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P0819 Identification of herpes simplex virus type 1 by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS)

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Background: Whereas genome detected has been implanted on viral field, proteomic detection has been developed on others microbiology areas. MALDI-TOF, a simple and no expensive method is really a very usefful tool in bacterial and fungal clinical laboratories.

In order to introduce this method in this area, the aim of this study was create a library for HSV-1 strain and apply it in clinical samples after cell culture.

Materials/methods: 5 HSV-1 strains grown in MRC-5 cells monolayer previously identified by conventional methods (qPCR or inmunofluorescence) were used to create an in-house library following manufacturer´s recommendations (Bruker Daltonics, Germany). Cell cultures monolayer non-infected was also used to define a background spectrum.

Then 28 HSV-1, 14 HVS-2, 12 Adenovirus, and 2 Cytomegalovirus were assayed according standars instructions and confronted with the HSV-1 created library.

Results: The spectra generated from HSV-1 cell cultures, analysed in the molecular weight range 2000–20000 Da, revealed the presence of some different peaks (9612/10712/15412) not overlapping those of uninfected cell cultures.

The protein spectra of 28 HSV-1 infected cell cultures were correctly identified with score values ≥1.9, even one of them with bacterial contamination, bacteria was also correctly identified. None of others showed any specific peak of HSV-1 library.

Conclusions: Library of HSV-1 was created with a specific spectrum. MALDI-TOF was able to identify and discriminate HSV-1 from culture. Therefore application to others viruses and over direct samples should be developed.