

Contribution of Atypical EPEC Cause of Diarrhoea among Children and their Characterization at Molecular Level

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Abstract

We have identified seventeen enteropathogenic *Escherichia coli* (EPEC) isolated from faecal sample of 396 children with and without diarrhoea. Out of 12 EPEC isolates from patient with diarrhoea, three (25 %) were atypical while nine (75 %) were typical EPEC. So typical EPEC is prevalent in children with diarrhoea in Delhi and NCR. Five atypical EPEC isolated from faecal sample of 100 healthy children which indicated that atypical EPEC strains are colonized in the intestine of healthy children and its isolation rates are more in healthy children in compare to children with diarrhoea. Interestingly all of the atypical EPEC isolates bearing large plasmid mostly comparable with the size of EPEC adherence factor (EAF). Multidrug resistance EPEC are emerging and atypical EPEC strains showed significantly less resistant to ampicillin, norfloxacin, cephotaxime, ceftriaxone, streptomycin, ciprofloxacin, tetracycline and nalidixic acid in compare to typical EPEC and all atypical EPEC are sensitive to chloramphenicol, gentamicin but none are resistant to furazolidone. Chloramphenicol, gentamicin and furazolidone are alternative drug of choice to treat the patient with diarrhoea caused by atypical EPEC. This study is an evidence of emergent atypical EPEC in Delhi. Appropriate antimicrobial agent is recommended stopping the emergence of resistance organism. This study further supports the opinion that Shiga toxin-producing *E. coli* (STEC) does not pose a major threat to children health in India as no STEC was detected by us. Polygenetic tree analysis of intimin gene sequences of our isolates with reported intimin genes revealed five groups of the closely related intimin genes: (i) 5 PD, 159 PD and *eae-α1* (ii) 102 PD, C 42-5, *eae-γ1*, 226-8 PD, C 84-a1 and *eae-γ2* (iii) 258 PD and *eae-λ* (iv) 216 PD, *eae-*

β 2, 283 PD, C 100c1 and *eae*- β 1 (ν) C 48-a and *eae*- κ . The 3' sequence analysis of *eae* gene from our isolates revealed that *eae*- β 1, *eae*- γ 1 and *eae*- γ 2 subtype are common in EPEC isolates with children with and without diarrhoea but *eae*- α 1, *eae*- β 2 and *eae*- λ could be common EPEC subtype prevalent in children with diarrhoea in Delhi, India. The present study appears to be the first report in India regarding detection of atypical EPEC from children without diarrhoea and also records the isolation of EPEC strains having intimin gene closely related to *eae*- γ and rare subtype *eae*- λ in India. Moreover the virulence determinants of atypical EPEC are relatively unknown, so it is important to analyze the exact role of this mega plasmid to understand the virulence determinants of atypical EPEC. Better characterization of variable 3' end of *eae* in a large collection of atypical EPEC isolated from children with and without diarrhoea may provide PCR tool for the diagnosis of few atypical EPEC subtype cause of diarrhoea in human.