Title: Potential virulence properties of human *Escherichia albertii* strains

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Abstract:

The new species *Escherichia albertii* comprises emerging animal and human pathogens. *E. albertii* was reported to share with other diarrheagenic *E. coli* pathotypes (DEC) some virulence factors, such as the *locus of enterocyte effacement* (LEE), which is responsible for *attaching/effacing* (AE) lesion formation in enterocytes. Due to difficulties in discriminating *E. albertii* isolates from other members of the *Enterobacteriaceae*, little is known regarding the potential virulence mechanisms of different isolates. WE evaluated potential virulence mechanisms of 5 *E. albertii* strains, formerly identified as atypical enteropathogenic *E. coli,* which had been isolated from diarrheic children. They were tested for the ability to adhere to and promote AE lesions (actin aggregation) in HeLa cells, and to invade and persist inside differentiated intestinal Caco-2 cells. Biofilm production on abiotic surfaces and resistance to 13 antibiotics were also examined. Plasmid profiles were assessed by electrophoresis of extracted DNA and presence of virulence genes of DEC and extra-intestinal pathogenic *E. coli* (ExPEC) were tested by PCR. The strains adhered to HeLa cells in a localized adherence (LA) (3 strains) or LA-like (loosen clusters) patterns (2 strains), and promoted actin aggregation. All strains adhered to and three invaded Caco-2 cells, but none persisted intracellularly. Biofilm was produced by 3 strains. All strains were sensitive to amikacin, amoxicillin/clavulanic acid, chloramphenicol, gentamicin and kanamycin, and resistant to cefalotin (5 strains), cefuroxime (3 strains), cefotaxime (2 strains); and amoxicillin, ampicillin, nalidixic acid, sulfazotrim, and tetracycline (1 strain each). Except for 1 strain with a single ~147 kb plasmid band, none of them carried plasmids. Among the 33 DEC virulence genes searched for, only *paa* (*porcine attaching and effacing associated*) (all strains), *shf* (*Shigella flexneri homologue*) (1 strain) and *efa1* (*E.coli factor for adherence*) (1 strain) were found. Among the 16 ExPEC genes, all strains carried *ompA* (outer membrane protein A-invasin), 3 carried *tsh* (heat-sensitive hemagglutinin), 2 carried *cvaC* (bacteriocin), 1 carried both *sitA* (*Salmonella siderofore*) and *traT* (Protein associated with complement resistance). Altogether, our data reveal the presence of potential intestinal and extra-intestinal virulence mechanisms in *E. albertii* strains thus reinforcing the importance of this species as potential human pathogens.

Keywords: *Escherichia albertii*, virulence mechanism, adhesion and invasion, DEC, ExPEC.

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