TITLE: MOLECULAR DIAGNOSIS AND VIRULENCE GENES PROFILE FROM *Campylobacter jejuni* INFECTION ISOLATED FROM CHILDREN WITH MODERATE TO SEVERE DIARRHEA IN FORTALEZA, CEARÁ, BRAZIL

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Campylobacter spp. infections are considered to be the most common cause of bacterial gastroenteritis caused by contamination of food in the world. *Campylobacter jejuni* is the most characterized specie. The aim of this study was to diagnose and identify the presence of virulence genes related to *Campylobacter jejuni* in children with moderate to severe diarrhea in the city of Fortaleza – CE, Brazil. The project was approved by the local and national ethical committees in Brazil (HIAS 80/06 and CONEPE 13523/2007, respectively). DNA was extracted directly from fecal samples arising from 436 children with moderate to severe diarrhea during May 2008 and April 2009, in Fortaleza, Ceará, Brazil. The diagnosis of *C. jejuni* was performed by conventional PCR using *hipO* gene. The detection of genes that encode proteins associated with virulence of *C. jejuni* was performed with uniplex and multiplex PCR techniques. *C. jejuni* was diagnosed in 14% (61/436) of the samples, presenting significant association between the presence of the pathogen in children aged 0-12 months (P = 0.0001) and children aged 12,1-24 months. 51 positive samples for *C. jejuni* were used for the detection of virulence genes. The prevalence of the *C. jejuni's* virulence-associated genes were: *flgE*, 92.2% (47/51) and *flaA*, 76.5% (39/51) – related to motility; *cheW*, 90.2% (46/51); *cheA*, 82.4% (42/51) and *cheR*, 66.6% (34/51) – related to bacterial chemiotaxis; *cadF*, 100% (51/51) and *jlpA*, 43.1% (22/51) – related to bacterial adhesion; *ciaB*, 96.1 % (49/51); *iamA*, 90.2% (46/51); *pldA*, 45.1% (23/51) and *pVir* 0% (0/51) – related to invasion; *cdtABC*, 94.1% (48/51) related to cytolethal distending toxin (CDT); *fur*, 66.6% (34/51); *cfrA*, 31.4% (16/51) and *ceuE*, 21.7% (11/51)– related to bacterial iron transport and regulation; *racR*, 100% (51/51); *sodB*, 96.1% (49/51); *dnaJ*, 88.2% (45/51) and *katA*, 66.6% (34/51);– related to oxidative stress. The distribution profiles of *C. jejuni's* virulence did not correspond to the patient's clinical presentation abdominal pain. But the association of *cfrA* and *dnaJ* genes was correlated with fever (P=0,0214), *jlpA* e *katA* gene was correlated with vomiting (P=0,0211) and *pldA* and *ceuE* genes was correlated with the presence of blood in stool (P=0,0013), suggesting that relationships might be related to the severity of infection by this microorganism. New studies about the expression of proteins associated with the virulence genes must be carried to better understand the pathobiology mechanisms of *Campylobacter jejuni* infections.

Keywords: *Campylobacter jejuni*, virulence, diarrhea.

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