PROTEIN EXPRESSION IN CUMULUS CELLS AS INDICATOR OF PREGNANCY SUCCESS

Assumto Iaconelli Jr.1,2, Daniela P. A. F. Braga1,2,3, Amanda S. Setti1,2,4, Elaine C. Cabral5, Marcos N. Eberlin5, Fernanda B. Cordeiro3, Edson Lo Turco3, Edson Borges Jr.1,2

1 Fertility Medical Group, Sao Paulo, Brazil, 2 Instituto Sapientiae – Centro de Estudos e Pesquisa em Reprodução Assistida, Sao Paulo, Brazil, 3 Universidade Federal de São Paulo (UNIFESP), São Paulo, Brazil, 4 Faculdade de Ciencias Medicas da Santa Casa de Sao Paulo, Sao Paulo, Brazil, 5 Chemistry Institute - ThoMSon Mass Spectrometry Laboratory, Universidade Estadual de Campinas, Campinas, Brazil

INTRODUCTION
The knowledge that cumulus cells (CC) have a central role in the support of oocyte development and maturation has led various groups to focus their research on the analysis of CC. Protein synthesis is the major outcome of gene expression and is directly associated with the observed phenotype. Earlier embryonic proteomic studies utilized 2D gel electrophoresis in combination with analysis of gel images. For known proteins or to correlate protein phosphorylation with embryonic development, Western blot analysis has been used. More recently, mass spectrometry (MS) fingerprinting has been demonstrated to provide a reliable approach for the identification of groups of proteins within limited amounts of samples.

OBJECTIVE
The objective of this study was to utilize the analytical power of MS to predict the pregnancy outcome by differential protein expression in CC.

MATERIALS AND METHODS

CONCLUSION
From the results of this study, potential biomarkers for the pregnancy outcome have been suggested. In a next step these proteins may be individually identified and its frequency in subjects may be determined. In conclusion, CCs proteomics may be a useful tool for the prediction of ICSI cycles outcomes.

RESULTS
Overall, 72 different proteins were detected, of which 19 were expressed exclusively in the Positive-Group and 16 other were expressed exclusively in the Negative-Group. Thirty seven other proteins were expressed in both groups, and of these, 16 were equally expressed between the groups and 21 were differentially expressed between groups.

This research was funded by FAPESP: Pesquisa Inovativa em Pequenas Empresas (PIPE). 2013/50052-7