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Antibiogram of *Salmonella* serotype *Typhi* and *Paratyphi* isolated from patients suspected of enteric fever

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Enteric fever is an ancient disease but still it is an important public health problem in developing countries including Nepal. A changing antibiotic susceptibility pattern of *Salmonella Typhi* and *Salmonella Paratyphi A* and emergence of multi drug resistance has increased to a great concern globally. The present study was conducted to determine the antibiogram of *Salmonella* serotype *Typhi* and *Paratyphi* isolated from patients suspected of enteric fever. A prospective study was carried out from July 2012 to August 2012. The positive samples of *Salmonella* were collected from Alka Hospital by streaking in Nutrient agar slant and transported aseptically to the Nepal Academy of Science and Technology (NAST) laboratory for the further identification of strains and antibiotic susceptibility testing. Antibiotic susceptibility test was performed by modified Kirby-Bauer disc diffusion method and results were interpreted by Clinical Laboratory Standards Institute (CLSI), 2012 guideline. A total of 47 *Salmonella* serotype isolated from 896 blood culture samples revealed almost equal infection in male and female. Age wise infection rate indicated higher among the age group less than 10 years. *S. Typhi* was isolated in 46.81% of cases while *S. Paratyphi A* in 53.19% of cases. Both *S. Typhi* and *S. Paratyphi A* were found to be 100% susceptible to drugs amoxicillin, chloramphenicol and ceftriaxone. Susceptibility to ofloxacin was 100% in *S. Typhi* and only 64% in *S. Paratyphi A*. Similarly susceptibility of gentamicin, co-trimoxazole, ampicillin and nalidixic acid was 95.45%, 86.36%, 90.90% and 13.64% and 76%, 88%, 64% and 4% for *S. Typhi* and *S. Paratyphi A* respectively. *Salmonella Paratyphi A* was observed as a rapidly emerging pathogen of enteric fever. There is increasing resistance of *S. Typhi* and *S. Paratyphi A* to many antibiotics and also there is re-emergence of chloramphenicol sensitivity in both strains of *Salmonella*.

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Novel approach to investigate syphilis pathogenesis, a neglected but devastating infectious disease

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Syphilis is caused by a spirochete, *Treponema pallidum* and is one of the oldest infectious diseases known to the mankind. It is estimated that >10 million new cases of syphilis occur every year worldwide with more than 900,000 new cases of congenital syphilis. In addition neurosyphilis remains a major problem in the developing World. The successful control of syphilis requires identification of important virulence factors of *T. pallidum* and knowledge of circulating strains in human populations. Inability to culture this pathogen *in vitro* and its genetic intractability has resulted in poor understanding of syphilis pathogenesis. We have taken advantage of a bioluminescent strain of *Borrelia burgdorferi* generated in our laboratory to examine expression and function of an immunogenic *T. pallidum* lipoprotein. *B. burgdorferi* causes Lyme disease and is physiologically and structurally closely related to *T. pallidum*. In addition, it is feasible to culture and genetically manipulate *B. burgdorferi*. Therefore, we considered it ideal to study the location and role of the *T. pallidum* lipoprotein in pathogenic mechanisms. We found that the selected *T. pallidum* lipoprotein is a bifunctional protein which plays a role in adherence to the host cells when expressed on the bacterial surface. This model heterologous expression system will allow us to reveal the function of other virulence factors of *T. pallidum* to better understand syphilis pathogenesis. We expect that we will be able to identify and characterize critical virulence factors and antigens of *T. pallidum* to produce a successful vaccine against syphilis in the future.

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