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Molecular epidemiology of Cryptosporidium spp. in North Lebanon

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Abstract

Cryptosporidium spp. are enteroparasites with worldwide distribution that infect the gastrointestinal tract of several vertebrates including humans. Human to human, zoonotic, foodborne and waterborne are reported as the main transmission routes of this parasite. Cryptosporidium spp. have been recognized as the predominant cause of waterborne and foodborne outbreaks. However, the epidemiological situation of cryptosporidiosis is not well known in Lebanon, a developing country with a population often affected by intestinal parasitic infections. This study was devoted to determine the prevalence and the genetic diversity of Cryptosporidium spp. in symptomatic hospitalized patients and in two children populations with different socio-economic level in North-Lebanon, as well as the risk factors associated with cryptosporidiosis.

Fecal samples obtained from these populations were examined microscopically by modified Ziehl-Neelsen staining as well as nested PCR were done for the detection of Cryptosporidium oocysts. Out of 163 symptomatic hospitalized patients and 249 children, Cryptosporidium was present in 11% and 10.4% respectively according to microscopy examination and/or molecular tests. The genotyping showed the predominance of Cryptosporidium hominis in both populations. Subgenotype analysis of the isolates at the gp60 locus identified three subtypes IaA19, IbA10G2 and IaA18R3 for C. hominis and two subtypes IIaA15G1R1 and IIaA15G2R1 for C. parvum. Moreover, cryptosporidiosis was correlated with having meals outside home and presence of gastrointestinal symptoms especially diarrhea (p <0.05).

This work constitutes the first molecular epidemiology study outlining risk factors associated with cryptosporidiosis in Lebanon. These findings support a need of a control program to prevent the circulation of this parasite.

Key words: Cryptosporidium spp.; molecular epidemiology; risk factors; Lebanon.


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