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pEntYN10 a plasmid of *Escherichia coli* O169:H41 associated with adherence and toxin production

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In this issue of *Virulence*, Ban E *et al*. described the complete sequence of the pEntYN10 plasmid of *Escherichia coli* O169:H41. The plasmid has 182 coding sequences (CDs); among the identified CDs, some were identified as colonization factors (CFs), one was an enterotoxin and others were insertion sequences (IS). In this editorial, the main findings, as well as the epidemiological significance and spontaneous loss of pEntYN10 plasmid of *E. coli* O169:H41 strains are discussed.

Ban et al.[1] described the complete sequence results of the pEntYN10 plasmid of *Escherichia coli* O169:H41, which was isolated from an epidemic outbreak of diarrhea in Osaka, Japan in 1991. Since then, other outbreaks have been reported in different countries including the Republic of Korea,[2] Japan[3] and the USA.[4] From 1996 to 2003, 16 epidemic outbreaks related to the transmission of enterotoxigenic *E. coli* (ETEC) in food were reported in the USA, and 10 of these were associated with ETEC O169:H41.[4] These observations suggest that ETEC-related diarrhea is no longer just a problem of travelers to developing countries, but it is now an endemic problem in the region as a whole.[5] In Japan, where the association of *E. coli* O169:H41 with food borne intestinal infection was first identified in 1991,[6,7] a series of new epidemic outbreaks of *E. coli* O169:H41-related diarrhea were reported.[3,8] Recently in the Republic of Korea (2012) in the area of Incheon City, an outbreak of intestinal infection related to *E. coli* O169[2] was reported in 7 schools that affected 230 students after eating Kimchi distributed by a food manufacturer. Infections produced by ETEC strains are a worldwide problem and this pathotype is considered to be the second most important etiological agent responsible for infantile diarrhea in the world, after Rotavirus and *Shigella*.[9] Ban et al.[1] describe the complete sequence of the pEntYN10 plasmid identified in the *E. coli* O169:H41 strain. Its analysis revealed that the plasmid has 145,082 base pairs with 182 coding sequences (CDs), and contains 43.15% guanine and cytosine. Among the coding sequences, some were identified as colonization factors (CFs), one was an enterotoxin and others were insertion sequences (IS). Furthermore, the plasmid presented *psiAB* and *relE* genes both related to stability but different from those (*stbAB, psiAB, relE, mok/hok/soc*) found in ETEC H10407 (O78:H11). With respect to the colonization factors, the authors found the presence of CS6, CS8 (CFAIII)-like, K88 (F4)-like encoded redundantly in the plasmid. In the case of CS8 (CofA) that shows a high structural homology with TcpA from *Vibrio cholerae* and had a similar amino acid sequence to that of the pSH1134 plasmid from ETEC 206-1 strain. In addition, 2 paralogous copies of the *faeG* gene related to the main component of the fimbrial structure of K88 were identified; the structure was similar to *Salmonella enterica* serovar Infantis. Despite the presence of *psiAB* and *relE* genes, which are related to the stability of the pEntYN10 plasmid, stability is lost fairly easily after passing the *E. coli* YN19 strain 7 times through trypticase soy broth (TSB). Analysis of the clones that lost the plasmid showed that ST toxin expression, as well as the adherence capacity of the aggregative pattern in HEp-2 cells, disappeared. Based on this last observation, the authors proposed that the genes present in pEntYN10 contribute to bacterial adherence to HEp-2 cells, probably related to the expression of CS6, CS8 (CFAIII)-like and K88 (F4)-like. Previous reports relating to *E. coli* O169:H41 strains isolated from epidemic outbreaks in Japan[3] in which the spontaneous loss of a 100 MDa plasmid was observed, concluded that this loss was associated with the inability to produce the ST toxin and adherence of the aggregative pattern to HEp-2 cells. Although these observations are in keeping with those reported by Ban et al.[1] more studies are required to define the participation of the plasmids in the expression properties of *E. coli* O169:H41 wild strains as they relate to the bacteria's virulence.

Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

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