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ePoster Session

Clinical parasitology news

**Detection and genetic characterization of *Cryptosporidium* spp. among patients infected with HIV and renal transplant recipients, by conventional and molecular techniques**

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**Background:** *Cryptosporidium* species is an important cause of diarrhea in immunocompromised patients such as patients with Human immunodeficiency virus (HIV) and renal transplant (RT) recipients. Till date around nine species of *Cryptosporidium* has been known to infect patients with HIV, *C. parvum* and *C. hominis* being the commonest ones. However, there is scanty data on this issue in RT recipients. Genetic characterization of *Cryptosporidium* is essential to investigate the genetic diversity and might aid in tracing source of infection, thus helping to control its spread. Conventional microscopy can not differentiate the different species. Molecular techniques such as polymerase chain reaction (PCR) and real-time PCR are required. Therefore, this study was designed to detect *Cryptosporidium* by microscopy and genetic characterization by PCR and real-time PCR.

**Material/methods:** A total of 550 patients (including 360 RT recipients, 190 HIV positive patients), 200 healthy controls (HC) and 140 immunocompromised patients (patients with HIV infection and RT recipients) without cryptosporidiosis were recruited and evaluated for *Cryptosporidia* by microscopy, SSU rRNA gene, *Cryptosporidium* oocyst wall protein (COWP) gene PCR- RFLP and real time PCR melting curve analysis (qPCR- MCA). COWP PCR-RFLP and qPCR MCA were also used for genetic characterization of the parasite (for detecting *C. hominis*, *C. parvum*, *C. meleagridis*, *C. wrairi*, *C. felis*, *C. baileyi*, *C. muris*, *C. andersoni* and *C. serpentis*). PCR results were confirmed by sequencing.

**Results:** *Cryptosporidium* parasite was detected in 74/550 (13.5%) (HIV and RT) patients by both microscopy and SSU- PCR. COWP PCR-RFLP detected 66/ 550 (12%) and qPCR detected 75/ 550 (13.6%) cases of *Cryptosporidia*. Taking microscopy as the gold standard sensitivity, specificity, positive predictive value and negative predictive values were 100%, 100%, 100% and 100% of SSU-PCR, 89%, 100%, 100% and 98.3% of COWP- PCR and 100%, 99.7%, 98.6% and 100% of qPCR respectively. Microscopy also detected four cases of mixed infection (two with *Cystoisospora belli*, one with *Cyclospora cayatanensis* and another with *Strongyloides stercoralis*). Thus, 71 (28 HIV [28/ 190, 14.7%], and 43 RT [43/360, 11.9%]) patients showed mono-infection with *Cryptosporidium* spp. None of the HC was infected with *Cryptosporidium*. Thus, *Cryptosporidium* spp. was more frequent in immunocompromised patients than HC (75/ 550, 13.6% vs. 0/ 200, 0%,  $p < 0.001$ ). *Cryptosporidium hominis*, *C. Parvum* and mixed infection were detected in 52/75 (69.33%), 21/75 (28%) and 2/75 (2.6%) patients by qPCR-MCA and 48/66 (72.7%), 16/66 (24.2%) and 2/66 (3.03%) patients by COWP- PCR- RFLP respectively.

**Conclusions:** Thus, *C. hominis* and *C. parvum* were the *Cryptosporidium* species detected among patients with HIV infection and RT recipients in our setup. *C. hominis* was most prevalent among RT recipients, as in patients with HIV infection. Molecular tools, especially qPCR- MCA are mostly helpful for genetic characterization of the parasite.