

ORIGINAL ARTICLE

Detection of unprecedented level of antibiotic resistance and identification of antibiotic resistance factors, including QRDR mutations in *Escherichia coli* isolated from commercial chickens from North India

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Abstract

Aim: This study aimed to investigate the occurrence of antibiotic resistance phenotype and simultaneously understand its genetic basis in *Escherichia coli* isolated from the cloacal swabs of commercial chickens from north India.

Methods and Results: *Escherichia coli* isolates were assessed for susceptibility to 14 different antibiotics using the disc-diffusion technique and were screened for the presence of 22 antibiotic resistance genes (ARGs) by employing PCR. Isolates were found to be highly resistant to fluoroquinolones (nalidixic acid 91%, norfloxacin 73% and ciprofloxacin 66%), tetracycline (71%), beta-lactams (ampicillin 49% and amoxicillin/clavulanic acid 37%), co-trimoxazole (48%), streptomycin (31%) and chloramphenicol (28%); and comparatively less resistant to cefazolin (13%), amikacin (10%), aztreonam (4%), gentamicin (4%) and ceftriaxone (3%). Sixty-three percent of isolates were resistant to more than four different drugs. Abundance of plasmid-borne ARGs like *tetA* (83%), *suL3* (44%), *aadA1* (44%), *strA* (43%), *strB* (41%), *qnrS* (38%), *suL2* (28%) and *aac(6)-Ib-cr* (15%) was observed among the isolates. Forty-five percent of isolates possessed more than five different ARGs. Quinolone resistance-determining region (QRDR) mutations within *gyrA* and *parC* genes were found to be the major determiners of quinolone resistance. QRDR mutations included leu83, asn87 and gly87 within gyrase-A polypeptide and ile80 and lys84 within topoisomerase IV (encoded by *parC*).

Conclusions: Our findings suggest the abuse of antibiotics as feed additives and prophylactic drugs in Indian poultry sector. It also projects this industry as an active hotspot for the replication and selection of ARGs.

Significance and Impact of the Study: Our findings would provide evidence to the authorities for formulating effective strategies for restricting antibiotic usage as non-therapeutic agents in food animals. Occurrence of both plasmid-borne and chromosome-borne resistance towards quinolones can drive movement of resistance phenotype across bacterial species and vertical movement of resistance along the bacterial generations, respectively, which can pose mitigation challenges.

Nitish Rawat and Anjali have equal contributions and both should be considered as first authors.

Self Attested
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