

Multidrug-Resistant Strains of *Salmonella enterica* Serotype *typhi* Are Genetically Homogenous and Coexist with Antibiotic-Sensitive Strains as Distinct, Independent Clones

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ABSTRACT

Objective: The goal of this study was to report the molecular analysis of antibiotic-sensitive and multidrug-resistant (MDR) strains of *Salmonella typhi*, using pulsed-field gel electrophoresis (PFGE), with a particular emphasis on the coexistence of these strains in a typhoid-endemic region of Karachi, Pakistan.

Methods: One hundred isolates of *S. typhi* in humans (50 MDR and 50 antibiotic-sensitive isolates) from sporadic cases of typhoid fever were analyzed by Vi-phage typing, antibiograms and PFGE.

Results: The MDR *S. typhi* strains were resistant to ampicillin, chloramphenicol, and trimethoprim-sulfamethoxazole. Analysis by PFGE showed that 50 MDR isolates of *S. typhi* had a single, homogenous PFGE profile, which was distinctly different from that of 50 antibiotic-sensitive isolates obtained in the same time frame from the same area. This latter group of isolates showed much greater diversity of PFGE profiles, as has been observed in other endemic regions.

Conclusions: Multidrug-resistant and antibiotic-susceptible strains of *S. typhi* can coexist in endemic areas as epidemiologically independent pathogens and are not in competition for continued persistence and transmission.

Key Words: antibiotic resistant, MDR *Salmonella typhi*, molecular typing, PFGE

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With regard to emerging infectious diseases, typhoid fever caused by multidrug-resistant (MDR) strains of *Salmonella typhi* presents a serious problem in many developing countries of the Third World.^{1,2} Multidrug-resistant strains of *S. typhi* resistant to chloramphenicol, ampicillin, and trimethoprim-sulfamethoxazole, with additional resistance to streptomycin, sulfonamides, and tetracyclines began to appear in the late 1980s in the South Asian region and have now spread widely to the Middle East, Africa, and Asia.¹⁻⁴ The problem is particularly acute on the Indian subcontinent, where approximately 60 to 65% of strains isolated are MDR strains. In addition, the disease associated with MDR strains tends to be more severe, with patients registering a higher morbidity score and a higher mortality rate, often with unusual complications.^{3,5,6} To design rational strategies to control dissemination of such MDR strains, and also to better understand their biologic characteristics and epidemiology, the analysis of such strains, using a variety of recently available molecular methods, with higher discriminatory power compared to classic techniques, would seem to be a high priority. Molecular analysis of *S. typhi* from different parts of the world has been performed in recent years by several techniques, such as ribotyping, IS200 typing, polymerase chain reaction (PCR)-based methods, and pulsed-field gel electrophoresis (PFGE).⁷⁻¹¹ This article presents the molecular analysis of antibiotic-sensitive and MDR strains of *S. typhi* from Karachi, Pakistan, using PFGE, with a particular emphasis on the coexistence of these strains in a typhoid-endemic region.

MATERIALS AND METHODS

One hundred isolates of *S. typhi* in humans obtained from blood were used in this study. These isolates were obtained from sporadic cases of typhoid fever occurring in patients admitted to the pediatric unit of the Aga Khan University Medical Center in Karachi, and consisted of 50 antibiotic-sensitive and 50 MDR isolates. The isolates were obtained between March 1996 and April 1997 from