Abstract

The restriction enzyme profiles of nested PCR products were used to analyze. Cryptosporidium species during the first two years of this project, the method can differentiate most of Cryptosporidium into species of genotypes, not bwtween C. wrairi and C. parvum bovine genotype. In this year, the new primers were designed for the single PCR to amplify the target sequence of just four species, then analyzed by RFLP to differentiate C. parvum bovine genotype and C. wrairi.

The method was used on the samples collected from central Taiwan (Rona, Donpu, Hopien and Zhen-ai village) during the second year with new-designed single PCR to analyze, the conclusion shows that the samples from the four places are all positive for Cryptosporidium. After RFLP analysis, we found there were only C. parvum bovine genotype in the village Rona and Hopien, however there were mixed genotypes of C. parvum human and C. parvum bovine in the village Donpu and Zhen-ai. This year, samples collected from village Wu-lai and Zhen-shi , all are negative for Cryptosporidium and Cyclospora, even detected with nest PCR or single PCR.

In the 341 samples from AIDS patients, four samples are Cryptosporidium positive, the preference is 1.17%. After RFLP analysis, 2 samples are C. partum human genotype and another 2 samples are C. muris and C. meleagridis, increasing the possibility infected from animals.

This project constructs the detecting model of Cryptosporidium and Cyclospora successfully for water and fecal samples; by the way , also design the whole methods to differentiate species and genotypes of Cryptosporidium and Cyclospora .

Keywords：Cryptosporidium；Cyclospora；polymerase chain reaction；RFLP；genotype