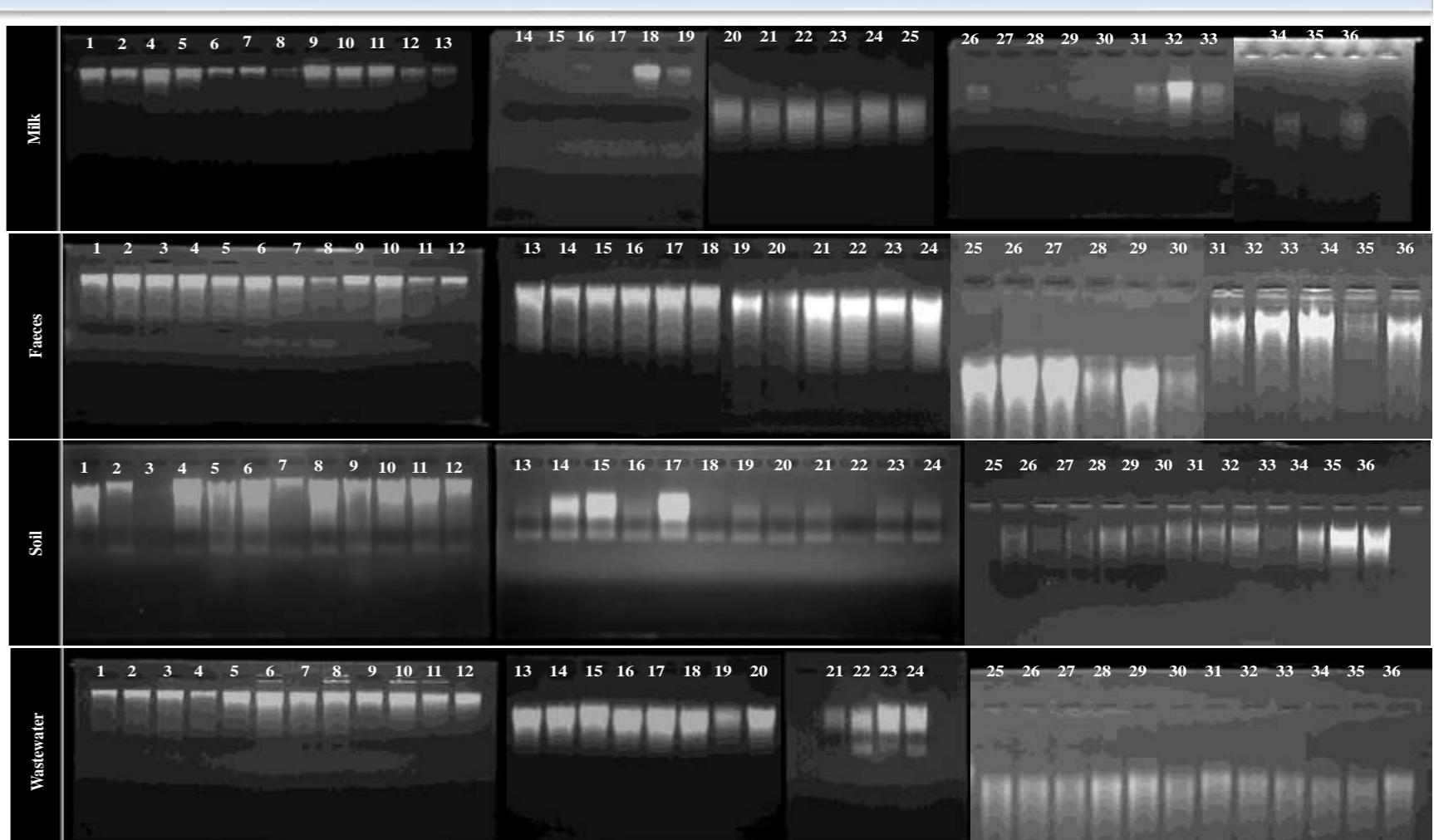
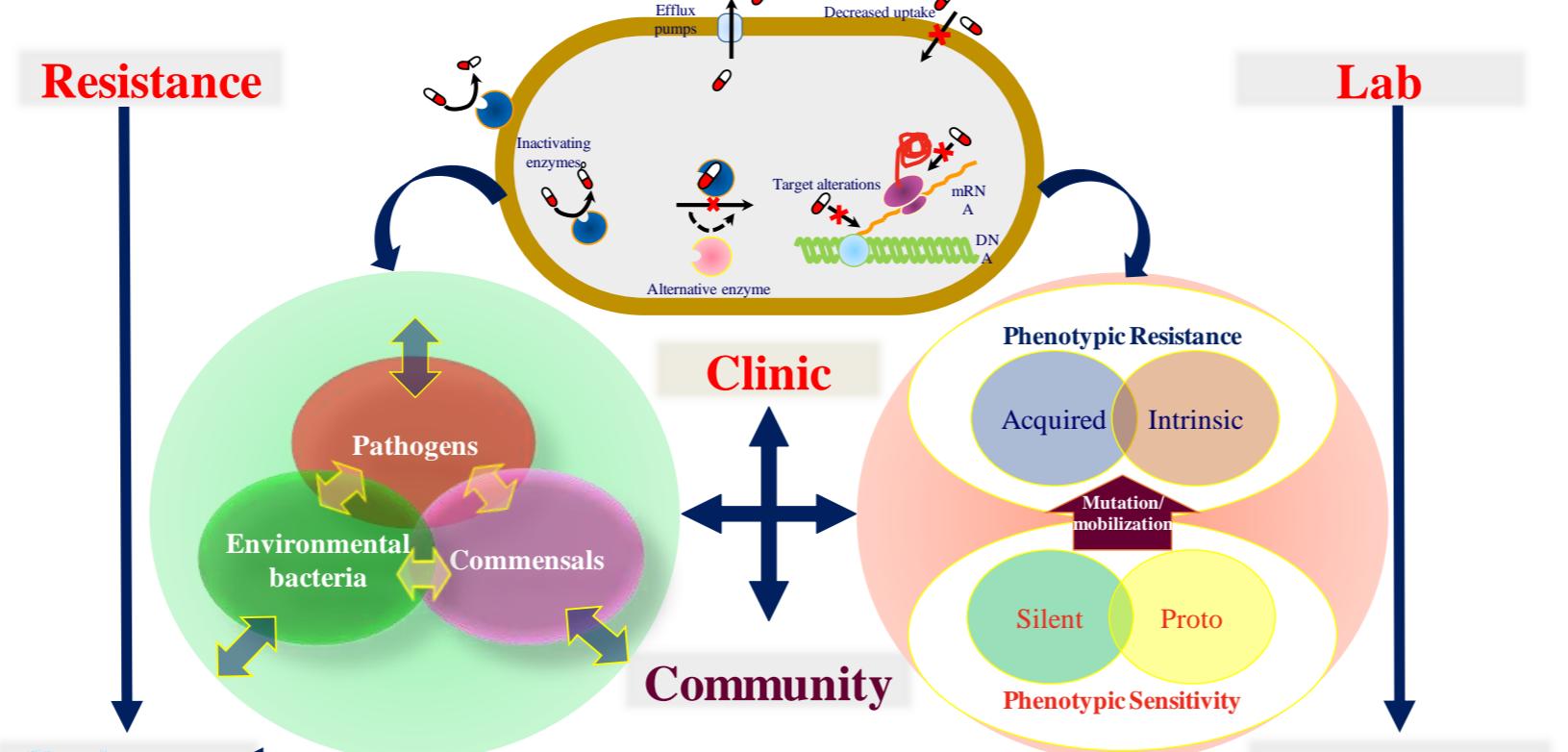
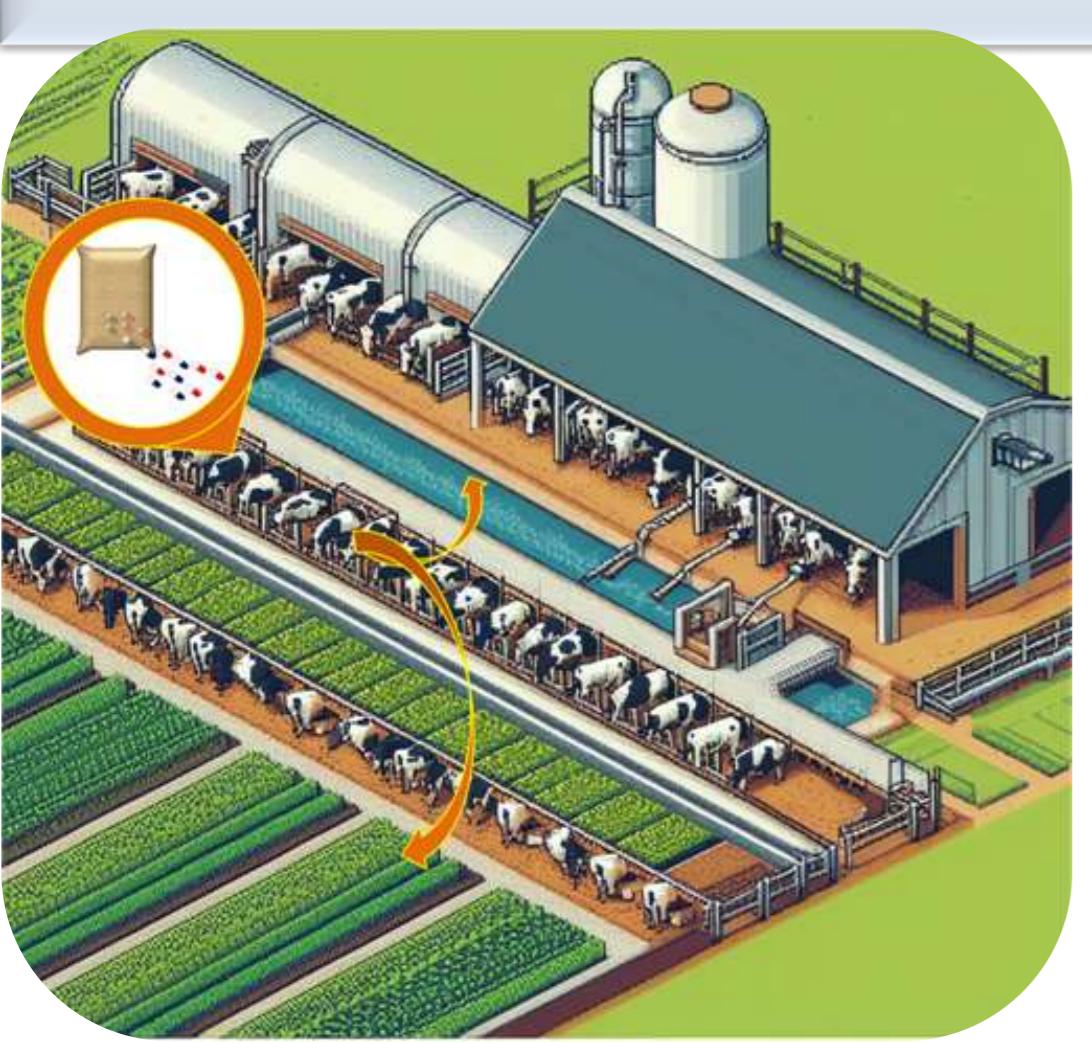


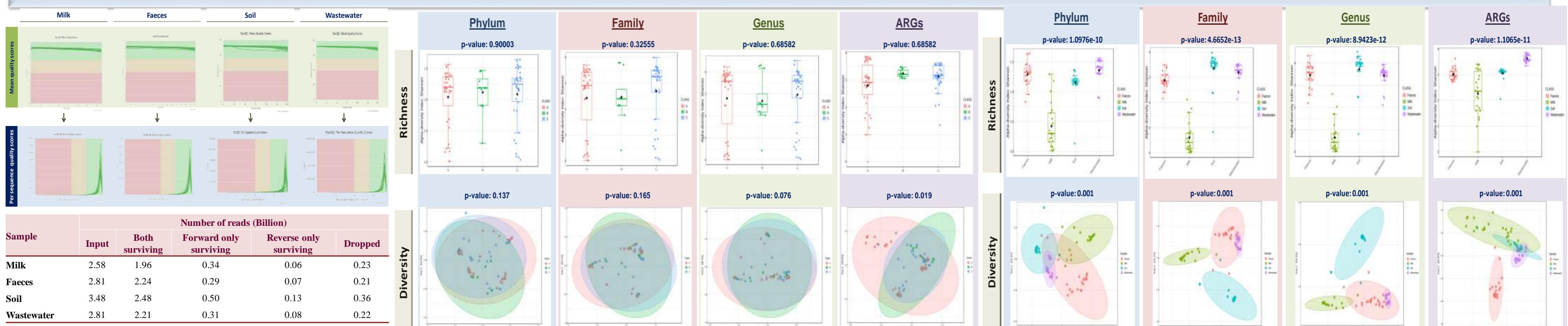
Metagenomic Insights into the Antibiotic Resistome of an Organized Dairy Production System

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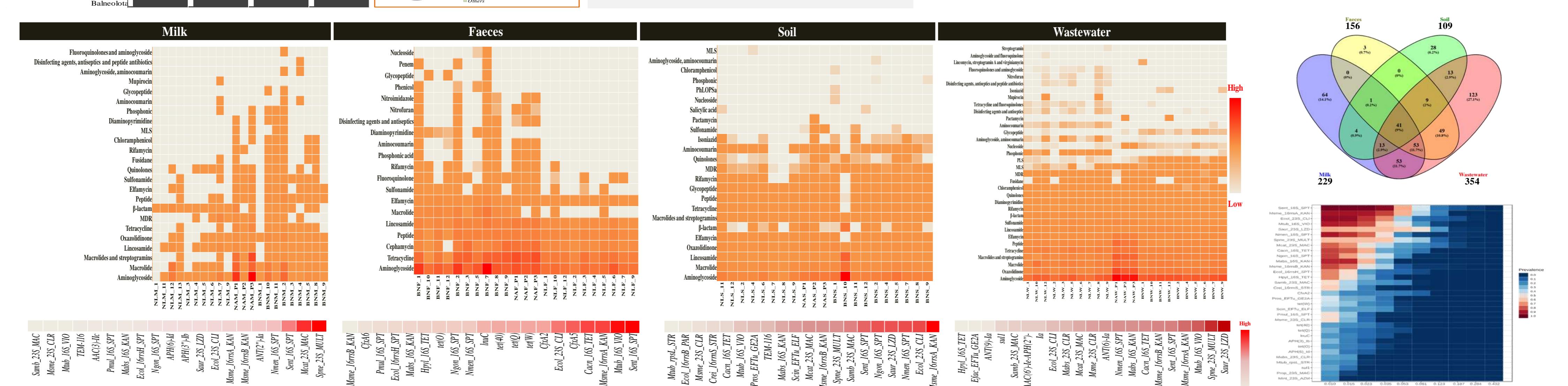
Study Overview



Microbiome and Resistome Ecological Indexes of Dairy Production System



Microbiome and Resistome of Dairy Production System



Conclusions

- ✓ Aminoglycoside resistant genes were most abundant and common among all the sample types
- ✓ Antibiotic target alteration was the most predominant antibiotic resistant mechanism
- ✓ The most abundant antibiotic resistant genes were present in wastewater, followed by faeces, soil and milk
- ✓ In dairy production system, wastewater is the reservoir of antibiotic resistant genes

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Declaration

There is no conflict of interest for authors in poster publication.

