

# A comparative study on co-trimoxazole resistance among bacteria isolated from UTI patients and hospital wastewater

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## ABSTRACT

Antibiotic resistance, a natural phenomenon, is the ability of microorganisms to resist the effect of an antibiotic to which they were once sensitive. Resistance to first-line antibiotics and, more recently, last-line treatments, and even combination drugs could be fatal in case of minor infections. Co-trimoxazole, a combination of two antifolate compounds - sulfamethoxazole and trimethoprim, is effective against Gram-negative and Gram-positive bacteria. There are multiple reports of co-trimoxazole resistance among clinical as well as environmental bacteria making it difficult to treat bacterial infections. Horizontal gene transfer (HGT) occurs through transformation, conjugation and transduction is mainly responsible for the widespread of antibiotic resistance genes among bacterial isolates. HGT also decipher the finding of antibiotic resistant bacteria (ARB) and genes (ARG) in different environments and livestock through the transfer from environmental into the clinical pathogens. The transmission of ARGs among different bacterial species is a global human threat. This study aims at determining the prevalence and diversity of co-trimoxazole resistant bacteria in clinical and STP receiving hospital wastewater. Furthermore, this works highlights the acquisition of genetic factors viz. *dfp* and *sul* genes conferring resistance to co-trimoxazole among urinary tract infection (UTI) causing bacterial pathogens and wastewater bacterial isolates. The study will further provide in-sights into the antibiotic resistance spread in clinical and environmental samples and how these two systems interlink.