Biotype and Antimicrobial Susceptibility of *Shigella sonnei* in Malaysia

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Abstract

Bacteria of the genus *Shigella* are the etiologic agent of shigellosis, an acute intestinal infection. *Shigella sonnei* was reported to be increasingly prevalent in Malaysia. This study aimed to determine the degree of diversity that exists among Malaysian *S. sonnei* based on phenotypic characters such as biotypes and resistotypes. Two *S. sonnei* biotypes were identified in this study, i.e. biotype *a* (n=29, 73%) and biotype *g* (n=11, 27%). The biotype *a* strains were subtyped into eight resistotypes whereas all the *S. sonnei* biotype *g* strains shared an identical resistotype of streptomycin - trimethoprim-sulfamethoxazole - tetracycline. All the *S. sonnei* strains remained susceptible to kanamycin, ceftriaxone and ciprofloxacin. Highest resistance rate was observed for streptomycin (67.5%), followed by tetracycline (40%), trimethoprim-sulfamethoxazole (37.5%), ampicillin (10%), and chloramphenicol (10%).

Introduction

Bacteria of the genus *Shigella* are the etiologic agent of shigellosis, an acute intestinal infection. This genus consists of four species, i.e. *S. dysenteriae*, *S. flexneri*, *S. boydii*, and *S. sonnei*. Shigellosis is a major public health concern, especially in developing countries. Shifting of *Shigella* dominance from *S. flexneri* to *S. sonnei* was reported in developing and developed countries (WHO, 2009). Increasing prevalence of *Shigella sonnei* has also been reported in Malaysia (Banga Singh et al., 2011). Therefore, the present work aimed to determine the degree of diversity that exists among Malaysian *Shigella sonnei* strains based on phenotypic characters such as biotypes and resistotypes.

Materials and Methods

Forty epidemiologically unrelated clinical *S. sonnei* strains collected during the period 1997-2009 in Malaysia were analyzed. Biotyping was performed and biotypes were designated according to methods described by Nastasi et al. (1993). Antimicrobial susceptibility testing was performed using Kirby-Bauer disc diffusion method (Clinical and Laboratory Standards Institute, 2010) using eight antimicrobials: ampicillin, chloramphenicol, streptomycin, tetracycline, ciprofloxacin, kanamycin, ceftriaxone, and trimethoprim–sulfamethoxazole.

Results and Discussion

Two *S. sonnei* biotypes were identified, i.e. biotype *a* (n=29, 73%) and biotype *g* (n=11, 27%). These two biotypes were commonly reported in Australia from 1990-2009 (Valcanis, 2010). In many other countries, an increasing prevalence of *S. sonnei* biotype *g* since the 1990s was reported (Mammina et al., 2006; Izumiya et al., 2009). More Malaysian strains need to be studied to obtain a more accurate depiction of the different *S. sonnei* biotypes in Malaysia. The biotype *a* strains were subtyped into eight resistotypes whereas all the *S. sonnei* biotype *g* strains shared an identical resistotype of streptomycin - trimethoprim-sulfamethoxazole - tetracycline. All the *S. sonnei* strains remained susceptible to kanamycin, ceftriaxone and ciprofloxacin. Highest resistance rate was observed for streptomycin (67.5%), followed by tetracycline (40%), trimethoprim-sulfamethoxazole (37.5%), ampicillin (10%), and chloramphenicol (10%). Nine strains (22.5%) were susceptible to all the antimicrobials tested. Fifteen (37.5%) were multidrug-resistant strains (resistant to three or more classes of antimicrobials). Resistance to trimethoprim-sulfamethoxazole and tetracycline are common in *S. sonnei* (Seol et al., 2006; Izumiya et al., 2009). However, the resistance rates to these two antimicrobials in this study were relatively low.

Conclusion

*Shigella sonnei* biotype *a* was the predominant biotype detected in this study. The resistotypes of these strains were more diverse compared to the biotype *g* strains.

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References


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