Author's response to reviews

Title: Prevalence and Genetic Characterization of Cryptosporidium, Enterocytozoon, Giardia and Cyclospora in Diarrheal Outpatients in China

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Dear Editor,

According to the “requesting consent statement” by the editor, we have stated in the Methods section about written informed consent for participation in the study.

We would like to submit the enclosed manuscript “Prevalence and Genetic Characterization of Cryptosporidium, Enterocytozoon, Giardia and Cyclospora in Diarrheal Outpatients in China”, which we wish to be considered for publication in *BMC* infectious disease. All co-authors have seen and agree with the contents of the manuscript and there is no financial interest to report. We certify that the submission is original work and is not under review at any other publication. We know that your journal has high publication standards, so we have already had the language of this paper corrected by a professional language editing service that specializes in scientific manuscripts.

Cryptosporidiosis, microsporidiosis, giardiasis and cyclosporiasis are emerging infectious diseases. *Cryptosporidium* spp., *Enterocytozoon* spp., *Giardia* spp. and *Cyclospora* spp. are globally distributed diarrhea-causing intestinal protozoan parasites of humans, livestock, companion animals and wildlife. Thus far, no study has confirmed whether *Cryptosporidium andersoni*, *Enterocytozoon* spp. and *Giardia* spp. assemblage C could infect human outpatients on a large scale. In this study, we investigated fecal specimens from 252 diarrhea patients in a pediatric clinic (169) and an intestinal clinic (83) of a hospital in Pudong, Shanghai, China, from October 2012 to March 2013. *Cryptosporidium* spp. and *E. bieneusi* were detected in 13.49% of the 252 diarrhea patients, whereas the *Giardia* infection rate was 6.75%. Our data
indicated the first outbreaks of cryptosporidiosis caused by Cryptosporidium andersoni and of microsporidiosis caused by E. bieneusi in China. Thus, Cryptosporidium andersoni should be considered the fourth major Cryptosporidium species infecting humans in the world.

We believe that our findings could be of interest to the readers of BMC infectious disease. We hope that the editorial board will agree on the interest of this study.

Your kind consideration would be greatly appreciated.

Sincerely,

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