

Scientists use machine learning to help fight antibiotic resistance in farmed chickens

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Scientists have used machine learning to find new ways to identify and pinpoint disease in poultry farms, which will help to reduce the need for antibiotic treatment, lowering the risk of antibiotic resistance

transferring to human populations.

The study, published in *The ISME Journal*, was led by Dr. Tania Dottorini from the School of Veterinary Medicine and Science and Future Food Beacon at the University of Nottingham.

The rapid increase in [poultry](#) production to meet growing demand in China has resulted in extensive and indiscriminate use of antibiotics. This has led to a worrying increase in cases of antimicrobial resistance (AMR) diagnosed in animals, which could potentially spread to humans via direct contact, environmental contamination, and food consumption.

With [antibiotic resistance](#) now one of the most threatening issues worldwide, effective and rapid diagnostics of bacterial infection in chicken farming can reduce the need for antibiotics, which will reduce epidemics and AMR.

In this project, researchers in Nottingham collected samples from the animals, humans and environment on a Chinese farm and its connected slaughterhouse. This complex "big" data has now been analyzed for new diagnostic biomarkers that will predict and detect bacterial infection, insurgence of AMR, and transfer to humans. This data will then allow early intervention and treatment, reducing spread and the need for antibiotics.

The study produced three key findings. Firstly, several similar clinically relevant [antimicrobial resistance genes](#) (ARGs) and associated mobile [genetic elements](#) (antibiotic resistance genes able to move within genomes and between bacteria), were found in both human and broiler chicken samples. In particular, eleven types of clinically important antibiotic resistance genes, with conserved mobile ARG gene structures were found between samples from different hosts.

Dr. Dottorini said, "These similarities would have been missed if we only used large-scale conventional comparative analysis, which in fact showed that microbiome and resistomes differ across environments and hosts. Overall, this finding suggests the relevance of adopting a multi-scale analysis when dissecting similarities and differences of resistomes and microbiomes in complex interconnected environments."

Secondly, the study showed that by developing a machine learning-powered approach integrating metagenomics data with culture-based methods, the team found the existence of a core chicken gut resistome that is correlated with the AMR circulating in the farms. These results supported the hypothesis that correlations exist between resistance phenotypes of individual commensal and pathogenic [bacteria](#) and the types of ARGs in the resistome in which they exist.

Finally, using sensing technology and machine learning, the team uncovered that the AMR-related core resistomes are themselves associated with various external factors such as temperature and humidity.

Dr. Dottorini said, "The food production industry represents a major consumer of antibiotics, but the AMR risks within these environments are still not fully understood. It is therefore critical to set out studies and improved methods optimized to these environments where animals and humans may be in close contact. Precision farming, cost-effective DNA sequencing and the increased adoption of machine learning technologies offer the opportunity to develop methods giving a better understanding and quantification of AMR risks in farming environments."

More information: Alexandre Maciel-Guerra et al, Dissecting microbial communities and resistomes for interconnected humans, soil, and livestock, *The ISME Journal* (2022). [DOI: 10.1038/s41396-022-01315-7](https://doi.org/10.1038/s41396-022-01315-7)

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