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Molecular basis and mechanism of resistance to Ciprofloxacin by *Staphylococcus Aureus* strains isolated from pregnant women

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Staphylococcus aureus can cause worrisome infections especially for the immune compromised pregnant woman and her fetus but worse problems are posed by the drug-resistant strains. This study was carried out to determine the molecular basis and mechanism of resistance of *Staphylococcus aureus* to ciprofloxacin; a quinolone with broad-spectrum antimicrobial activities. Five known ciprofloxacin-resistant *Staphylococcus aureus* strains isolated from pregnant women attending antenatal clinics in Imo State Nigeria were used for this study. Their antibiotic resistance profiles were confirmed using disc diffusion method. Minimum inhibitory concentration (MIC) of ciprofloxacin on test isolates was also obtained using standard microbiological tests. This was followed by molecular studies which involved; Genomic DNA extraction, polymerase chain reaction, gel electrophoresis, and gene sequencing. Analysis of the sequences obtained was done using the clcbio main workbench software to obtain their statistics, basic alignment, and phylogeny. Results revealed resistance to ciprofloxacin to be genetic with all the isolates harbouring the quinolone resistance determinant region, (QRDR) found on Gyr A and Par C genes. BLAST results with related genes in the gene bank showed mutations at the quinolone target site suggestive of modification of the target site as a mechanism of resistance observed. Phylogenetic analysis revealed that the genes studied were from one ancestor hence possible horizontal transfer of resistance genetic materials among the isolates. The public health importance of this cannot be overemphasized.

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