

POSTER PRESENTATION

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Analysis of protein profile expressed on the membrane surface of plasma cells, stromal cells and mononuclear cells from bone marrow microenvironment of multiple myeloma patients by mass spectrometry

Fabricio de Carvalho^{1*}, Adriana FP Leme², Alisson L Matsuo³, Sandra S Matsuda¹, Bianca A Pauletti², Walter MT Braga¹, Edgar J Paredes-Gamero⁴, Maria de Lourdes LF Chauffaille¹, Gisele WB Colleoni¹

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Background

Multiple Myeloma (MM) is a malignant proliferation of B-cells with plasma cell differentiation. Interactions of plasma cells with stromal cells and other cells in bone marrow (BM) microenvironment are responsible for MM progression. Screening of proteins expressed on the membrane surface of plasma cells, stromal cells and mononuclear cells from MM patients by mass spectrometry (MS) may identify new prognostic and therapeutic targets in this incurable disease.

Materials and methods

BM from eight MM patients, five normal BM from donors and seven tonsils of children submitted to tonsillectomy (controls) were collected. Plasma cells (CD138+) from MM patients and tonsils, stromal cells (CD105+) and mononuclear cells from MM patients and normal BM were isolated by magnetic cell sorting (MACS). Stromal cells were *in vitro* expanded and characterized by immunocytochemistry and flow cytometry (CD105, Vimentin, CD45 and cytokeratin [CK]). Proteins were obtained by Pierce Cell Surface Protein Isolation kit and quantified by Pierce 660nm Protein Assay.

Results and conclusion

In vitro expansion of stromal cells was possible for four MM and four normal BM samples. Stromal cells were CD105+, Vimentin+, CD45- and CK-, without contamination with other cell types. Plasma cell pool from MM patients or tonsils (control), stromal cell pool and mononuclear cell pool from MM patients or normal BM (control) were subjected to protein extraction (yield ranged from 50µg to 100µg). Analysis of proteins will be performed by LTQ (Linear Ion Trap Quadrupole) Orbitrap Velos Mass Spectrometry and the spectra MS/MS will be obtained using Mascot.

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Author details

¹Department of Clinical and Experimental Oncology, Hematology and Hemotherapy, Universidade Federal de São Paulo, UNIFESP/EPM, São Paulo, Brazil. ²Mass Spectrometry Laboratory, Bioscience Laboratory, CNPEM/ABTLuS, Campinas, Brazil. ³Department of Microbiology, Immunology and Parasitology, Cell Biology, UNIFESP/EPM, São Paulo, Brazil. ⁴Department of Biochemistry, Molecular Biology, UNIFESP/EPM, São Paulo, Brazil.

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* Correspondence: fabrocarvalho@gmail.com

¹Department of Clinical and Experimental Oncology, Hematology and Hemotherapy, Universidade Federal de São Paulo, UNIFESP/EPM, São Paulo, Brazil

Full list of author information is available at the end of the article

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