

Methods & Materials: A novel series of thiazole derivatives were rationally designed by Computer Assisted Drug Design (CADD) approach (VLife Science®). The optimized scaffold was synthesized in multiple steps from thiosemicarbazide and was suitably cyclized to get corresponding active 2,4-di-substituted thiazole derivatives. Metal complexes of thiazoles were further prepared using salts of d-block compounds (copper, nickel and cobalt) as per protocol designed in our laboratory. The modern analytical techniques (UV-Vis, IR, NMR, MS, RS, XRD, AAS, MM, MC) revealed that the results were in full agreement with their assigned chemical structures. All the synthesized compounds were screened for their anti-microbial activity according to standard protocol against bacterial strains (*E. coli*, MTCC-1687; *S. aureus*, MTCC-2940; *B. subtilis*, MTCC-441; and *K. pneumonia*, MTCC-3040). The nucleolytic activity of compounds and metal complexes were evaluated using gel electrophoresis employing *E. coli* plasmid pBR322.

Results: Among them, *para*-substituted (halogenated) thiazoles exhibited excellent anti-bacterial activity against *E. coli*, *S. aureus*, and *K. pneumonia*. Nearly all compounds exhibited moderate to high nuclease activity. The copper complexes showed moderate nuclease activity while cobalt and nickel complexes displayed excellent nuclease activity. The *in silico* docking study performed revealed the binding orientations of these compounds at active site amino acid residues ASN 165 and GLU 40 (PDB ID: 1AHP), amino acid residues TYR 151 and GLY 18 (PDB ID: 2C44) and amino acid residues ARG 73 and ASP 76 (PDB ID: 1K6W) of crystal structure of *E. coli* metabolic enzymes.

Conclusion: From this study, it can be concluded that the novel molecules have tremendous anti-microbial and nuclease activity. This research helps in understanding mechanism of action of thiazole based anti-microbials and it may possibly be used as template for searching potent anti-microbial agents in future.

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Incidence of SHV and CTX-M Extended spectrum β -lactamases producing gram negative bacterial isolates from antenatal mother with asymptomatic bacteriuria

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Background: Asymptomatic bacteriuria (ABU) occurs in 2 to 10% of cases during pregnancy and the risk of onset of bacteriuria is maximum between 9th to 17th week of gestation. ABU will lead to adverse anomalies if left untreated such as acute pyelonephritis, low birth weight infants (LBW) and premature delivery. The incidence of Extended Spectrum Beta-Lactamases (ESBLs) such as TEM-1, SHV-1 and CTX-M type producing uropathogenic bacteria have been increasing over years. Thus this study was carried out to analyze the population of ESBL producing MDR Gram negative bacteria and to ascertain the most prevalent ESBL gene in our geographical region among antenatal women with asymptomatic bacteriuria.

April and September 2015 were included in this study. Their mid-stream urine samples were collected during the 16th week of gestation and processed in the Department of Clinical Microbiology, MGMCRI following standard methods. Gram negative pathogens were isolated and phenotypically confirmed for ESBL production. All those ESBL positive isolates were screened by PCR for the presence of *bla*_{CTX-M}, *bla*_{SHV} and *bla*_{TEM} with specific primers and the amplicons were subjected to sequencing.

Results: Out of 637 antenatal mothers with asymptomatic bacteriuria, 54 urine samples were not included due to improper sample collection and 268 samples were found to be sterile. Remaining 315 samples showed significant growth of single pathogenic bacteria. Among these, 44 were Gram positive isolates and 271 were Gram negative pathogens. ESBL production was phenotypically observed among 35% (n=95) of these GNB. Out of these 95 ESBL isolates, 73% were MDR isolates, none of them carried *bla*_{TEM} and the presence of *bla*_{CTX-M} and *bla*_{SHV} were observed in 69.4% and 20% of isolates respectively. All the *bla*_{CTX-M} and *bla*_{SHV} amplicons were confirmed through sequencing followed by BLAST analysis (<http://blast.ncbi.nlm.nih.gov/Blast.cgi>).

Conclusion: Presence of *bla*_{CTX-M} and *bla*_{SHV} genes reflects their prevalence among the community. Periodic and continuous antenatal follow-up only can reduce the complications of asymptomatic bacteriuria among antenatal mothers. This study urges the need for the regional antimicrobial practicing policy by the stakeholders to implement and to monitor.

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Molecular detection of azithromycin resistance mechanisms in typhoidal salmonellae



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Background: Antibiotic resistance in enteric fever continues to pose major therapeutic challenge with increase in ciprofloxacin resistance. Azithromycin has been used to treat enteric fever as an alternate treatment option without any guidelines for laboratory interpretation. In 2015 issue CLSI has added breakpoints for testing azithromycin susceptibility in typhoidal Salmonellae. We aimed to assess the prevalence of resistance to azithromycin in *S. Typhi* and *S. Paratyphi A* in a collection of strains to characterize the mechanisms underlying resistance.

Methods & Materials: A total number of 224 *S. Typhi* and *S. Paratyphi A* isolates were available in the cryopreserved stock