Abstract

Typhoid fever is a unique human septemic infection caused by *Salmonella typhi*. Typhoid fever is still an important public health problem in many developing countries.The continuing presence of the disease in endemic areas and emergence of multidrug- resistant strains in many developing countries as well as the increasing reports from developed countries has renewed the interest to better understand the epidemiology of typhoid fever and some aspects of its pathogenesis. Characterization of *S. typhi* strains in different epidemiological settings depends largely on the utility of highly precise molecular typing tools.

A convenient, versatile and safe method for preparing bacterial DNA for ribotyping, pulsed- field gel electrophoresis (PFGE), IS200 typing and gene hybridization of restricted DNA analysis has been described in this study.

PFGE analysis, IS200 typing, ribotyping, amplified fragment length polymorphism (AFLP) analysis and gene hybridization profile typing clearly demonstrated the high genetic diversity among geographical isolates of *S. typhi*, indicating the existence of multiple clones of *S. typhi* in different regions of the world. On the other hand, limited diversity was observed among *S. typhi* strains isolated from patients in Papua New Guinea (PNG) with fatal and non- fatal typhoid fever by the same typing methods. This points to the fact that *S. typhi* strains circulating in PNG were possibly derived from single or closely related clones.

PCR- ribotyping and PCR- restriction fragment length polymorphism (RFLP) were found to be of limited value in subtyping *S. typhi*.

AFLP analysis of the PNG *S. typhi* strains from fatal and non- fatal cases of typhoid fever showed no association between genotypes (molecular profiles) and virulence (the