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Cytolethal Distending Toxins in Intestinal and Extraintestinal E. coli

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Abstract: Introduction: Cytolethal distending toxins (CDTs) represent intracellular acting proteins which interfere with cell cycle of eukaryotic cells. They are produced by Gram-negative bacteria with afinity to mucocutaneous surfaces and could play a role in the pathogenesis of various diseases. CDTs induce DNA damage probably through DNAse activity, which causes cell cycle arrest and leads to further changes (cell distension and death, apoptosis) depending on the cell type. Five subtypes of CDT (I to V) were reported in E. coli. Methods: We examined 252 E. coli strains belonging to four different groups. Of these strains, 57 were isolated from patients with diarrhea, 65 from patients with urinary tract infections (UTI), 65 from patients with sepsis and 65 from patients with other extraintestinal infections (mostly surgical wounds, decubitus ulcers and respiratory tract infections). Identification of these strains was performed by MALDI-TOF analysis and detection of genes encoding CDTs and determination of the phylogenetic group was performed by PCR. Results: In this study, we detected presence of cdt genes in 11 of 252 E. coli strains tested (4,4 %). Four cdt positive E. coli strains were confirmed in group of UTI (6,15 %), three cdt positive E. coli strains in groups of diarrhea (5,3 %) and other extraintestinal infections (4,6 %). The lowest incidence, one cdt positive E. coli strain, was observed in group of sepsis (1,5 %). All cdt positive E. coli strains belonged to phylogenetic group B2. Conclusion: CDT-producing E. coli are isolated in a low percentage from patients with intestinal and extraintestinal infections, including sepsis and our results correspond with these studies. A weak prevalence of cdt genes suggests that CDTs are not major virulence factors but in combination with other virulence factors may increase virulence potential of E. coli. We suppose that all 11 cdt positive E. coli strains represent real pathogens because they belong to the phylogenetic group B2 which is pathogenic lineage for bacteria E. coli.

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