

The Lebanese LSICDM

Molecular epidemiology of *Cryptosporidium* spp. in North Lebanon

Marwan Osman^{1,2}, Sadia Benamrouz^{2,3}, Karine Guyot², Dima El Safadi^{1,2}, Hassan Mallat¹, Fouad Dabboussi¹, Monzer Hamze¹, Eric Viscogliosi², Gabriela Certad^{2,4}

¹ Laboratoire Microbiologie Santé et Environnement (LMSE), Ecole Doctorale des Sciences et de Technologie, Faculté de Santé Publique, Université Libanaise, Tripoli, Liban

² Institut Pasteur de Lille, Centre d'Infection et d'Immunité de Lille (CIIL), UMR CNRS 8204, INSERM U1019, Université de Lille, CHU de Lille, Biologie et Diversité des Pathogènes Eucaryotes Emergents (BDPEE), Lille, France

³ Ecologie et Biodiversité, Faculté de Gestion, Economie et Sciences (FGES), Université Catholique de Lille, Lille, France

⁴ Département de la Recherche Médicale, Groupement des Hôpitaux de l'Institut Catholique de Lille, Faculté de Médecine et Maïeutique, Université Catholique de Lille, Lille, France

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 IdA19, 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.

J Infect Dev Ctries 2018; 12(2S):34S. doi:10.3855/jidc.10014

(Received 04 December 2017 – Accepted 12 December 2017)

Copyright © 2018 Osman *et al.* This is an open-access article distributed under the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

Corresponding author

Gabriela Certad, MD. PhD.

Institut Pasteur de Lille, Centre d'Infection et d'Immunité de Lille (CIIL), UMR CNRS 8204, INSERM U1019, Université de Lille, CHU de Lille, Biologie et Diversité des Pathogènes Eucaryotes Emergents (BDPEE), 1 rue du Professeur Calmette, 59019 Lille cedex, France.

Phone: 03-20-87-79-61

Fax: 03-20-87-78-88

Email: gabriela.certad@pasteur-lille.fr

Conflict of interests: No conflict of interests is declared.