PROTEIN EXPRESSION IN CUMULUS CELLS AS INDICATOR OF PREGNANCY SUCCESS

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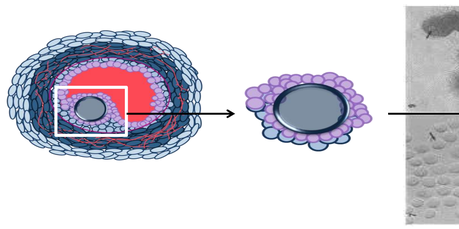
INTRODUCTION

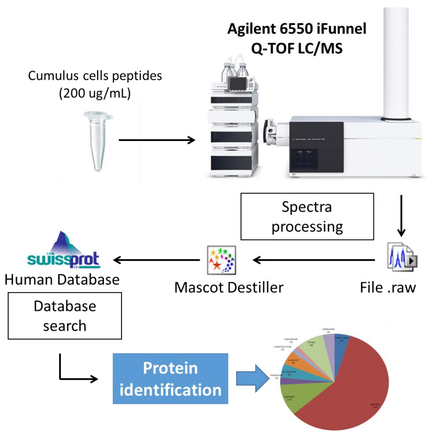
The knowledge that cumulus cells (CC) have a central role in the support of oocyte development and maturation has led various groups to focus their research on the analysis of CC. Protein synthesis is the major outcome of gene expression and is directly associated with the observed phenotype. Earlier 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





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.

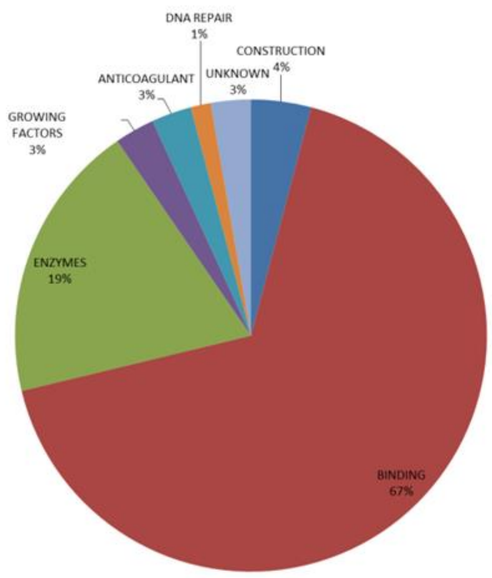


Fig.1: Protein distribution in patients who did and did not become pregnant

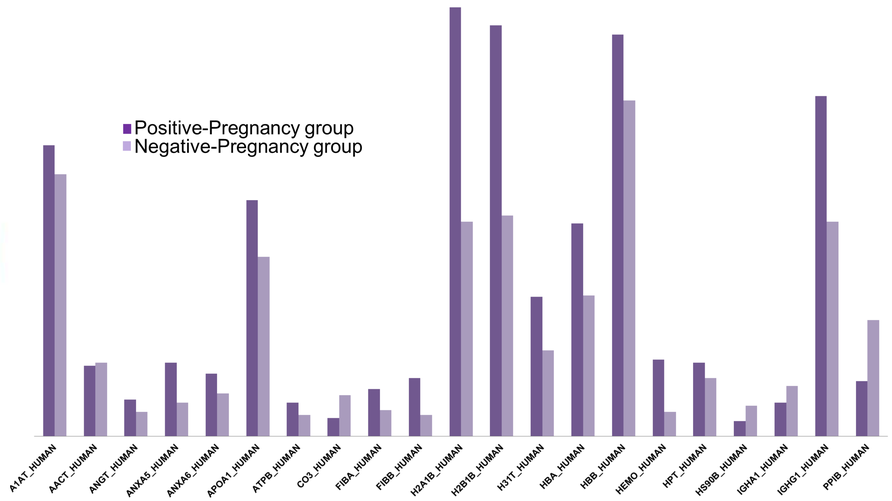


Fig.2: Proteins differently expressed between the groups

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.

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