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Paper Poster Session II

MALDI - TOF

MALDI-TOF mass spectrometry for the identification of *Trichomonas vaginalis*: preliminary study

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Objectives

Trichomonas vaginalis is a flagellated protozoa causing trichomoniasis, a common but overlooked sexually transmitted human infection, with around 170 million cases occurring annually worldwide. In diagnostic practice, the gold standard for the identification of *T. vaginalis* is the culture of the clinical sample on specific media. Recently, immunochromatographic assays for the detection of specific antigens, as well as PCR assays for the simultaneous detection of the DNA of *T. vaginalis* and sexually-transmitted bacteria and viruses, are also available. The well-known genome sequence of *T. vaginalis* has made possible the application of proteomic methods to the study focused on specific proteins of this parasite. However, few data are available about the overall proteomic expression profiling of *T. vaginalis.* The aim of this study was to obtain a proteic profile to identify *T. vaginalis* by MALDI-TOF MS.

Methods

In this preliminary study, MALDI-TOF MS was applied on the reference strain *T. vaginalis* G3 cultivated in “Trypticase-yeast extract maltose” medium and on 4 strains isolated in our laboratory from clinical samples by using “*Trichomonas* medium N.2” (Oxoid) and identified by microscopic examination. Aliquots of cultures of all the strains were submitted to formic acid/acetonitrile protein extraction. The spectra obtained with Microflex LT mass spectrometer (Bruker Daltonics, Germany) were analysed by FlexAnalysis software. The spectrum obtained for the reference strain was used to create a mean spectrum profile subsequently supplemented in the Bruker Daltonics database (version 3.1.2.0), not including any protozoa profiles.

Results

The proteic profile of the reference strain matched none of the existing profiles in the Bruker Daltonics database and no interference with the peaks of the 2 different culture media used in this study was found. This proteic profile was found to be reproducible over a second independent experiment analysing at least 10 replicates/time and no differences were observed when this strain was grown in different lots of media. The proteic profile of the reference strain was supplemented in the Bruker Daltonics database to be used for further blind identification of additional *T. vaginalis* isolates. The 4 field strains yielded an identifiable protein profile with an identification score value >1.7.

Conclusion

These results obtained testing 4 *T. vaginalis* strains isolated from clinical samples are very encouraging because they showed the ability of MALDI-TOF MS to correctly identify this protozoa even if some differences in the proteic profile of the different strains were observed. This preliminary study will be extended by testing the strains isolated in our laboratory during the period 2003-2014 in order to strengthen our results and to subsequently assess the usefulness of this methodology in the identification of this protozoan directly on clinical samples.