



Metagenomic and culture based insights into host and plasmid contexts of high risk ARGs in poultry farm environments

Yaling Wang^{1, 2#}, Lianwei Ye^{1, 3, 4#}, Linan He^{1, 2#}, Zhenlong Wu⁵,
Yiwen Yang^{6*}, Sheng Chen^{1, 2*}

¹Shenzhen Key Lab for Biological Safety Control,
The Hong Kong Polytechnic University Shenzhen Research Institute

²Department of Food Science and Nutrition, The Hong Kong Polytechnic University

³School of Laboratory Medicine and Life Science, Wenzhou Medical University

⁴One Health Innovation Center of Zhejiang Province

⁵State Key Laboratory of Animal Nutrition and Feeding, China Agricultural University

⁶Key Laboratory of Feed Biotechnology of Ministry of Agriculture and Rural Affairs,
Chinese Academy of Agricultural Sciences



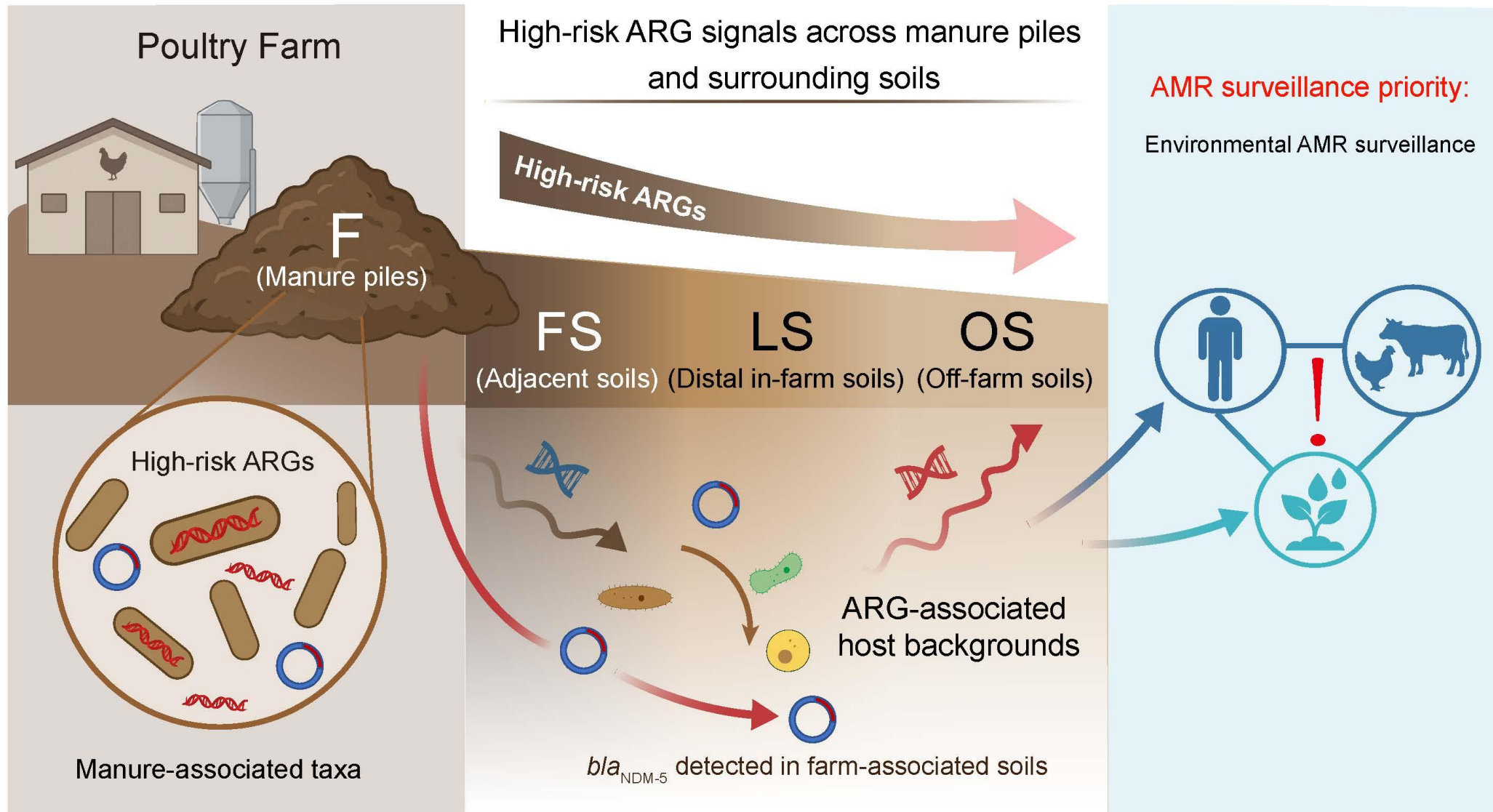
Yaling Wang, Lianwei Ye, Linan He, Zhenlong Wu, Yiwen Yang, Sheng Chen. 2026.

Metagenomic and culture based insights into host and plasmid contexts of high risk ARGs in poultry farm environments.

iMetaOmics 3:e70143. <https://doi.org/10.1002/imo2.70143>



Introduction



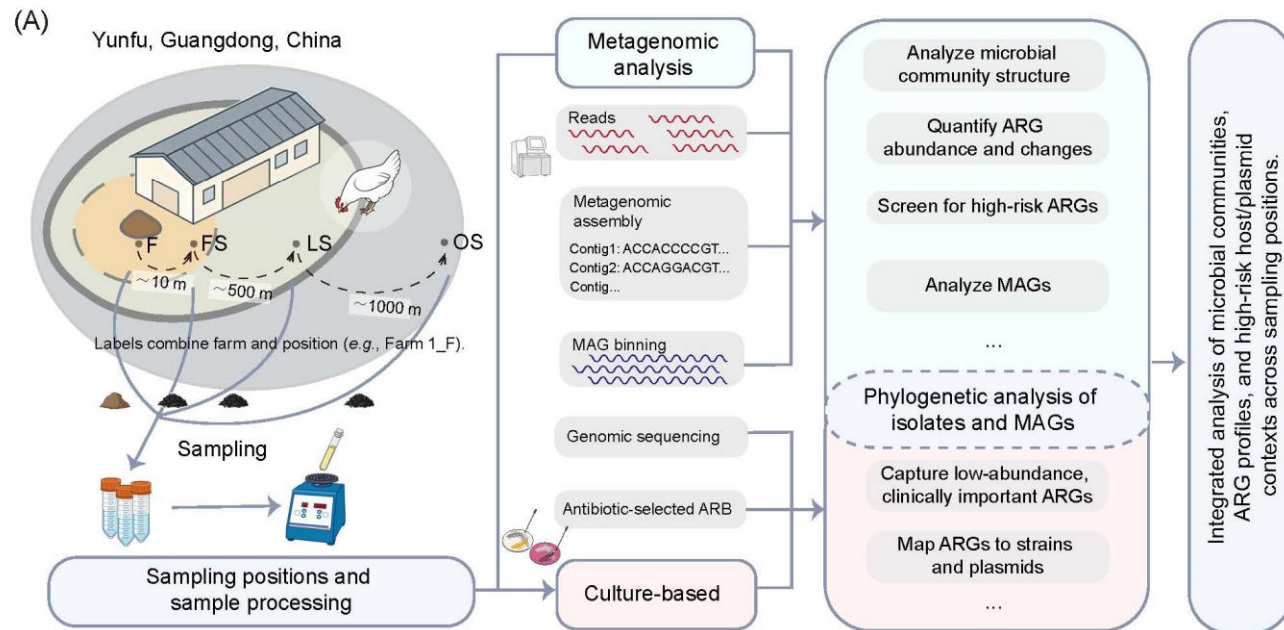
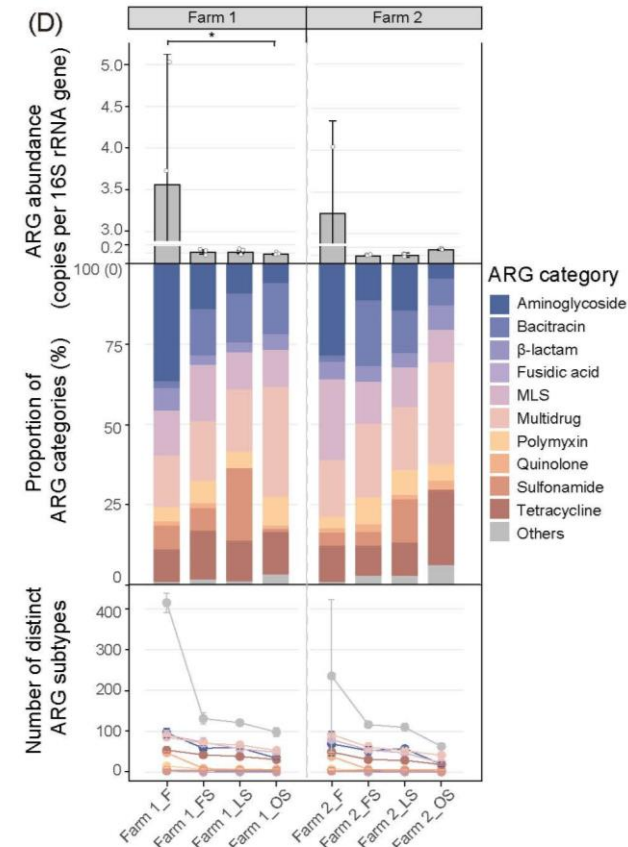
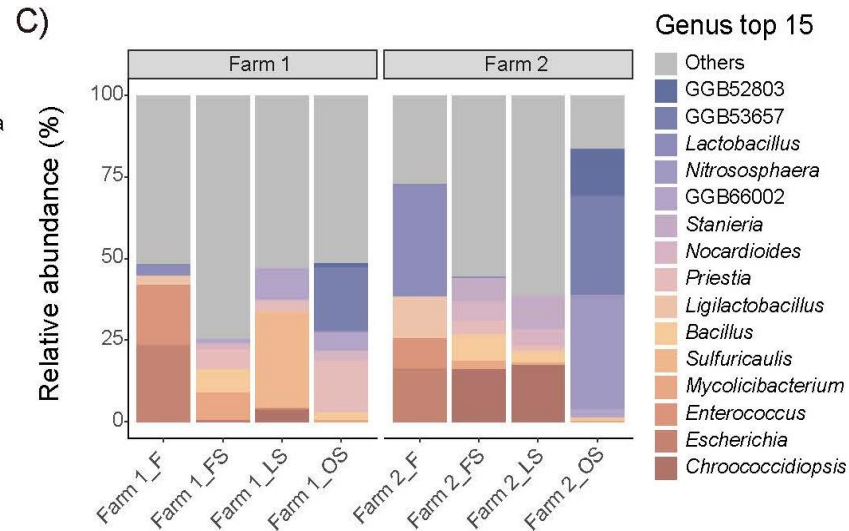
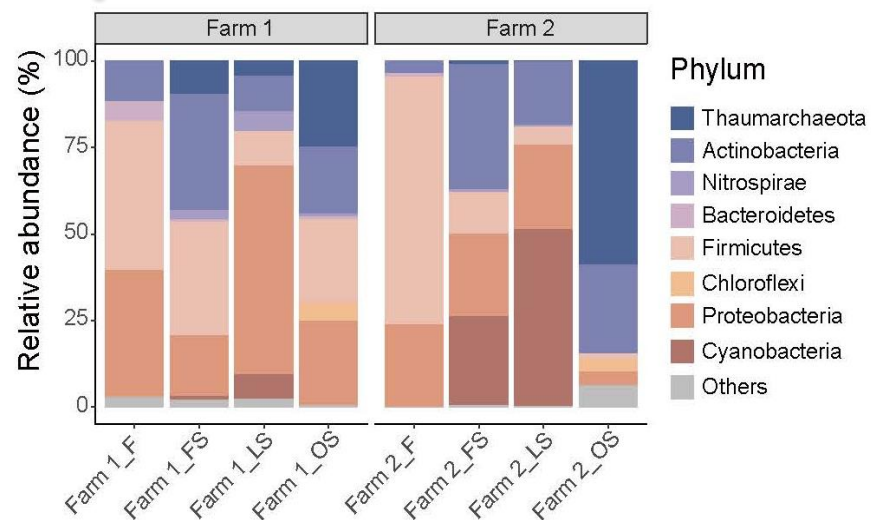


Highlights

- Metagenomic sequencing, culture-based isolation, and genomic analysis were combined to characterize ARG distributions in poultry manure and surrounding soils at both the community and strain levels, improving the detection of high-risk resistant bacteria and ARGs.
- Differences in microbial communities and high-risk ARGs were identified across sampling locations, and Enterobacteriaceae carrying important ARGs such as bla_{NDM} were isolated from soil, providing evidence for assessing AMR risks in poultry farm environments.
- Strain typing and plasmid analysis further characterized bla_{NDM-5}-positive strains and their IncHI2A-associated plasmid backgrounds, linking hosts, ARGs, and plasmids and providing a reference for surveillance of high-risk resistance determinants in poultry farms.



Result 1



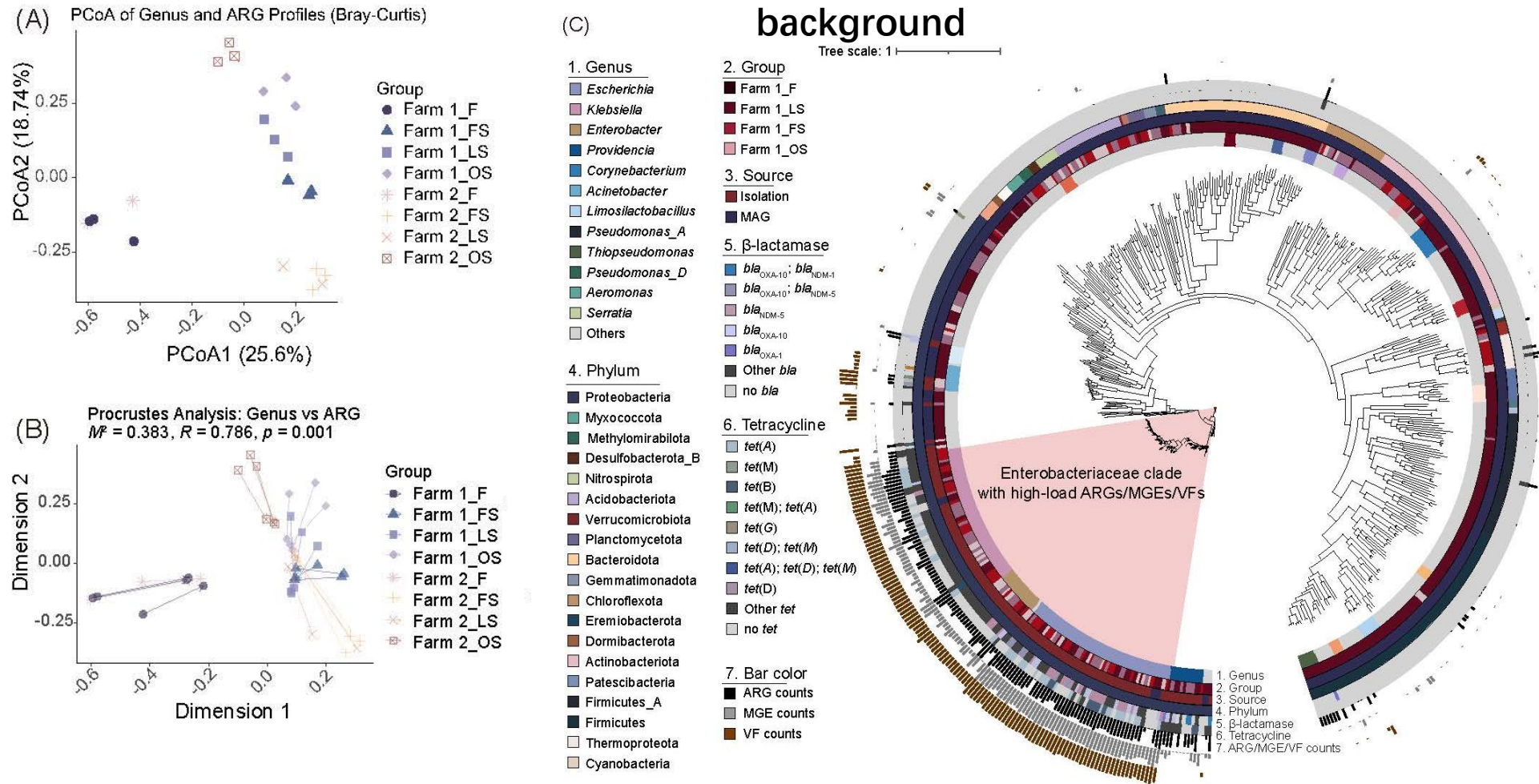
- Manure piles and surrounding soils showed distinct microbial community compositions, with manure piles enriched in typical manure-associated microbial groups.
- Microbial community composition and ARG profiles showed coordinated changes associated with sampling location.

- At both farms, manure piles had the highest total ARG abundance and number of ARG subtypes, with relatively high-risk ARG signals also observed in manure piles and adjacent soils.

➤ Microbial community and high-risk ARG profiles across manure piles and surrounding soil

Result 2

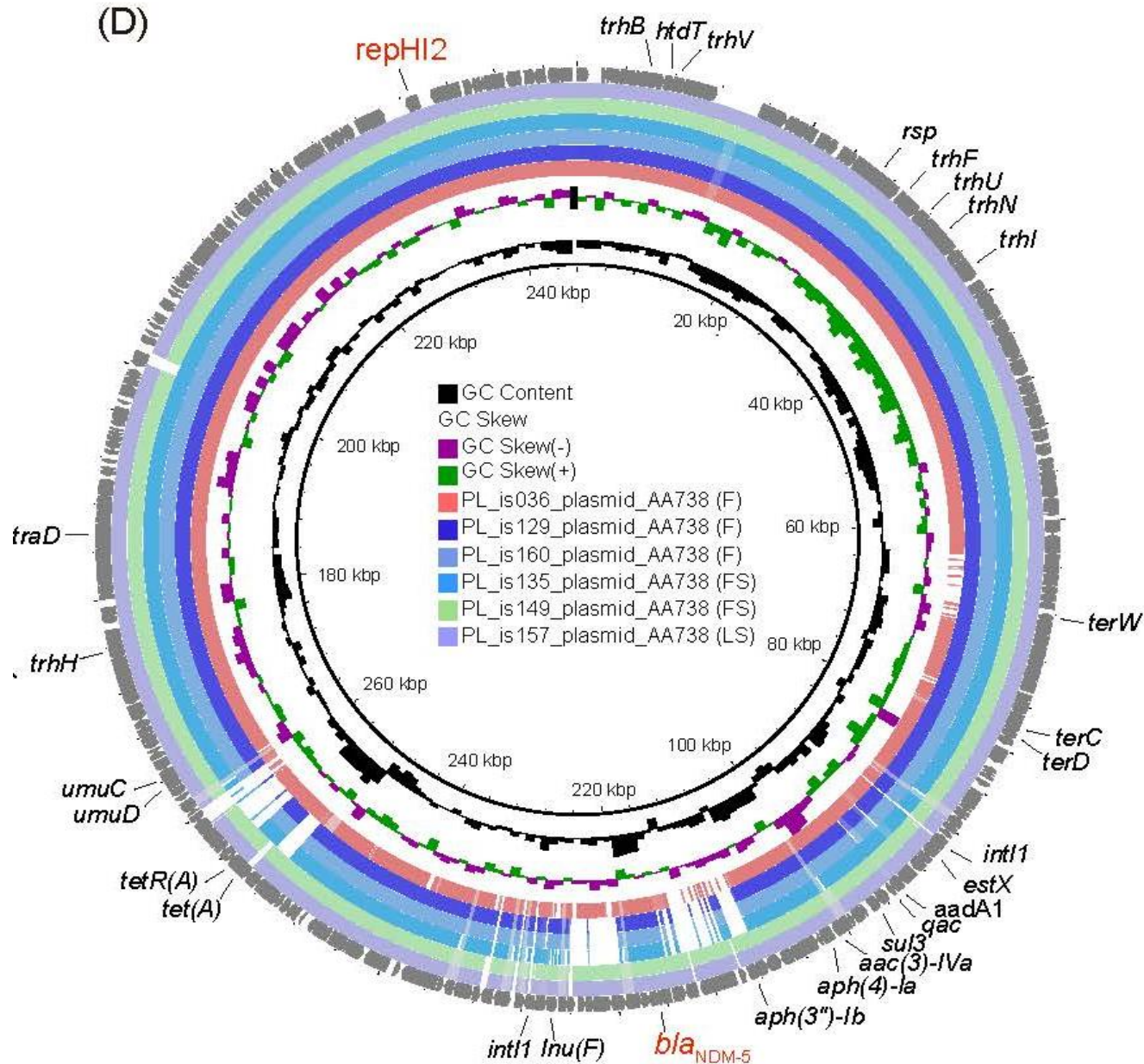
➤ Enterobacteriaceae as an antibiotic resistance gene/mobile genetic element/virulence factor-enriched host



- ❑ Culture-based isolation and isolate genome analysis detected additional ARGs not captured by metagenomics and identified culture-confirmed blaNDM-positive resistant hosts.
- ❑ Enterobacteriaceae represented a major host background enriched in ARGs, mobile genetic elements (MGEs), and virulence factors (VFs).
- ❑ In Farm 1, blaNDM-5-positive *E. coli* showed a cross-location, multi-sequence-type (ST) distribution.

Result 3

➤ IncHI2A-related plasmid backgrounds associated with *bla*_{NDM-5} in Farm 1



- ❑ Plasmid binning and replicon typing were further performed on bla_{NDM-5}-positive isolates from Farm 1.
- ❑ Most non-redundant bla_{NDM-5}-positive plasmid backgrounds carried IncHI2A and/or rep_cluster_1088-associated markers.
- ❑ Some plasmid bins showed high backbone similarity to the reference plasmid pJH51-1, further defining the plasmid context of bla_{NDM-5}.



Summary

- ❑ Complementary metagenomic and culture-based isolate genomics revealed high-risk ARG profiles in poultry manure piles and surrounding soils.
- ❑ bla_{NDM}-positive Enterobacteriaceae hosts and the multi-ST background of bla_{NDM-5}-positive E. coli were further characterized.
- ❑ ncHI2A plasmid backgrounds associated with bla_{NDM-5} were resolved, providing a basis for AMR surveillance of high-risk host–ARG–plasmid combinations in farm environments.

Yaling Wang, Lianwei Ye, Linan He, Zhenlong Wu, Yiwen Yang, Sheng Chen. 2026.
Metagenomic and culture based insights into host and plasmid contexts of high risk ARGs in poultry farm environments.
iMetaOmics 3:e70143. <https://doi.org/10.1002/imo2.70143>



“***iMeta***” launched in 2022 by iMeta Science Society, **impact factor (IF) 44.4**, **ranking top 47/22643 in the world**. It aims to publish innovative and high-quality papers with broad and diverse audiences. Its scope is similar to *Cell*, *Nature* and *Science*. Its unique features include video abstract, bilingual publication, and social media with 800,000 followers. Indexed by [SCIE/ESI](#), [PubMed](#), [Google Scholar](#) etc.

“***iMetaOmics***” launched in 2024, indexed by [ESCI](#), [PubMed](#), [Google Scholar](#), with a **target IF>15**, and its scope is similar to *Nature Communications*, *Science Advances*, *Advanced Science*, *Nucleic Acids Research*, etc.

“***iMetaMed***” launched in 2025, with a target IF>15, similar to *Med*, *Cell Reports Medicine*, *eBioMedicine*, *eClinicalMedicine* etc.



Society: <http://www.imeta.science>

Publisher: <https://wileyonlinelibrary.com/journal/imeta>

iMeta: <https://wiley.atyponrex.com/journal/IMT2>

Submission: iMetaOmics: <https://wiley.atyponrex.com/journal/IMO2>

iMetaMed: <https://wiley.atyponrex.com/journal/IMM3>



[iMetaScience](#)



[iMetaScience](#)



office@imeta.science

imetaomics@imeta.science



[Promotion Video](#)

Update
2026/6/17