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## Spectrum of mutations in Hbb gene among thalassemia major patients in a cohort of Nepalese population

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The thalassemias are the most common monogenic disorders with a genetically determined reduction in the rate of one or more types of normal hemoglobin polypeptide chain resulting in a decrease in the amount of hemoglobin involving the affected chain. Beta thalassemia is a highly heterogeneous disorder in its phenotype, geographical distribution and molecular mechanism. DNA was extracted from the 26 clinically diagnosed blood samples and Amplification Refractory Mutation System-Polymerase Chain Reaction (ARMS PCR) was used for amplification to analyze mutations in *Hbb* gene and 2% gel electrophoresis was used for visualization of PCR products. Among 26  $\beta$ -thalassemia major patients, 13 (50%) had IVS 1-5 (G>C) mutation, 8 (30.76%) had 619bp deletion, 2 (7.69%) CD 8/9 (+G), 1 (3.84%) CD 15 (G>A), 1 (3.84%) had -88 (C>T) mutation whereas CD41/42 (-TCTT) was not detected in any of the patients. Among the patients with 619bp deletions 2 (25%) were homozygotes and 6 (75%) were heterozygotes. This is the baseline study to assist in the regulation of proper new health policies which will impact in the proper diagnosis and treatment.

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## Susceptibility pattern of *Salmonella enterica* isolates towards fluoroquinolones, macrolides and cephalosporins

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Enteric fever caused by *Salmonella enterica* serovar Typhi and Paratyphi A is the most common clinical diagnosis among febrile patients presenting to hospital in Nepal. The aim of this study was to evaluate the susceptibility pattern of *Salmonella enterica* serovar Typhi and Paratyphi A isolates towards different classes of drugs. During the study period, 62 isolates of *S. enterica* serovar Typhi (68.8%) and 28 Paratyphi A (31.1%) were obtained from 1815 blood samples from clinically diagnosed enteric fever patients visiting to Kathmandu Model Hospital. All isolates were identified by conventional biochemical tests and serotyping. Antibiotic susceptibility testing to 10 antibiotics was performed by modified Kirby Bauer disc diffusion method and CLSI recommended interpretive criteria. Minimum inhibitory concentration (MIC) of ciprofloxacin, ofloxacin, nalidixic acid, cefixime and azithromycin were determined by agar dilution method. All the isolates were found to be 100% susceptible to first line drugs (amoxycillin, chloramphenicol and cotrimoxazole) and cephotaxime and highly susceptible towards ceftriaxone, cefixime and azithromycin. However, 12 (13.3%) and 13 (14.4%) isolates were resistant to ofloxacin and ciprofloxacin respectively. Of the total isolates 84 (93.3%) were nalidixic acid resistant. Nalidixic acid resistance was observed higher in *S. Typhi* (58/84) compared to *S. Paratyphi A* (26/84) ( $P < 0.001$ ). Difference in both MIC and inhibition zone diameter in fluoroquinolones, macrolides and cephalosporins sensitive and resistant isolates was statistically significant ( $P < 0.001$ ). The decreased susceptibility to fluoroquinolones of *Salmonella* was strongly correlated with resistance to nalidixic acid. However, third generation cephalosporins including cefixime and macrolides like azithromycin still remains as useful drugs for the treatment. Besides that, due to the re-emergence of susceptibility, conventional drug may play important role in the treatment of enteric fever.

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