



Max Planck Institute for Chemical Ecology

7th Central and Eastern European Proteomics Conference

13-16 October 2013 Jena, Germany



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Proteomic profile of human chorion derived mesenchymal stem cells by using ion trap mass spectrometry

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Key words: placenta, mesenchymal stem cells, ion trap mass spectrometry, proteomic

The human placenta and fetal membranes are reservoirs of mesenchymal stem cells. Summal cells from fetal tissues have significantly higher plasticity in comparison to adult stem cells [1]. Therefore, stem cells derived from placenta are promising candidates for the development of the future strategies in cell therapy.

The chorionic membranes was obtained from healthy female donors (n = 6) after the five caesarean section. The populations of mesenchymal stem cells were enzymatic isolated from tissues. On proteomic analysis were used cells from fourth passages. Whole cell protein from tions were identified utilizing a bottom-up approach. The tryptic peptides were separated by two-dimensional high-performance liquid chromatography and identified by ion trap mass spectrometry.

A total of 760 protein sequences were identified from whole cell fractions. The list of identified proteins has showed also proteins which higher expression is typical for placentary for membranes and which are related to cell growth, maintainance and to cytoskeletal organization. Other identified proteins include chaperones, metabolic enzymes, transporters, knowly proteases, cytoskeletal, adhesion and cellular defense proteins, transcription and translation initiation factors.

Knowledge about proteome of chorion derived mesenchymal stem cells are highly relevant for understanding properties and changes during cell processes like proliferation, different tiation and reaction on changes of experimental conditions, thereby giving highly relevant information in future developments of desired therapeutic methods.

Acknowledgements: This study was supported by Scientific Grant Agency of the Ministry of Liducation of Slovak republic (VEGA1/1109/11) and Agency of Slovak Ministry of education for the Structural Lunds of the EU under project ITMS: 26220220143 for the financial support of the research.

References

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