Abstract

Introduction. Diarrheagenic E. coli (DEC) are a major cause of diarrhea in children in developing countries. However, they are not part of routine diagnosis in clinical laboratories. Objectives. To determine the DEC prevalence in Peruvian children and to describe the genetic variability of these strains. Materials and methods. A total of 8,003 E. coli strains previously isolated from eight different studies of diarrhea in children, mainly from peri-urban areas of Lima, were analyzed. Diagnosis of DEC was done with Multiplex real-time PCR using genes for each of the 6 DEC groups. Conventional PCR was performed for the detection of additional virulence genes. Results. Globally, the mean prevalence in diarrhea samples (n=4,243) was: enteroaggregative E. coli (EAEC) 9.9%, enteropathogenic E. coli (EPEC) 8.5%, enterotoxigenic E. coli (ETEC) 6.9%, diffusely adherent E. coli (DAEC) 4.8%, Shiga toxin-producing E. coli (STEC) 0.8% and enteroinvasive E. coli (EIEC) 0.6%. The relative frequency of each pathogen varies according to the age and the type of study. The main pathotypes in control samples (n=3,760) were EPEC (10.9%) and EAEC (10.4%). An important variability in the virulence genes frequency and molecular resistance mechanisms for each pathotype was found, without differences between diarrhea and control groups. Conclusions. DEC are a major cause of diarrhea in Peruvian children. These pathogens are highly heterogeneous. Additional studies are required to determine the prevalence in rural areas of Peru and in severe diarrhea cases.

Keywords

Escherichia coli, Diarrhea, Child, Peru, Virulence.