

FOREWORD

Of the protozoan parasitic infections transmitted by the waterborne route, *Cryptosporidium* is recognised as a significant cause of diarrhoea in humans worldwide. It is responsible for between 250 to 500 million infections annually in Asia, Africa and Latin America, and can be life-threatening in immunocompromised hosts (e.g. individuals affected by Acquired Immune Deficiency Syndrome, AIDS). Currently, there is no effective specific drug treatment for cryptosporidiosis.

The broad host range for *Cryptosporidium* together with the high output of oocysts ensures a high level of contamination in the environment, which favours waterborne transmission. Transmission by the waterborne route can result in large numbers of consumers being infected, resulting in large outbreaks of waterborne disease. Oocyst contributions into water arise from both point and non-point sources and specific knowledge of oocyst sources which contaminate water catchments is helpful when attempting to determine the potential for exposure to oocysts at water treatment plants. Infected humans, domesticated animals and wildlife can be reservoirs of human infection, and together with infected indigenous hosts in a watershed and carriage by aquatic birds, all contribute to the pool of waterborne oocysts, yet not all waterborne *Cryptosporidium* oocysts are infectious to humans.

Molecular typing methods have provided much needed insight into the genus *Cryptosporidium* by supporting the validity of known species and identifying the presence of other species and cryptic species / genotypes, only some of which are human-infective. They can also assist us in determining the public health significance of oocysts present in catchments and water by identifying those species / genotypes that are human-infective. Now that these discriminatory tools are available, we must use them to understand the epidemiology of this parasite, particularly the range and abundance of species / genotypes present in hosts and our environment over time and space, which in turn will provide better insight into the contributors of waterborne oocysts.

In recent years a number of research groups have made significant advances in the development of genetic typing methods for *Cryptosporidium*. While different approaches have been adopted, each has been driven by the realisation that a more discriminatory typing system than currently exists is essential if we are to apply molecular technologies to understand the epidemiology of *Cryptosporidium* and cryptosporidiosis. Sequencing of the *Cryptosporidium* genome and other technological advances have further accelerated research and knowledge in this area.

The organisers of the workshop considered it opportune to consolidate these new approaches and examine their practicality as tools for routine monitoring and analysis of *Cryptosporidium* in the environment.

The aim of the workshop was to bring together leading researchers in the field of genetic fingerprinting, public health specialists and water utility microbiologists to evaluate recent advances and examine their practicality as tools for routine monitoring of catchments and water and for the analysis of waterborne events, incidents and outbreaks.

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