Insights into bacterial communities: multidrug-resistant and biofilm-forming bacteria in poultry droppings

Namrata Jiya[1], Swapnil Kajale[1], Kunal Jani[1], Abhishek Keer[1], Chahat Markan[1], Monica Chavan[1], Ashwin V. Khandare[1], Mahendra D. Jamdhade[1], Alimuddin Zumla[2] and Avinash Sharma[1,3,*]

[1]National Centre for Microbial Resource, National Centre for Cell Science, Pune 411 007, India
[2]Department of Infection, Division of Infection and Immunity, University College London, and NIHR Biomedical Research Centre, UCL Hospitals NHS Foundation Trust, London NW32QG, UK
[3]School of Agriculture, Graphic Era Hill University, Dehradun 248 002, India

An ever-increasing demand for high-quality protein sources like poultry products, along with excessive use of antibiotics in animal husbandry are contributing factors to the growing global problem of antimicrobial resistance (AMR). The overuse of antibiotics in poultry and the dissemination of poultry faecal waste in the environment results in the propagation and spread of multidrug-resistant (MDR) bacteria. We investigated the bacterial diversity of poultry droppings by targeted amplicon sequencing and determined the resistance pattern of 165 bacterial isolates against various types of antibiotics. We found that the species of genera *Enterobacter*, *Enterococcus*, *Escherichia*, *Proteus*, *Bacillus* and *Shigella* showed resistance against beta-lactams, cephalosporins, fluoroquinolones, sulphonamide, nitrofurantoin, polymyxin E and aminoglycosides. In addition, we detected strong biofilm-producing isolates of *Enterobacter*, *Bacillus*, *Proteus*, *Escherichia* and *Enterococcus*. The detection of biofilm-forming MDR bacteria in poultry droppings highlights the need for proactive measures to mitigate their growth and transmission. High-throughput sequencing revealed the differential prevalence of amplicon sequence variants belonging to *Lactobacillus*, *Corynebacterium* and *Bacteroides*. Functional imputations support the observed potential of biosynthesis of divergent antibiotics and drug resistance. Our findings highlight that poultry droppings harbour a diverse array of antibiotic-resistant bacteria, underscoring the significance of continuous surveillance and appropriate disposal methods to counteract the escalating problem of multidrug resistance under the 'One Health' approach.

Keywords: Antibiotics, antimicrobial resistance, biofilms, multidrug-resistant bacteria, poultry droppings.

in animal husbandry and unregulated ad hoc disposal of inadequately treated waste effluents in the environment are contributing factors to the local and global spread of AMR[1]. India has been one of the world's largest consumers of antibiotics, with around 5071 million defined daily doses (DDD) consumed in 2015 (refs 2, 3). An ever-increasing demand for high-quality protein products like milk, poultry meat and fish has led to the unregulated use of antibiotics in the animal production sector in India[2]. This contributes to continuing the spread of AMR, from animal food sources to humans and the environment at large, by the farm-to-fork approach. The most widely used antibiotics in poultry feed include aminoglycosides, beta-lactams, colistin, quinolones, sulfonamides and tetracyclines[4].

The use of antibiotics in poultry feed in conventional poultry farming practices to ensure flock health, growth promotion, and prophylaxis of diseases has led to the rise in AMR worldwide[5]. Thus, the recent methods adopted by various nations under the 'One Health' approach to curbing the growing AMR throughout the world use antibiotic-free (ABF) production or alternative to antibiotics like probiotics, prebiotics, essential oils, enzymes, etc. in poultry production[6]. The overuse of antibiotics in poultry production and dissemination of poultry faecal waste by direct land dumping in the environment can result in the propagation and spread of multidrug-resistant (MDR) bacteria. The biofilm formation potential of bacterial strains poses an additional health risk to humans and animals by increasing the AMR and the development of fatal infections.

The World Health Organization (WHO), Geneva, Switzerland, emphasizes surveillance studies due to the critical importance of monitoring the significant impact of