ORIGINAL RESEARCH

Evaluation of Microbial Profiling in Paediatric Patients with Infected Gut: An Institutional Based Study

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ABSTRACT

Background: Exposure to antibiotics in childhood is thought to alter the intestinal microbiome. Most of the data in literature are from case reports and small-sample cross-sectional studies; however, several recent short-term longitudinal studies have provided estimates of the incidence of adverse health events after enteric infections. Hence; under the light of abovementioned data, the present study was undertaken for assessing the microbiological profile of pediatric patients with infected gut.Materials &Methods: A total of 50 pediatric subjects within the age range of 6 to 16 years were enrolled. Complete demographic and clinical details of all the subjects were obtained. Inclusion criteria for the present study included pediatric subjects admitted because of gut infection. Subjects with presence of any other systemic illness, or any known drug allergy were excluded from the present study. Stool samples were collected prior to discharge home. All the samples were sent to microbiological department where Blood agar and Macconkey agar was used followed by incubation at 37 degrees centigrade for overnight with the aim of evaluating the microlocal growth. Quantification of the microbial growth was done. Results: A total of 50 subjects were analyzed. Mean age of the subjects was 10.3 years. 66 percent of the subjects were boys while the remaining were girls. Neutrophil count and lymphocyte count was 15.32 (x10³/µL) and 2.13 $(x10^{3}/\mu L)$ respectively. Salmonella was the main organism identified, found to be present in 46 percent of the cases. E.coli was found in 20 percent of the cases. Actinobacteria and Bacteroides were identified in 14 percent and 10 percent of the cases. Conclusion: In children presenting for emergency department care with acute gut infection, Salmonella was the main bacterium responsible for it.

Key words: Paediatric, Gut, Microbial.

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INTRODUCTION

Exposure to antibiotics in childhood is thought to alter the intestinal microbiome. Observational studies in high-income settings have suggested that there are alterations in the intestinal microbiome in children receiving antibiotics relative to those who have not received antibiotics. Antibiotics disrupt the composition of microbiota as they have activity against both commensal and pathogenic bacteria. Dysbiosis of the intestinal microbiome has been linked to multiple adverse health outcomes, including under nutrition and obesity, asthma, diabetes, and some forms of cancer. $^{\rm 1-\,3}$

Children with poor nutrition are at increased risk of complications. In Western countries children have increased rates of admission for gastroenteritis, malnutrition, comorbidity, and electrolyte disturbance (especially hypokalaemia) and a longer hospital stay than their non-indigenous counterparts. The cost of gastroenteritis to the community is huge but often underestimated if costs to the family, including lost time at work, are not considered.⁴⁻⁶

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Gastroenteritis leads to hospital admission in 7/1000 children under 5 years of age each year in the UK, and diarrhoea results in hospital admission in 1/23 to 1/27 children in the US by the age of 5 years. In Australia, gastroenteritis accounts for 6% of all hospital admissions in children under 15 years.⁷⁻⁹ Acute gastroenteritis accounts for 204/1000 general practitioner consultations in children under 5 years in the UK. In the US, rotavirus results in hospital admission in 1/67 to 1/85 children by the age of 5 years.^{7,8}

Most of these data are from case reports and smallsample cross-sectional studies; however, several recent short-term longitudinal studies have provided estimates of the incidence of adverse health events after enteric infections. These studies suggest that the increase in risk for sequelae is considerable.^{10,11}Hence; under the light of abovementioned data, the present study was undertaken for assessing the microbiological profile of pediatric patients with infected gut.

MATERIALS & METHODS

The present study was undertaken for assessing the microbiological profile of pediatric patients with infected gut. A total of 50 pediatric subjects within the age range of 6 to 16 years were enrolled. Complete

demographic and clinical details of all the subjects were obtained. Inclusion criteria for the present study included pediatric subjects admitted because of gut infection. Subjects with presence of any other systemic illness, or any known drug allergy were excluded from the presentstudy. Stool samples were collected prior to discharge home. All the samples were sent to microbiological department where Blood agar and Macconkey agar was used followed by incubation at 37 degrees centigrade for overnight with the aim of evaluating the microlocal growth. Quantification of the microbial growth was done. All the results were recorded in Microsoft excel sheet and were subjected to statistical analysis using SPSS software. Univariate analysis was done for evaluation of level of significance.

RESULTS

A total of 50 subjects were analyzed. Mean age of the subjects was 10.3 years. 66 percent of the subjects were boys while the remaining were girls. Neutrophil count and lymphocyte count was $15.32 (x10^3/\mu L)$ and 2.13 $(x10^3/\mu L)$ respectively. Salmonella was the main organism identified, found to be present in 46 percent of the cases. E.coli was found in 20 percent of the cases. Actinobacteria and Bacteroides were identified in 14 percent and 10 percent of the cases.

Table 1: Demographic profile

Variable	Number
Mean age (years)	10.3
Boys	33
Girls	17
Neutrophil count (x10 ³ /µL)	15.32
Lymphocyte count (x10 ³ /µL)	2.13

Table 2: Microbiological profile

Microbiological profile	Number	Percentage
Eubacteria	3	6
Bacteroides	5	10
Actinobacteria	7	14
Escherichia coli	10	20
Salmonella spp.	23	46
Streptococcus spp.	2	4
Total	50	100

DISCUSSION

Acute gastroenteritis is usually self-limiting, but if untreated it can result in morbidity and mortality secondary to water loss, and electrolyte and acid–base disturbance. Acute diarrhoea causes 4 million deaths each year in children aged under 5 years in Asia (excluding China), Africa, and Latin America, and more than 80% of deaths occur in children under 2 years of age.¹²⁻¹⁴

A total of 50 subjects were analyzed. Mean age of the subjects was 10.3 years. 66 percent of the subjects were boys while the remaining were girls. Neutrophil count and lymphocyte count was 15.32 $(x10^3/\mu L)$ and 2.13 $(x10^3/\mu L)$ respectively. Salmonella was the main

organism identified, found to be present in 46 percent of the cases. E.coli was found in 20 percent of the cases. Actinobacteria and Bacteroides were identified in 14 percent and 10 percent of the cases. In a study addressing the composition of the gut microbiota of children between the ages of 1 and 4 years and adults from the USA, it was found that members of the Actinobacteria, Bacilli, Clostridium cluster IV (Ruminococcaceae), and Bacteroidetes were more prevalent in children than in adults. In contrast, members of Clostridium cluster XIVa (Butyrivibriocrossotus and related bacteria) were more abundant in adults than in children. These findings suggest that some members of the microbiota may already be established in young children, whereas others are continuing to evolve. In another study, monitoring of the gut microbiota of 28 children was extended to the age of 5 years. Interestingly, microbial diversity at 5 years of age was still significantly lower than that in adults. These findings are consistent with the previous one, with the same taxa, including Actinobacteria, Bacilli, and Clostridium cluster IV, retaining abundances similar to those in infants, and others, such as Clostridium (Lachnospiraceae), cluster XIVa adopting а distribution more like that in adults.^{15, 16}

In another study conducted by Mathew et al, analyzed gut microbiome and clinical outcomes in young children suffering from viral or mixed viral-bacterial infection. They used a permutational multivariate analyses of variance to test the significance of group differences. Statistical analysis by overall relative abundance denoted lesser proportions of Bacteroides in the infected children, whereas Bifidobacteriaceae richness was more prominent in the bacterial-viral mixed infections. Pairwise differences of gut microbiota were significantly higher in RV+EAEC (P = 0.009) and NoV + EAEC(P = 0.009)coinfections, compared to EPEC mixed infection with both, RV (P = 0.045) and NoV (P = 0.188). Shannon diversity index showed considerable more variation in microbiome diversity in children infected with RV cohort compared to NoV cohort. Our results highlight that richness of Bifidobacteriaceae, which acts as probiotics, increased with the severity of the viralbacterial mixed infections. As expected, significant reduction of relative numbers of Bacteroides was characterized in both RV and NoV infections, with more reduction observed in co-infection pathogenic E. coli. Although mixed infection with EAEC resulted in significant microbiota differences compared to viral infection only or mixed infection with EPEC, the clinical condition of the children were worsened with both pathogen.¹⁶Tickell KD et al evaluated Shigellaassociated and dysentery-associated mortality, the diagnostic value of dysentery for the identification of Shigella infection, and the efficacy of antibiotics for children with Shigella or dysentery, or both.3649 papers were identified and 60 studies were included for analyses: 13 for mortality, 27 for diagnostic value, and 20 for treatment. Shigella infection was associated with mortality (pooled OR 2.8, 95% CI 1.6-4.8; p=0.000) whereas dysentery was not associated with mortality (1.3, 0.7-2.3; p=0.37). Between 1977 and 2016, dysentery identified 1.9-85.9% of confirmed Shigella infections, with sensitivity decreasing over time (p=0.04). Ten (50%) of 20 included antibiotic trials were among children with dysentery, none were placebo-controlled, and two (10%) evaluated antibiotics no longer recommended acute infectious for diarrhoea. Ciprofloxacin showed superior microbiological, but clinical, effectiveness compared with not pivmecillinam, and no superior microbiological and

clinical effectiveness compared with gatifloxacin. Substantial heterogeneity was reported for metaanalyses of the Shigella-associated mortality studies (I2=78·3%) and dysentery-associated mortality studies (I2=73·2%). Too few mortality studies were identified to meaningfully test for publication bias. No evidence of publication bias was found in this analysis of studies of diagnostic value.Current WHO guidelines appear to manage dysentery effectively, but might miss opportunities to reduce mortality among children infected with Shigella who present without bloody stool.¹⁷

CONCLUSION

In children presenting for emergency department care with acute gut infection, Salmonella was the main bacterium responsible for it.

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