

Molecular epidemiology of *Cryptosporidium* infections in Japan

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Molecular characterization has provided insights into the epidemiology of *Cryptosporidium*, which is one of the major causes of protozoal diarrhea in humans worldwide. By PCR amplification and sequence analysis of 18S rDNA and poly-threonine genes of clinical isolates, it has been demonstrated that three large-scale outbreaks and more than 60% of sporadic cases in Japan were caused by human-adapted genotype I (syn. *Cryptosporidium hominis*). In this study, the isolates were further characterized by sequencing of glycoprotein cpgp40/15, which showed the highest intraspecific diversity. As a result of this analysis, 37 clinical isolates were placed in 9 distinct clusters. This suggests that this analytical method is a promising tool for outbreak characterization and traceback investigation. The 18S rDNA gene would be suitable as the target molecule for species identification and cpgp40/15 gene for subgenotype differentiation. The availability of molecular characterization of intestinal protozoa will have a major impact on our knowledge of *Cryptosporidium* epidemiology and point to new methods of control.