eP480
ePoster Viewing
MALDI-TOF

MALDI-TOF MASS SPECTROMETRY ANALYSIS FOR THE DIFFERENTIATION OF THE PATHOGENIC INTESTINAL AMOEBA ENTAMOEBA HISTOLYTICA FROM THE NON-PATHOGENIC ENTAMOEBA DISPAR ISOLATED FROM BIOLOGICAL SAMPLES.

A. Calderaro[1], M. Piergianni[1], C. Gorrini[1], G. Piccolo[1], M. Buttrini[1], S. Montecchini[1], M.C. Medici[1], M.C. Arcangeletti[1], C. Chezzi[1], F. De Conto[1]

[1]Clinical and Experimental Medicine, University of Parma, Parma, Italy

Objectives. The detection of *Entamoeba histolytica*,the causative agent of invasive amoebiasis, is an important goal of theclinical parasitology laboratory. The identification of *Entamoeba dispar* as a morphologically identical but non-pathogenicspecies has highlighted the need for non-microscopic detection methods able todifferentiated the 2 organisms. Matrix-assisted laser desorption/ionizationtime-of-flight mass spectrometry (MALDI-TOF MS) recently emerged as afirst-line method for the accurate identification of bacteria, but few data are available for protozoa. Thepotential role of MALDI-TOF MS for therapid identification of specific biomarkers of *E*. *histolytica*distinguishing it from *E*. *dispar* was investigated in this studyanalysing strains isolated from clinical samples.

Methods. In this preliminary study, MALDI-TOF MS wasapplied on 2 strains: *E*. *histolytica* strain 8026 and *E*.*dispar* strain 1557, isolated inour laboratory by using Robinson's medium and characterized by molecularmethods. Aliquots of cultures of these strains were submitted to formicacid/acetonitrile protein extraction. The spectraobtained with the instrument Microflex LT mass spectrometer (Bruker Daltonics,Germany) were analyzed and subsequently imported into theClinProTools software version 2.2 (Bruker Daltonics, Germany) to perform astatistical analysis in order to verify the presence of specific peaks for eachof the tested strains.

Results. Both the strains yielded a proteinprofile, including unique peaks, which was found to be original. These proteinprofiles were found to be reproducible over four, independent experimentsanalyzing at last 20 replicate/time and no differences were observed when thestrains were grown in different lots of Robinson's medium. Five discriminatingpeaks between *E*. *histolytica* and *E*. *dispar* strains were found; inparticular, 2 peaks (8,250 and 8,300 Da) were found only in the *E*.*histolytica* profile and 3 (5,400, 5,500 and 5,550 Da) only in the *E*.*dispar* profile.

Conclusion. Thesepreliminary results obtained for 2 *Entamoeba*spp. strains are very encouraging becausethey showed the ability of MALDI-TOF MS to detectdifferences in protein profiles allowingto differentiate the pathogenic species *E*. *histolytica* from the non-pathogenic species *E*.*dispar*, distinguishable only at the genetic level. Being MALDI-TOF MS more rapid and lessexpensive than genetic methods such as PCR, it could be used for the differentiation of *E*. *histolytica*from *E*. *dispar* field isolates. Future perspectives of our study willconcern the analysis by MALDI-TOF MS of several *E. histolytica* and *E. dispar* wellcharacterized strains isolated in our laboratory during the period 2000-2013 in order to assess theusefulness of this methodology in the differentiation of these two species.