Molecular Analysis of *Shigella dysenteriae* Type 1 Strains by Using Pulsed-Field Gel Electrophoresis

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Objective: Determine the use of pulsed-field gel electrophoresis (PFGE) in molecular typing of *Shigella dysenteriae* type 1 strains from sporadic outbreaks and epidemic periods from different geographical location of the world.

Methodology: Genomic DNA of *S. dysenteriae* type 1 strains was analyzed using PFGE. The use of PFGE in a Not-I-digested DNA fragments clearly distinguished isolates involved in the epidemic from the non-epidemic strains. Genomic DNA was digested by Not-I restriction enzyme and the fragments separated using the contour-clamped homogenous electric field method on a CHEF-DRII system on 1% agarose.

Results: One hundred thirteen isolates of *S. dysenteriae* type 1 (18 from epidemic and 95 from sporadic outbreaks) were typed by the PFGE method. These isolates were classified into 8 PFGE type A to H, comprising 1 to 22 patterns, and 25 patterns were identified in total. The major groups consisted of A and B. Type A was predominantly detected (in 51 of 56 strains) among the strains isolated in Bangladesh, while type B was rare (in 2 of 56 strains) and isolated only from Rangpur during the epidemic period in 1984. Among the very recent isolates (1995-1997) in Bangladesh, there were no type A pattern 2 isolates. This pattern was present among the epidemic strains isolated in Rangpur and in the Hooghly district of West Bengal, in 1984.

Conclusion: The results of the analysis suggest that a clonal relationship existed between these strains during the epidemic period in Bangladesh and West Bengal in 1984. Thus, the PFGE technique could be used as an epidemiologic tool for identifying epidemic-associated strains as well as for molecular subtyping of epidemiologically unrelated strains.

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Clonal Groups of Enteropathogenic *Escherichia coli* Isolated in Case-Control Studies on Diarrhoea in Bangladesh

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Objective: Investigate the clonal status of enteropathogenic *Escherichia coli* (EPEC) strains isolated from case-control studies in Bangladesh.

Methodology: Eighty EPEC isolates from children with diarrhoea and 14 isolates from matched healthy controls from two case-control studies were analyzed. The first study, conducted during 1991-1992, comprised 451 children aged up to five years with diarrhoea and 602 matched control children without diarrhoea. The second study, conducted during 1993-1994, comprised 546 children with diarrhoea and 215 matched healthy children recruited from the same neighbourhood. The EPEC isolates were characterized by serogrouping, enterobacterial repetitive intergenic consensus (ERIC) sequence PCR, and biochemical fingerprinting method (the automated phene plate or PhP system).

Results: Twelve EPEC serogroups were found with O114 (n=19) and O127 (n=23) being the dominant serogroups. Most strains of O114 serogroup belonged to the same PhP and PCR types. Strains of O127 serogroup contained those producing cytolethal distending toxin CDT (n=16) and those which did not (n=7). Both were found among the patients and the controls. The results of PCR and PhP typing showed that the CDT-positive strains belonged to the same clonal group and were related to one of the two PhP/PCR types of CDT-negative O127 strains. Thirty-one