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Opinion Article

# Genetic Mobility and Resistance in Poultry Wastewater Microbiomes

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## DESCRIPTION

Antimicrobial resistance (AMR) has emerged as a global health crisis, threatening the effective treatment of infectious diseases. A significant contributor to the spread of AMR is the environmental discharge of antimicrobial compounds and resistance genes from anthropogenic sources, such as livestock farming and poultry processing facilities. Poultry slaughterhouse wastewater (PSWW) represents a hotspot for AMR propagation, harboring diverse microbial communities and genetic material, including plasmids capable of mediating resistance. This study explores the metagenomic landscape of plasmid-mediated AMR in PSWW, with a particular focus on its implications for the dissemination of tuberculosis-associated resistance mechanisms.

### The role of plasmids in antimicrobial resistance

Plasmids are extrachromosomal DNA elements capable of Horizontal Gene Transfer (HGT) between bacteria. They often carry genes conferring resistance to multiple antimicrobial agents, making them pivotal in the evolution and spread of AMR. Plasmid-mediated resistance is particularly concerning because it can facilitate the rapid dissemination of AMR genes across diverse bacterial populations, including pathogenic strains. In the context of PSWW, plasmids play a critical role in the transfer of resistance genes within and beyond the microbial community. The presence of antibiotics and other selective pressures in wastewater promotes the survival and proliferation of resistant bacteria, further amplifying the risk of HGT.

### Metagenomics as a tool for studying AMR

Metagenomics provides a comprehensive approach to studying the genetic composition of microbial communities in complex environments like PSWW. Unlike traditional culture-based methods, metagenomics allows the detection of unculturable microorganisms and their associated resistance genes. This technique involves the extraction, sequencing, and analysis of total DNA from environmental samples, enabling researchers to:

1. Identify the diversity of microbial species and genes present.
2. Characterize the resistome the collection of all AMR genes in a given sample.
3. Detect mobile genetic elements, such as plasmids, that facilitate gene transfer.
4. Assess the co-occurrence of resistance genes with specific bacterial hosts or other functional genes.

### Plasmid mediated AMR in poultry slaughterhouse wastewater

Poultry slaughterhouse wastewater contains a complex mixture of organic matter, antibiotics, disinfectants, and microbial communities. These conditions create an ideal environment for the proliferation and exchange of plasmid-mediated AMR genes. Key findings from metagenomic studies on PSWW include:

**Diverse resistome:** Studies have identified resistance genes conferring resistance to antibiotics such as tetracyclines, beta-lactams, aminoglycosides, and macrolides. Many of these genes are associated with plasmids, highlighting their role in resistance dissemination.

**Co-selection mechanisms:** The presence of heavy metals and biocides in PSWW can co-select for AMR, as resistance genes for antibiotics and these compounds are often located on the same plasmid.

**Potential pathogens:** Plasmid-mediated AMR genes have been detected in opportunistic pathogens such as Escherichia coli, Klebsiella pneumoniae, and Salmonella spp., which are commonly found in PSWW. These pathogens pose a risk to human and animal health if transmitted through contaminated water or food.

**Cross-resistance to tuberculosis drugs:** While poultry-associated bacteria are not directly linked to tuberculosis (Mycobacterium tuberculosis), the presence of resistance genes in PSWW could have indirect implications. For instance, resistance genes for aminoglycosides and fluoroquinolones-antibiotics also used in tuberculosis treatment-may spread to environmental mycobacteria or other bacteria capable of interacting with M. tuberculosis in clinical settings.

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## Environmental and public health implications

The discharge of untreated or inadequately treated PSWW into the environment exacerbates the spread of AMR. Resistance genes and plasmids released into water bodies can persist and be taken up by environmental bacteria, creating reservoirs of AMR. This poses a significant risk to public health, as these genes can re-enter the human food chain or water supply.

Moreover, the overlap between AMR genes in PSWW and those involved in tuberculosis treatment underscores the need for a "One Health" approach integrating human, animal, and environmental health to address AMR comprehensively.

## Strategies for mitigating AMR in PSWW

To curb the spread of plasmid-mediated AMR in poultry slaughterhouse wastewater, several interventions are recommended:

1. Enhanced wastewater treatment: Advanced treatment technologies, such as membrane bioreactors, constructed wetlands, and advanced oxidation processes, can reduce the microbial load and remove genetic material from wastewater.
2. Antibiotic stewardship: Reducing the use of antibiotics in poultry farming and promoting alternative measures, such as probiotics and vaccines, can minimize selective pressure for resistance.
3. Surveillance and monitoring: Regular monitoring of AMR genes and plasmids in PSWW using metagenomics can provide early warning signs of emerging resistance trends.
4. Policy and regulation: Implementing stringent regulations on the discharge of PSWW and the use of antimicrobials in agriculture is crucial for limiting environmental contamination.

Metagenomic studies of plasmid-mediated AMR in poultry slaughterhouse wastewater provide critical insights into the mechanisms and risks associated with the spread of resistance. These findings highlight the need for integrated strategies to mitigate AMR at the interface of agriculture, environment, and public health. By addressing the issue of AMR in PSWW, we can take a significant step toward safeguarding the efficacy of antibiotics and protecting global health.