EXECUTIVE SUMMARY

The protozoan parasite Cryptosporidium parvum is transmitted via contact with infected animals, recreational waters or contaminated drinking water or food and represents a significant public health problem. Approximately 6000 cases are reported each year in the UK. The number of cases in the UK is likely to be underreported. In the absence of available specific treatment of human cases, research has been directed towards developing molecular methods to characterise parasites so that sources and origins of infections can be identified and appropriate measures put in place to control routes of infection. To support the underlying scientific process of the development of Cryptosporidium parvum genotyping, a national collection of Cryptosporidium parvum oocysts and DNA, with a supportive database of patient data, has been established.

The aims of the project were several-fold.

- To develop a national collection of oocysts of Cryptosporidium parvum.
- To isolate & identify a series of highly polymorphic markers that are able to identify different isolates of Cryptosporidium parvum.
- To use the selected markers in the analysis of the variation between the isolates collected from clinical cases.
- To analyse whether the multilocus system could be used to identify sources of infection and in particular differentiate point sources.
- To pilot the transfer of any such developed typing system to the PHLS Cryptosporidium Reference Unit.
- To initiate testing the performance of the developed typing system on samples from England and Wales
- To extend the application of the typing system to the investigation of field isolates in England and Wales.
A large collection of well-documented *Cryptosporidium* sp. isolates (1172 from Scotland, 5001 from England and Wales) has been collected and archived providing not only a comprehensive picture of the prevalence and distribution of human and livestock cases of the disease but also an essential archive of material for future development of molecular epidemiological tools. The results have shown that the application of molecular fingerprinting using the new highly polymorphic markers provides much greater definition and resolution of the differences between *Cryptosporidium parvum* isolates than has been possible previously.