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ANTIBIOTIC RESIDUES IN THE ENVIRONMENT: DRIVERS OF ANTIMICROBIAL RESISTANCE IN ECOSYSTEMS - A SYSTEMATIC REVIEW

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INTRODUCTION & AIM

The widespread use of antibiotics in human medicine, agriculture, and aquaculture has resulted in the accumulation of antibiotic residues in environmental matrices such as soil, surface water, sediments, and wastewater. These residues act as environmental contaminants that exert selective pressure on microbial communities, thereby promoting the emergence and dissemination of antimicrobial resistance (AMR).

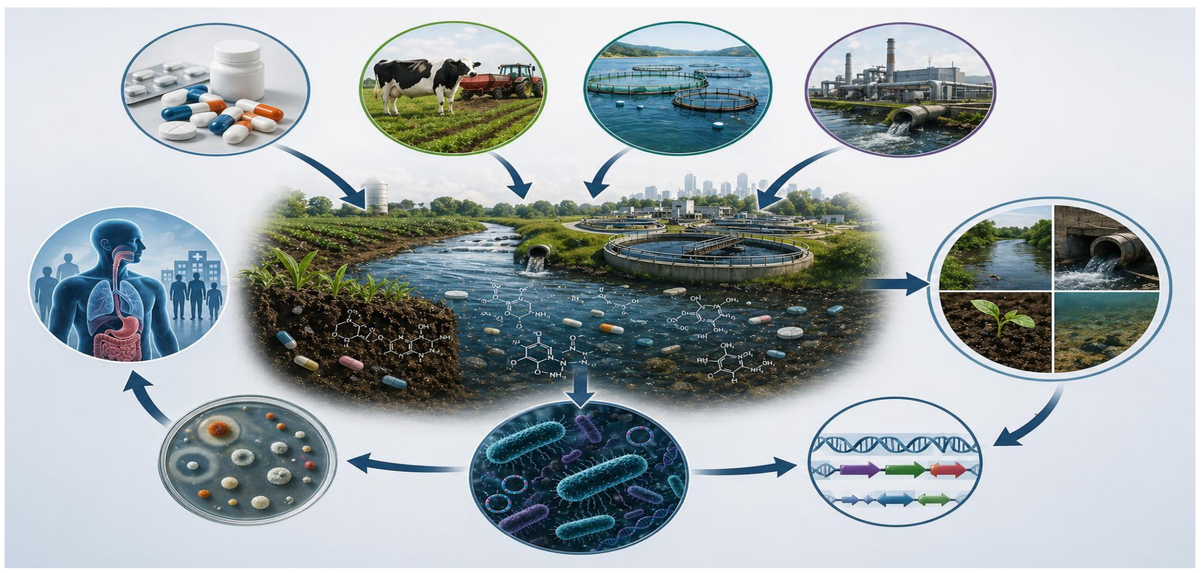


Fig.1: Pathway of antibiotic residues in the environment and their role in driving antimicrobial resistance across ecosystem.

METHOD

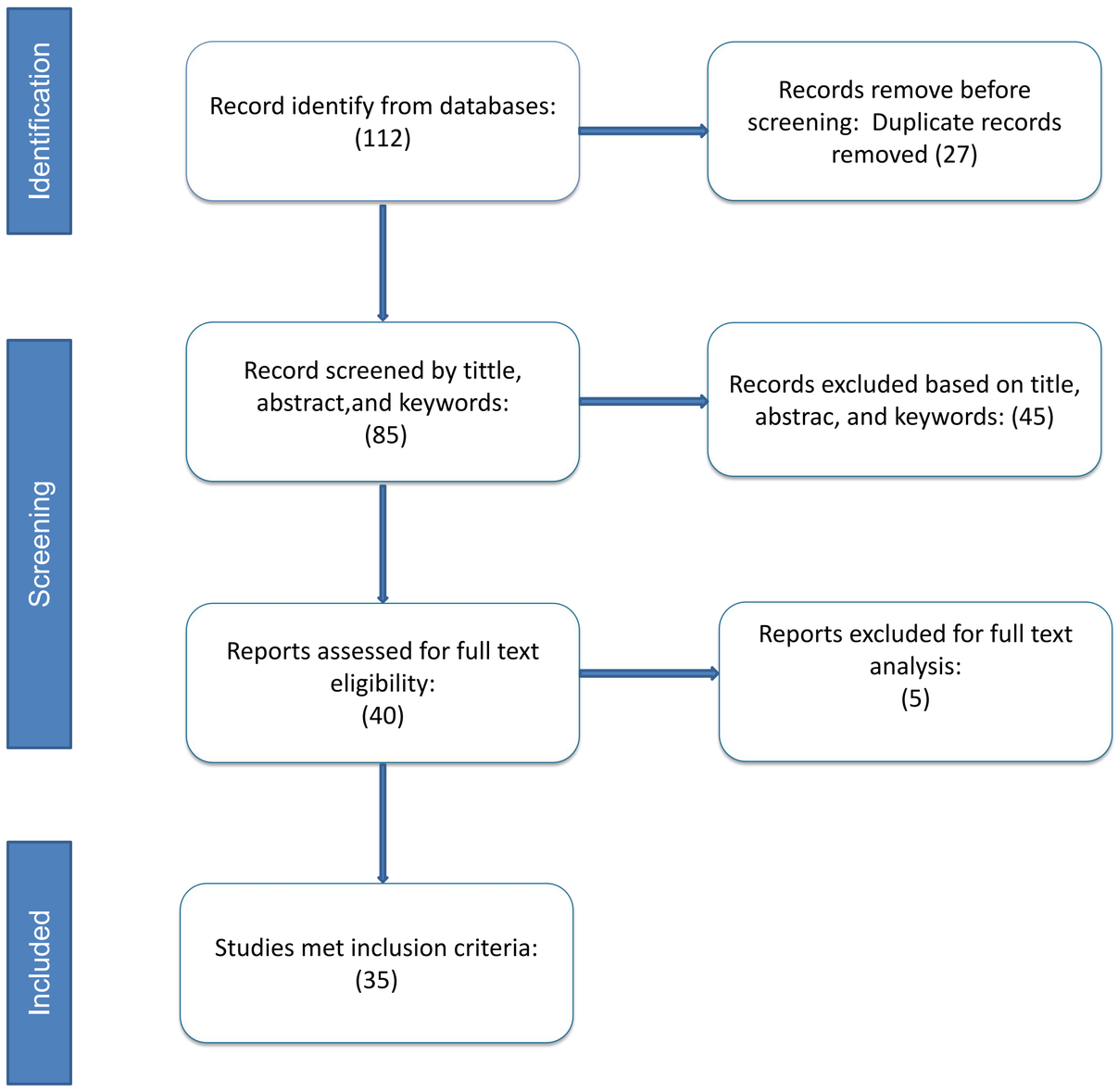
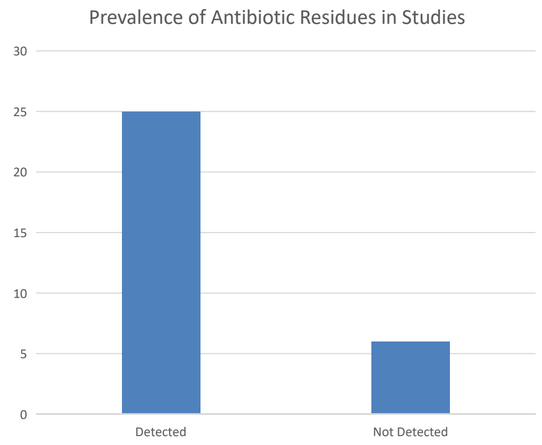
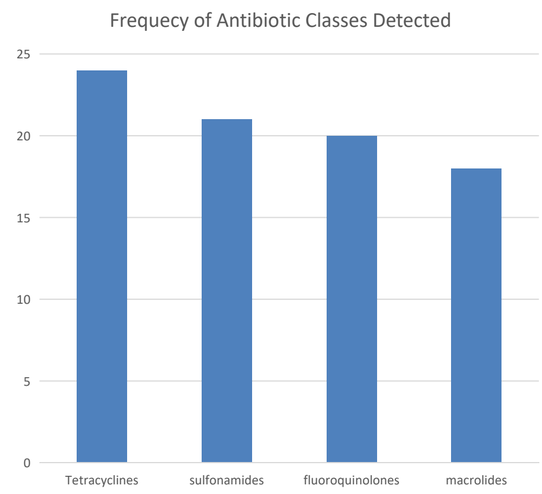
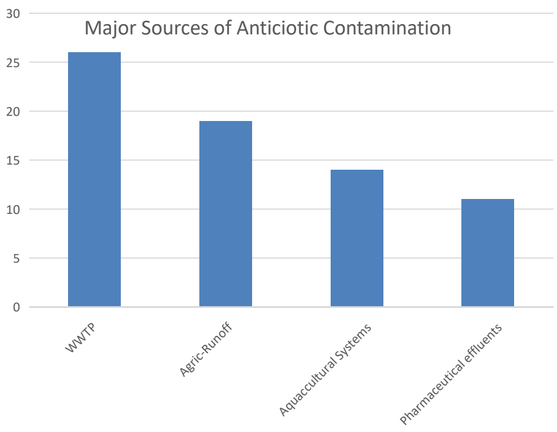


Fig.2: Flow chart for the methodology followed for the identification and selection of studies, according to the preferred reporting items for the systematic review (PRISMA).
Numbers within the bracket indicate the number of records

RESULTS & DISCUSSION







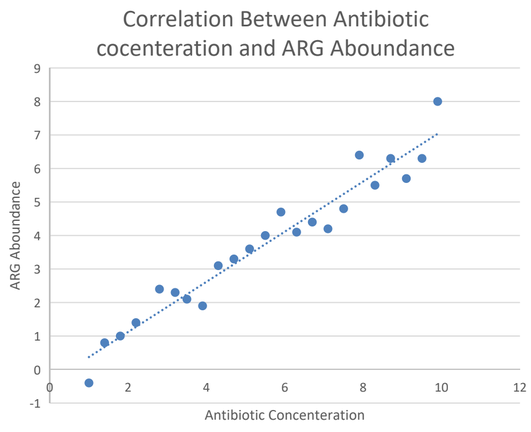


Fig.3: The study reviewed showed Antibiotic residues were reported in 29 of the 35 studies, with concentrations ranging from 1–500 ng/L in aquatic environments and up to 1200 µg/kg in soils and sediments. Tetracyclines (24 studies), sulfonamides (21), fluoroquinolones (20), and macrolides (18) were the most frequently detected classes. Antimicrobial resistance genes (ARGs), particularly tet, sul, and bla, were identified in 23 studies, with significant positive correlations (r = 0.60–0.88) between antibiotic concentrations and ARG abundance. Major contamination sources included wastewater treatment plants (26 studies), agricultural runoff (19), aquaculture systems (14), and pharmaceutical effluents (11).

CONCLUSION

Antibiotic residues are widely distributed across environmental matrices, including water, soil, and sediments, and play an important role in the emergence and dissemination of antimicrobial resistance (AMR). The consistent detection of resistance genes and their strong correlation with antibiotic concentrations explain the environment as an important reservoir and transmission pathway for resistance. Major anthropogenic sources are wastewater treatment systems, agricultural activities, aquaculture, and pharmaceutical discharges

FUTURE WORK / REFERENCES

Future research should focus on standardizing methods for detecting antibiotic residues and antimicrobial resistance genes (ARGs), as well as expanding long-term environmental monitoring. Advanced tools such as metagenomics are needed to better understand resistance pathways, while improved wastewater treatment technologies should be developed to reduce environmental contamination. Greater attention is also required in low- and middle-income regions, alongside integrated One Health approaches to effectively link environmental, animal, and human health in combating antimicrobial resistance.