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Toxins of extra intestinal *Escherichia coli* isolated from blood culture

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Extraintestinal pathogenic *Escherichia coli* (ExPEC) is one of the main etiological agents of bloodstream infections caused by Gram-negative bacilli. ExPEC pathogenicity is due to the presence of genes, located on plasmids or chromosomes that encode virulence factors. E. coli virulence factors such as adhesins, toxins, invasins etc. are able to modify the metabolism of host cell, contributing to disease. In this study, 80 strains of E.coli were isolated by haemoculture from septicemic patients and investigated by polymerase chain reaction (PCR) to identify virulence factors genes encoding toxins and to determine phylogenetic group. We characterized genes encoding 3 different types of toxins: hemolysin A (hlyA), cytotoxic necrotizing factor type 1 (cnf1) and cytolethal distending toxins (cdt-I to cdt-V). 23.75% of E. Coli strains contained cnf1gene and 22.5% contained hlyA. Genes cdtI and cdtIVwere detected in 1 of 80 strains. Phylogenetic classification showed that E. Coli strains fall into to 4 groups (A, B1, B2, D) based on PCR detection (chuA and yjaA genes and DNA fragment TSPE4.C2). Virulent ExPEC mainly belong to groups B2 and D. The presented study results confirmed that 56% of E. Coli strains belonged to group B2 and 24% belonged to group D.

Biography

Katarina Curova has completed her PhD degree at the age of 27 years from Department of Medical and Clinical Microbiology, University of Pavol Jozef Safarik University in Košice in 2007. She is a teacher at the same Department. Her area of research interest is Virulence of Escherichia coli. She has participated in two international and many national conferences and has published 4 articles in current contents journals.

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