

## **Synthesis: The Methodological Gap**

The foregoing review reveals a critical methodological gap at the intersection of computational approaches and environmental AMR surveillance.

### Comparative Summary of Related Studies

Author	Title	Year	Unsupervised	Supervised	Focus	Contribution
Nguyen et al.	ML for Predicting Antimicrobial MICs	2018	No	Yes	Genomic AMR	Salmonella MICs
Ardila et al.	Systematic Review of ML in AMR	2025	No	Yes	Systematic review	RF/GBDT
Parthasarathi et al.	Clustering-Based AMR Gene Analysis	2024	Yes	Yes	AMR gene clustering	Silhouette 0.82
Kou et al.	Spatial Epidemiology of E. coli	2025	No	No	Spatial epidemiology	Spatial autocorrelation
Abada et al.	Ward's Clustering for Agricultural MDR	2025	Yes	No	Agricultural MDR	Ward's clustering
Abamo et al.	INOHAC AMR Project Two	2024	No	No	Environmental surveillance	Multi-regional dataset
<b>Current Study</b>	<b>Pattern Recognition of AMR</b>	<b>2026</b>	<b>Yes</b>	<b>Yes</b>	<b>Water-fish-human nexus</b>	<b>Hierarchical + RF</b>

Table 1: Comparative Summary of Computational Approaches to AMR Analysis

*The current study uniquely integrates unsupervised pattern discovery with supervised validation for multi-regional environmental surveillance.*

**Limitations of Existing Approaches.** Supervised methods achieve high accuracy but cannot identify novel resistance patterns absent from training data. Unsupervised clustering, while effective in agricultural and clinical settings, has rarely been applied to multi-regional One Health surveillance. Spatial epidemiology operates on aggregated metrics rather than phenotypic profiles. Philippine surveillance has relied on conventional MDR classification, leaving the INOHAC dataset's pattern discovery potential unrealized.

**The Present Study's Contribution.** This study addresses these gaps through a hybrid unsupervised-supervised framework for environmental AMR surveillance. Ward's hierarchical clustering discovers resistance archetypes without predefined labels, while Random Forest classification validates whether clusters represent biologically coherent structures. Applying this methodology to isolates spanning multiple Philippine regions and ecological compartments (water, fish, human) enables characterization of resistance phenotypes specific to the One Health nexus. This integrated approach advances beyond purely supervised prediction or unsupervised clustering alone, offering a reproducible framework for future surveillance studies.