

**SHORT COMMUNICATIONS**

**Virulence Characteristics and Molecular Epidemiology of Diarrheagenic  
*Escherichia coli* (DEC) Associated with Sporadic Cases  
in a Tertiary Care Hospital in Manipal-Southern India**

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Diarrhoea continues to be one of the most common causes of morbidity and mortality among infants and children in developing countries contributing to the deaths of 3.3 to 6 million children annually. Detection of the etiological agents is important for all therapeutic aspects and for implementing appropriate control strategies. In developing countries, DEC are said to be commonly associated with endemic form of diarrhea. The DEC belong to different categories of pathotypes which are classified based on their clinical features, virulence mechanism and serotypes into ETEC, EPEC, EaggEC, EHEC and EIEC [1-3].

Serogrouping was once the widely used method for identifying the DEC strains and was also used as the epidemiological marker. But now molecular epidemiological markers like PCR, PFGE and Dendrogram are used for tracing genetic relatedness among the different DEC strains.

A total of 180 *E. coli* strains from infants and children with persistent diarrhea for more than 2 weeks were included for the present study. *E. coli* strains from 75 age matched infants and children without diarrhea for the past 3 weeks were included as controls. A multiplex PCR targeting the specific virulence genes was carried out [4]. of the total 180 *E. coli* strains, 28 (15.6%) were Eagg Coli, 9 (5%) EPEC and the remaining 4 (2.2%) were ETEC pathotypes. Serogrouping showed that Eagg *E. coli* belonged to 0128 and 086a, EPEC to 0114 and ETEC to 028ac serogroups which are the most common serotypes found in most of the geographical areas in India. Antibiotic susceptibility testing of the pathotypes was carried out according to NCCLS guidelines and were found to be multiple drug resistant. The ATCC strains *E. coli* 25922 and *Staphylococcus aureus* 25923

were used as quality control strains. The DEC were sent to NICED, Kolkata for PFGE and clonal analysis [5, 6]. Two strains of ETEC ( serogroup 025, 028ac) and two strains of Eagg *E. coli* ( serogroup 086a) pathotypes were closely related according to clonal criteria as they showed difference with less than two bands in the PFGE and showed more than 50% similarity in the dendrogram and were placed in the same cluster. Such a trend has been observed previously among the DEC strains isolated from an outbreak and among the pandemic *Vibrio parahaemolyticus* strains [7, 8]. In contrast to our findings, a study conducted at Kolkata on the strains collected from different geographical areas in India, revealed that the strains of the same pathotype of DEC are not monophyletic ie not confined to a single cluster in the dendrogram.revealing that there is no correlation between pathotypes and serotypes as well as the place of isolation of DEC strains.

Detection of clonality in DEC is a useful approach as it gives information such as source of contamination, nature of strains in the population etc. Thus the molecular epidemiology compares the genetic profiles of DEC belonging to different pathotypes giving information among the prevailing clonal diversity among the isolates

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