



Escherichia Coli Molecular Characterization and Antimicrobial Susceptibility Associated with Diarrhea among Children in Babil Province: Genotype, Phenotype, and Virus Genes Markers

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Abstract

Escherichia coli (DEC) strains that cause diarrhoea in children have been identified and classified in comparatively few investigations in Babil. This study looked on DEC among Babil children who were hospitalized and under the age of two. Using culture on MacConkey and EMB agar, the faeces of 200 children with diarrhea and 75 children without diarrhea were analyzed, and the E. coli isolates were checked for the presence of diarrheagenic E (Kaper JB et al., 2004). coli types and antibiotic susceptibility patterns. PCR for the detection of virulence genes. The detection of 10 different virulence genes for five different pathogroups of DEC, including enteroaggregative (EAEC), enteropathogenic (EPEC), enterotoxigenic (ETEC), enteroinvasive (EIEC), and enterohemorrhagic Escherichia coli, was done using a multiplex PCR system approach (EHEC). With typical EAEC and typical EPEC predominating, this investigation showed a significant prevalence of antibiotic resistance among normal intestinal E. coli isolates as well as a high incidence of diarrhea genic E. coli isolates (Aranda KRS et al., 2004). The sensitivity for detecting ETEC strains in hospitalized children can be determined by using primers for both ST variants.

Keywords: Diarrhea genic, Antimicrobial-Resistance genes, Escherichia coli, Virulence genes, Phylogenetic grouping, Antibiotic susceptibility, Diarrhea, Babil, DEC, EPEC, EHEC, ETEC, EAEC

INTRODUCTION

One of the main contributors to significant problems among children in the underdeveloped countries is diarrhea. In the underdeveloped world, it was believed that more than 4 million children died from diarrhea every year between the 1950s and 1970s death as a result. The main causes of diarrhea were bacteria, viruses, and parasites. Diarrhea genic bacteria were the most prevalent cause. The most significant etiologic agent of childhood diarrhea is Escherichia coli (DEC), which is a significant public health issue in underdeveloped nations. Differentiating these organisms from nonpathogenic elements of the normal gut flora is necessary for DEC strain identification (Ishii S et al., 2007).

On the basis of unique molecular, clinical, and pathological characteristics, DEC strains can be categorised into six main groups: enteroaggregative E. coli (EAEC), enterohemorrhagic (Shiga-toxin producing E. coli (EHEC/STEC), enteroinvasive (EIEC), enteropathogenic (EPEC), enterotoxigenic (ETEC), and diffusely adherent E. coli (DAEC).

The primary causative agent of paediatric diarrhea, Escherichia coli, is a significant public health issue in developing nations. Since they are identical to the non-pathogenic E. coli frequently found in human faeces, diarrhea genic E. coli cannot be accurately detected or identified using solely culture, biochemical, and serotyping techniques. Because of this, only DNA-based methods, such as the polymerase chain reaction (PCR) assay, which have a high sensitivity and specificity for their detection, can

be employed for quick and accurate diagnosis (Nweze EI, 2009). Geographical differences affect the epidemiological relevance of various DEC pathotypes in pediatric diarrhea. Numerous researches have looked at the clinical significance of ETEC-related diarrhea in particular areas.

The majority of the times, DEC, which naturally occurs in warm-blooded animals' digestive systems and is discharged into the environment through faecal material deposition, are used as indicators of faecal contamination of rivers. *E. coli* host sources in a typical mixed watershed can include people, agricultural animals, wildlife, and pets, among others. Until recently, it was thought that *E. coli* could not live in the environment and did not develop in secondary habitats like soil, surface water, or sediment. These hosts are typically referred to as primary habitats. It has been demonstrated that *E. coli*, even in temperate conditions, may grow in water, sediment, and soil and endure in the secondary habitats for protracted periods of time.

Since DEC cannot be accurately identified using standard procedures like culture and biochemistry, it is challenging to identify these strains, in contrast to polymerase chain reaction (PCR) methods that are utilized to find several genes important for the virulence characteristic of DEC. Multiplex PCR experiments made to find the virulence genes of EPEC, ETEC, EAEC, EHEC, and EIEC.

Our study's goals were to determine the prevalence of DEC diarrhea genic *E. coli* in hospitalized children as well as to look into the microbial sensitivity profiles of *E. coli* isolates. By using PCR, virulence-encoding genes in DEC diarrhea genic *E. coli* isolates were identified based on their phylogenetic isolation (Albert MJ et al., 2009).

DISCUSSION

Our research revealed that only children of all ages and genders had diarrhea genic *E. coli* isolates, while some of these isolates were also found in the group of control children. In addition, the study found that (ETEC), (EAEC), (EIEC), and (EHEC) were present, as opposed to the two categories.

In contrast to other studies conducted in Kuwait and Jordan, which had shown that EAEC was not a cause of diarrhea in their examined pediatric population, the rate of EAEC and ETEC among diarrheal cases in our study is in agreement with other similar studies recently reported from Iran,

Kuwait, and Egypt. The lack or low incidence rate of EIEC in the study's diarrhea cases and controls, however, is consistent with findings from other research from Egypt, Kuwait, and Jordan.

According to the study's findings, MDR *E. coli* made up a significant portion of all isolates and had high rates of antimicrobial resistance (1–91%) to various antimicrobial classes, including generation cephalosporins. These findings are consistent to some degree with numerous recent research conducted in other Arabic nations. The bla(CTX-M) genes have emerged as the most common ESBLs among multidrug resistant organisms globally over the past ten years. They first appeared in a few European and South American nations before spreading to India, China, and other nations.

CONCLUSIONS

We recommended that all patients with diarrhea should routinely be surveyed for causative pathogens, especially children under the age of two and in those specimens in which no other pathogen can be identified. The prevalence of EPEC and ETEC in our study revealed to be unexpectedly elevated in Babil. We also show how to employ a brand-new multiplex PCR to identify diarrhea genic *E. coli* in stool samples.

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