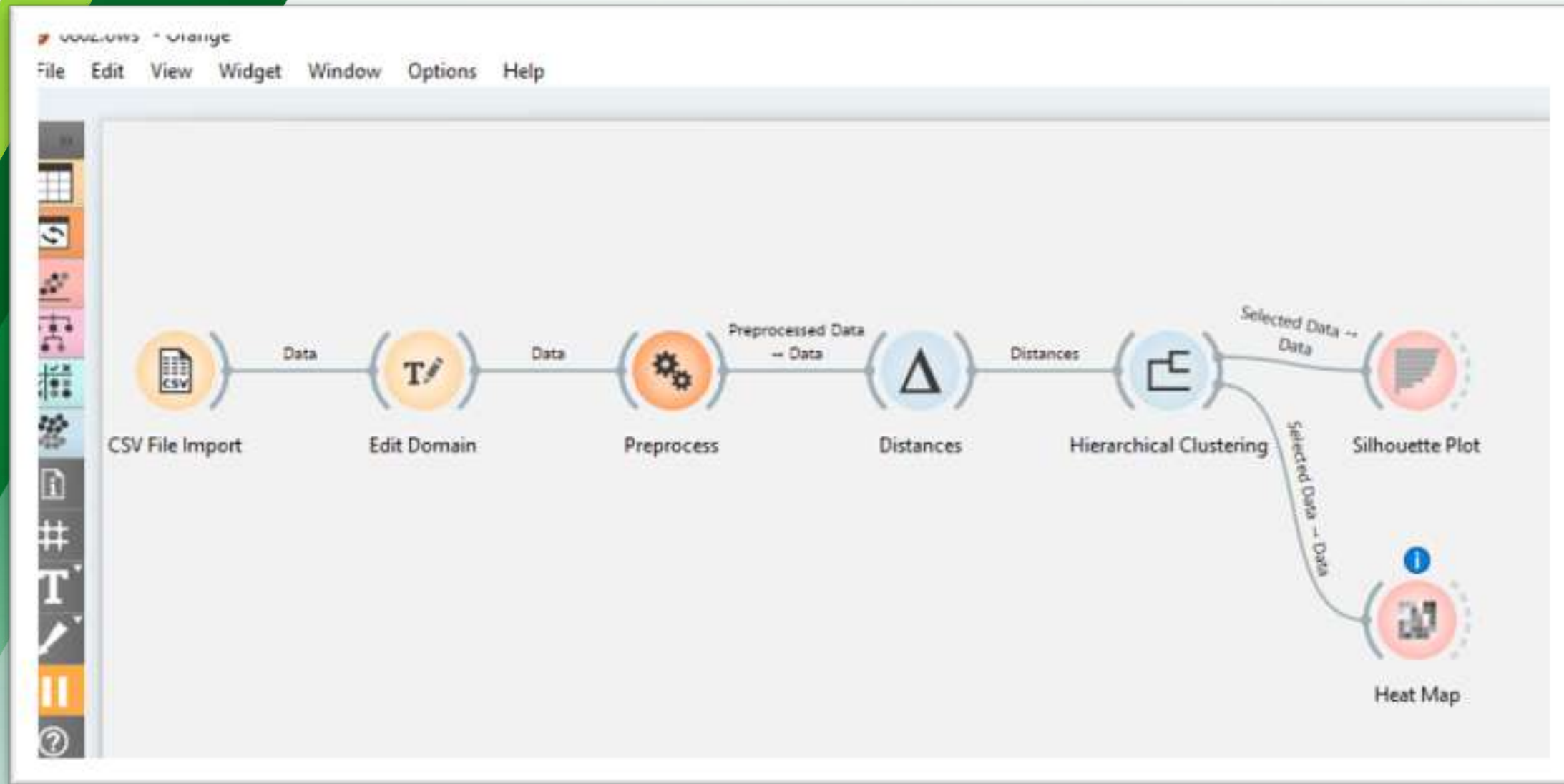
$$= (q_1 - p_1)^2 + (q_2 - p_2)^2$$



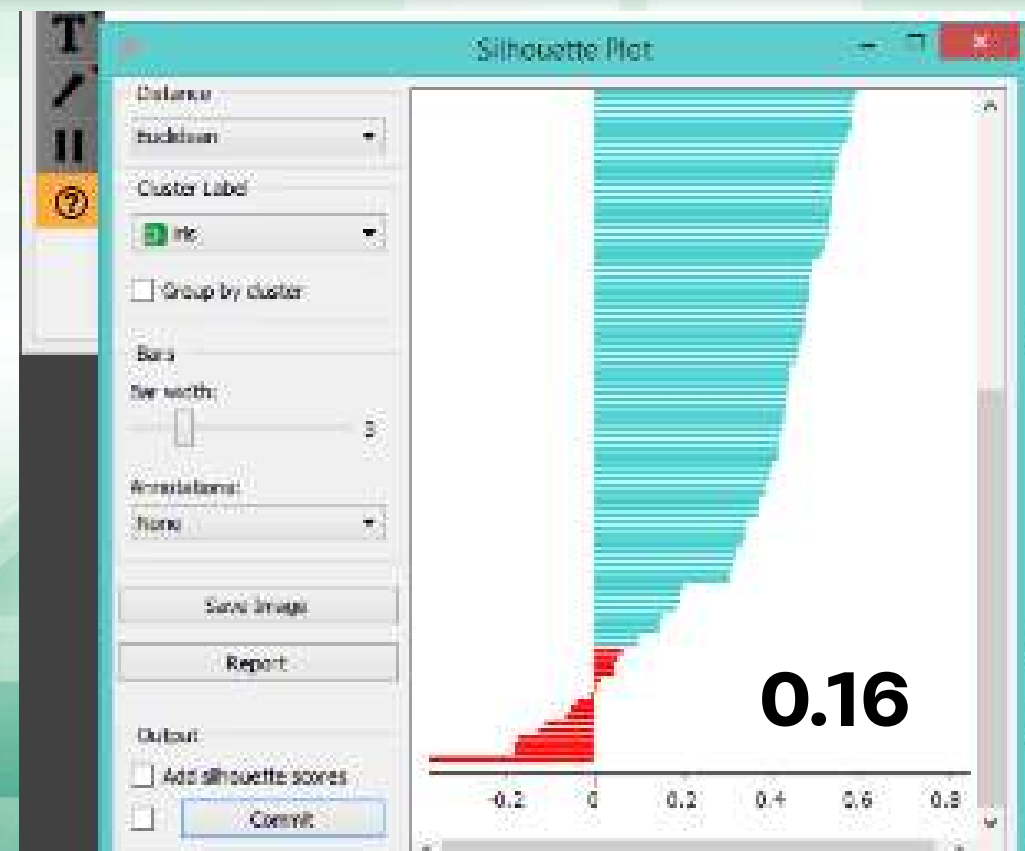
- **Data Pre-processing:** MIC values were converted into ordinal scales and normalized to the 0–1 range to ensure equal weighting across all antimicrobial agents.
- **Distance & Linkage:** The analysis employed Euclidean distance and Ward's linkage for cluster construction.
- **Study Findings –** The analysis identified five distinct clusters of isolates, supported by a Silhouette coefficient of 0.16, indicating a meaningful though moderately separated clustering structure.

Agglomerative Clustering

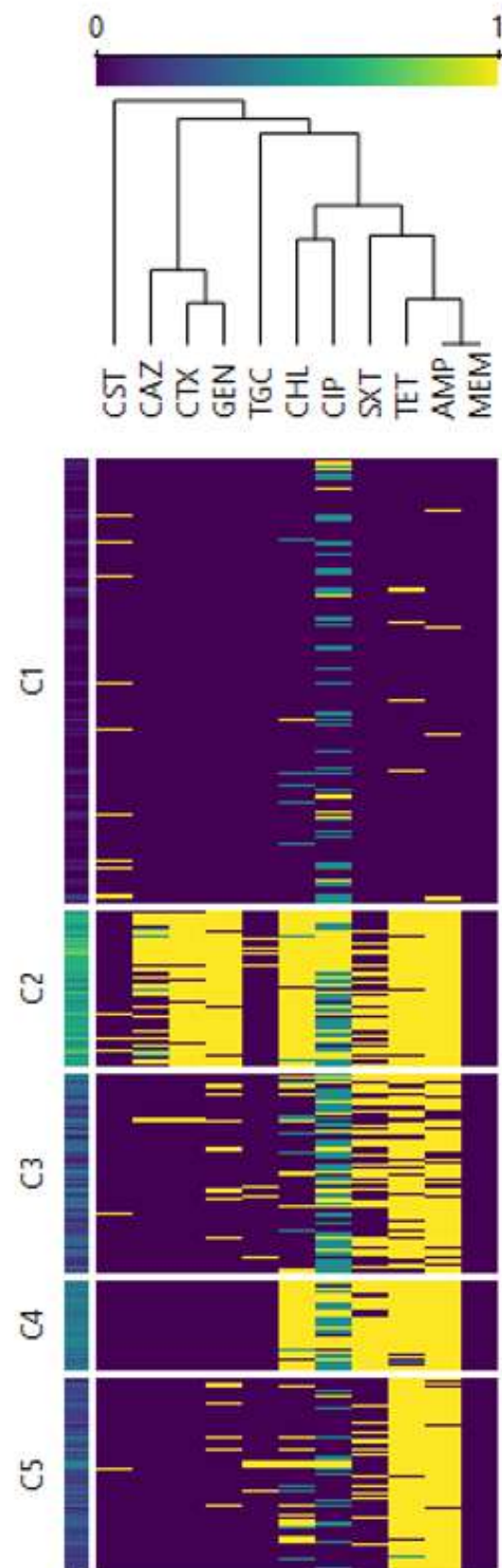




orange
DATA MINING

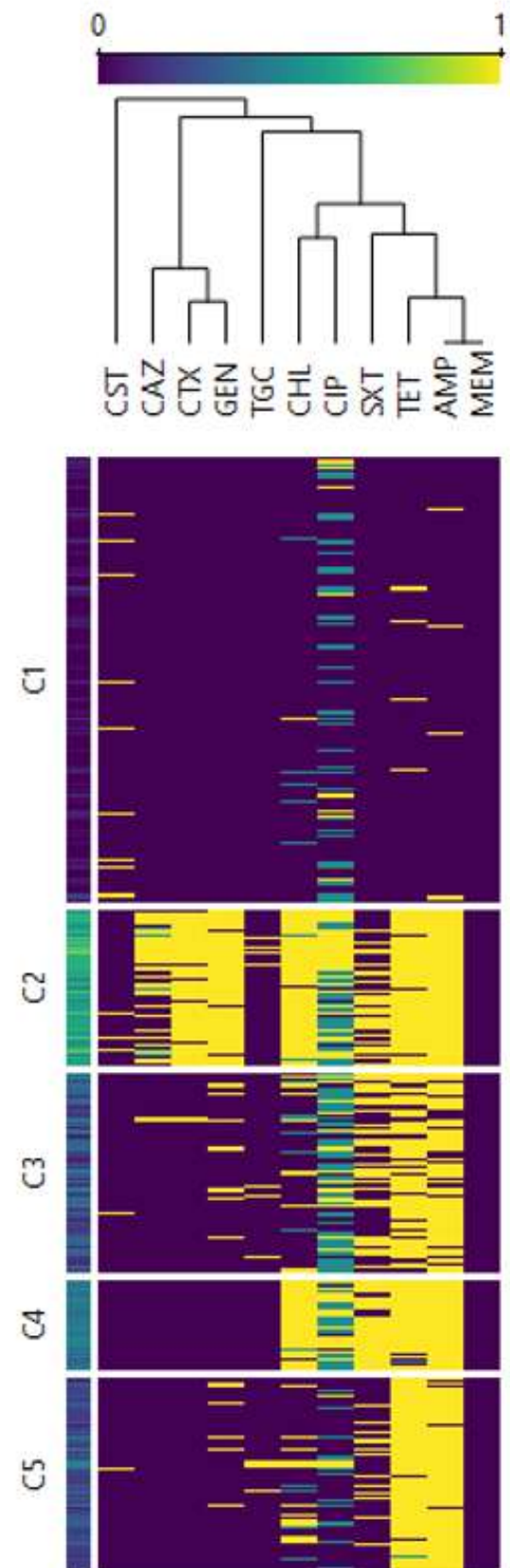


Study Results: Overview of the Five Clusters



- **Cluster 1 (n = 183):** This was the largest cluster, characterized by very low antimicrobial resistance, with resistance rates below 6% across all tested drugs.
- **Cluster 2 (n = 64):** Identified as the most critical cluster, representing extensive multidrug resistance (MDR). Isolates in this group exhibited near-complete resistance to multiple agents, including AMP (100%) and CHL/GEN/TET (>95%), and notably showed very high resistance to CTX (>92%).

Study Results: Overview of the Five Clusters



- **Cluster 3 (n = 82):** Displayed moderate resistance to AMP (78%) and TET (76%), while remaining fully susceptible to cephalosporins.
- **Cluster 4 (n = 37):** Demonstrated high resistance to older antimicrobials – AMP 100%, CHL 95%, TET 89%, and SXT 86% – but showed full susceptibility to CTX, CAZ, CST, GEN, and MEM.
- **Cluster 5 (n = 80):** Exhibited a resistance pattern similar to Cluster 3 but with markedly higher resistance to AMP (95%) and TET (96%).

Epidemiological Risk Analysis

Pork showed the highest risk

Pork samples had a **2.16**-fold higher likelihood of containing *MDR Salmonella* compared to poultry ($p < 0.001$).



2.16x
Higher Risk



Higher Likelihood of
MDR Salmonella

MDR Salmonella

=
VS



Lower Risk



Lower Likelihood of
MDR Salmonella



Sampling location: No significant difference in antimicrobial resistance levels was observed between samples collected from slaughterhouses and retail markets.

95% CI 1.47–3.19

Summary and Recommendations

- **Data-driven clustering – Appropriate analysis clearly separated resistance patterns and provides a strong base for future genomic work.**
- **Pork MDR risk – Pork showed a higher likelihood of MDR *Salmonella* contamination than poultry.**
- **Key resistant drugs – AMP, CHL, TET, and SXT were the main antimicrobial groups with high resistance.**

Acknowledgements

- สำนักตรวจสอบคุณภาพสินค้าปศุสัตว์
- กองควบคุมอาหารและยาสัตว์
- ปศุสัตว์จังหวัดในพื้นที่เขต 7
- ห้องปฏิบัติการตรวจวิเคราะห์คุณภาพเนื้อสัตว์





Thank you