

Cryptosporidiosis in children is pandemic to unique level.

Lihua Ling*

Department of Microbiology, Faculty of Medicine, Kuwait University, Safat, Kuwait

Abstract

Fecal samples from 62 Kuwaiti children with gastrointestinal symptoms who tested positive for *Cryptosporidium* infection by microscopy were genotyped and subtyped using a 60-kDa glycoprotein-based DNA sequencing tool and a small subunit rRNA-based PCR-restriction fragment length polymorphism analysis. The median age of afflicted children was 4.5 years old, and 77% of infections took place from November to April, when the weather was chilly. One youngster had both *Cryptosporidium parvum* and *C. hominis*, while three other kids had *Cryptosporidium parvum*. 13 subtypes of *C. parvum* and *C. hominis* were identified in total, with 92% of the samples falling under the common allele family IIa and the uncommon allele family IIc. Both in poor and industrialised countries, cryptosporidiosis is a substantial contributor to diarrheal illnesses. The transmission of cryptosporidiosis in people and the importance of *Cryptosporidium spp.* in animals and the environment for public health have both been improved by recent molecular epidemiologic investigations of the disease. Five species of *Cryptosporidium* have been identified as being the main cause of human illnesses using genotyping methods. The two most prevalent species among these five are *Homo sapiens* and *C. parvum*. The characterisation of *Cryptosporidium* at the species level is helpful in determining infection and contamination sources since these five.

Keywords: Gastrointestinal symptom, *Cryptosporidium parvum*, Glycoprotein.

Introduction

In this investigation, stool samples from 62 Kuwaiti kids who had *Cryptosporidium* diagnosed were used. With the exception of four specimens, which were obtained in 1997 and 1998, they were all collected between January 2001 and February 2004. Each stool sample came with the very minimum of clinical information, such as the patient's age and gender, any significant clinical symptoms, and the date the sample was taken. Due to gastrointestinal issues, many kids sought care at public hospitals [1,2].

Cryptosporidium genotyping

All samples were initially genotyped using the PCR-RFLP method. This method uses nested PCR to amplify an 830-bp fragment of the SSU rRNA gene and uses banding patterns in restriction analysis of the secondary PCR products with the enzymes SspI and VspI to distinguish between different *Cryptosporidium* species or genotypes [3].

Accession numbers for nucleotide sequences

In the nested PCR investigation of the SSU rRNA gene, DNA preparations of all 62 specimens produced results of the predicted size. With the help of the restriction enzymes SspI and VspI, RFLP analysis of the secondary SSU rRNA PCR products revealed that 58 of the kids had *C. parvum*, three had

C. hominis, and one had both *C. parvum* and *C. hominis*. Three *C. parvum* PCR products and one *C. hominis* PCR product that underwent DNA sequencing produced SSU rRNA sequences that were identical to those that had previously been reported for *C. parvum* and *C. hominis*, respectively [4].

Distribution of *C. parvum* and *C. hominis* subtypes in Kuwaiti children

Children from Kuwait showed a total of 13 subtypes from seven *C. parvum* and *C. hominis* allele groups. Nearly equal proportions of kids were infected with each allele of the *C. parvum* subtype family IIa or IIc, which made up the majority of the youngsters. Only two of the children who had allele IIa parasites had the subtype IIaA15G1R1, the majority of them had IIaA15G2R1. Only two of the children with allele IIc had the subtype IIcA18G1, but the majority of them had GP60 sequences with 20 copies of the TCA repeat and one copy of the TCG repeat. The sequence type IIcA20G1 had four subtypes, all of which belonged to IIcA20G1a whereas the majority of earlier specimens belonged to IIcA20G1b, IIcA20G1c, and IIcA20G1d. There were just one or two kids from the other five allele families. Three children exhibited mixed subtype infections; specimens 5627 and 5636 each had IIaA15G2R1 and IbA10G2, while specimen 8896 had IIcA20G1a and an unidentified subtype [5].

*Correspondence to: Lihua Ling, Department of Microbiology, Faculty of Medicine, Kuwait University, Safat, Kuwait, Email: Lihualing6754@cdc.gov

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Conclusion

Water borne transmission is regarded as a key route in the epidemiology of cryptosporidiosis in these places. In tropical nations, the transmission of *Cryptosporidium* in children is typically related with the rainy season. However, Kuwait receives relatively little precipitation, and the chilly season, which lasts from November to April, is when *Cryptosporidium* is most commonly transmitted. The fact that Kuwait's primary source of drinking water is desalinated water suggests that waterborne transmission plays a less significant role in this situation. In order to determine the risk factors associated with acquiring a *Cryptosporidium* infection and to provide some of the answers to the concerns raised above, a well-designed case control research with extensive data collecting on water and food sources and animal interaction would be beneficial. Water and household animals should also be sampled. The degree of zoonotic transmission of cryptosporidiosis in Kuwaiti children must be determined, in particular, by subtyping *C. parvum* from domestic animals in Kuwait.

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