Salmonellosis among Pediatric Population in Qatar: Prevalence, Antibiotic Resistance and Molecular Epidemiology

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BACKGROUND
Salmonellosis is a significant public health burden worldwide and being one of the most common bacterial diarrheal illnesses among infants and young children (Wang et al. 2017). Qatar reports multiple incidences of salmonellosis outbreaks among the pediatric population every year, coupled with a significant increase of multidrug-resistant (MDR) among gram-negative bacteria including Salmonella in the last few years, resulting in a serious public health hazard. Salmonella ranks among the four commonly isolated Enterobacteriaceae from clinical samples at Hamad Medical Corporation (HMC). The identification of Salmonella isolates into specific serovars is essential for epidemiologic studies, and tracing the source of outbreaks (Hong et al., 2003) but it is laborious and time-consuming. Many genotyping techniques, including pulsed-field gel electrophoresis (PFGE), random amplified polymorphic DNA (RAPD), restriction fragment length polymorphism (RFLP), multiplex PCR and whole-genome sequencing have been applied as alternative methods for Salmonella subtyping. Data relevant to these typing methods are scarce in Qatar. The recurrent Salmonella outbreaks in Qatar and the increasing number of salmonellosis cases (MOPI, Salmonella Work Shop, 2017, Qatar) mandates more attention and efforts to hinder the spread of these bacteria. This partially depends on the understanding of the bacterial phenotypic and genotypic characteristics that influence its pathogenicity and transmission with the potential to cause an outbreak.

OBJECTIVES
This study aims to
• Characterize the phenotypic resistance profile of Salmonella to relevant antibiotics among pediatric population.
• Elucidate the molecular mechanisms underlying resistance to ceftriaxone, cefepime, amoxicillin-clavulanate, tetracycline, trimethoprim-sulfamethoxazole, chloramphenicol, colistin and azithromycin in Salmonella isolates identified from pediatric among 2 – 16 years old in Qatar.
• Characterize the 16s rRNA gene region by restriction fragment length polymorphism (RFLP) to investigate if this region constitutes an appropriate ‘coincidental’ marker to distinguish important pathogenic Salmonella species.
• Determine the lineages of Salmonella species and evolutionary relationships among bacteria classified within the same genus.

Methods

Phenotypic profile of antibiotic
• 246 Salmonella isolates were collected from children under 16 years old during Jan. 2018 - Dec 2019, presented with gastroenteritis at Hamad Medical Corporation.
• Isolates were tested for antibiotic susceptibility against nineteen relevant antibiotic using E-test.

Genotypic of AMR
• Isolates that harbor antibiotic resistance were confirmed using PCR specific primers for 38 genes.
• In addition, the variable region of class 1 and 2 integrons were studied by PCR among amoxicillin-clavulanate (AMO) resistance samples.

Restriction fragment length (RFLP)
• 16s rRNA PCR amplicons were enzymatically digested with 7 restriction enzymes including AluI, BglII, BspHI, EcoRI, Smal, HinfI & HaeIII according to instructions of the manufacturer.

Conclusions
• Our results indicate a high antimicrobial resistance pattern of Salmonella, which necessitates the development of regulatory programs to combat antimicrobial resistance.
• In particular, our results showed high resistance to Class (1) AMC cassette that involves the transmission and expression of the resistance. This might lead to a concern of increased multidrug resistance in the future.
• This study provides evidence guidance to activate and implement the pillars of an antimicrobial stewardship program in animal and human health to reduce MDR salmonellosis

References

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