

Antibiotic Resistance: A Comparative Genetic Approach in *E. coli*

Prashant Alte¹ and Daiwshala Kamthane^{*2}

Department of Microbiology, N. S. B. College, Nanded, Maharashtra, India¹

Head, Department of Microbiology, S. G. B. College, Purna, Parbhani, Maharashtra, India²

Correspondence: udnimati@gmail.com

Abstract: *The antibiotic resistance in Escherichia coli is a critical clinical and environmental problem because these bacteria exhibit an extraordinary genetic malleability, which enables them to accumulate and spread the antimicrobial resistance genes. In this work, we used a comparative genetic strategy to study the molecular and structural mechanism of resistance in MDR E. coli isolated from different clinical and environmental origins. Resistome, antimicrobial resistance genes, plasmid replicons and chromosomal mutations are investigated with whole-genome sequencing and bioinformatics analyses and compared to a reference collection. Work on protein structure modelling and molecular dynamics simulations have also contributed to show that the impact of particular mutations in porins, β -lactamases, efflux pump components and quinolones target proteins on protein conformation, antibiotic interaction or cellular permeability. The investigation will describe associations between genomic variation, stress-adaptation pathways and phenotypic resistance, improving genotype–phenotype relationships. By combining comparative genomics with structural analysis, this study contributes to the understanding of E. coli antibiotic resistance mechanisms and identifies possible therapeutic targets as well as surveillance strategies for AMR.*

Keywords: *Escherichia coli*; antimicrobial resistance; comparative genomics; whole-genome sequencing; resistance genes; plasmids; protein structure modelling; molecular dynamics; evolution; stress-response pathways

