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CUMULUS CELLS PROTEOMICS AS A TOOL FOR SELECTION OF PATIENTS FOR EXTENDED EMBRYO CULTURE PROGRAMMES

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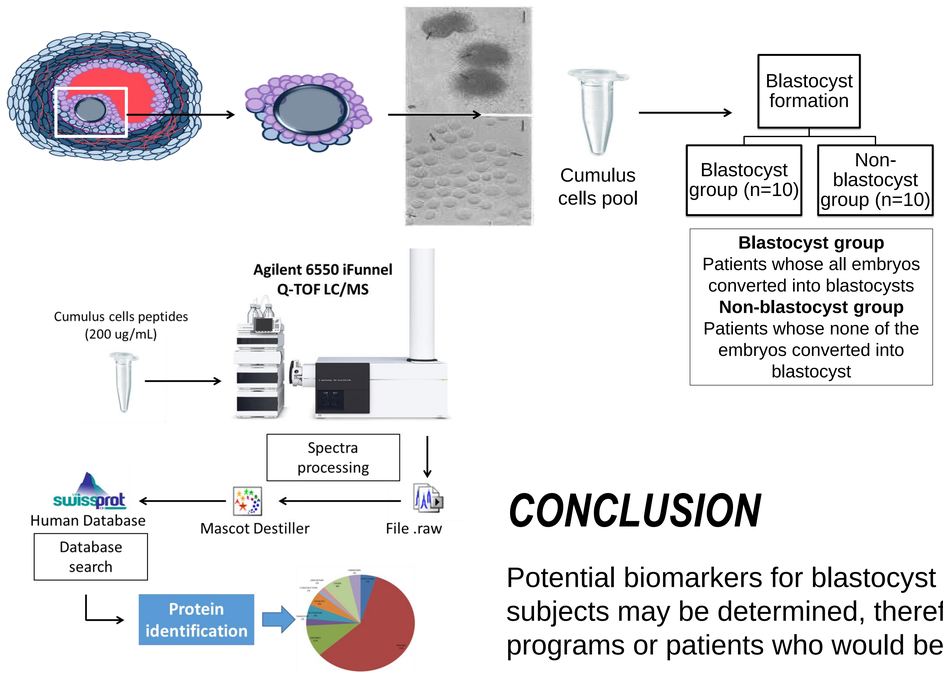
INTRODUCTION

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 identify patients that would benefit from extended embryo culture programs and blastocyst-stage embryo transfers.

MATERIALS AND METHODS



RESULTS

Overall, 87 different proteins were detected, of which 17 were expressed exclusively in Non-blastocyst group and 30 other proteins were expressed exclusively in the Blastocyst group. The remaining 40 proteins were expressed in both groups, and from those, 6 proteins were equally expressed between the groups and another 34 were differentially expressed between groups.

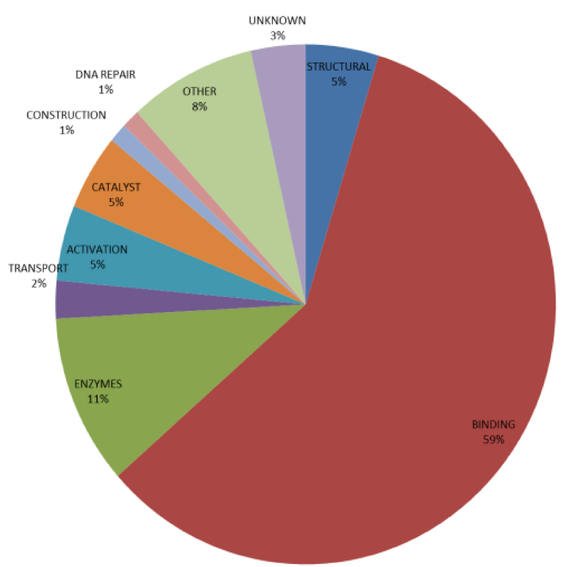


Fig.1: Protein distribution in Blastocyst and Non-blastocyst groups

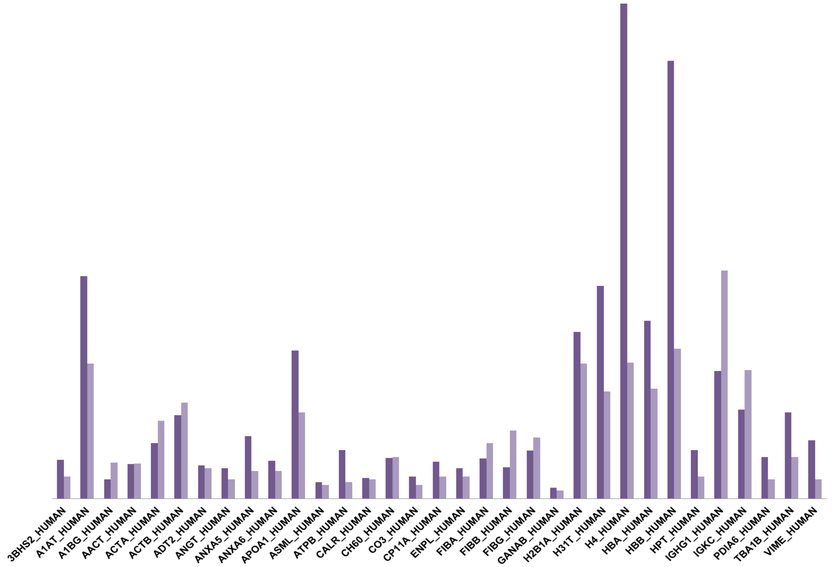


Fig.2: Proteins differently expressed between the groups

CONCLUSION

Potential biomarkers for blastocyst formation chance have been suggested. In a next step these proteins may be individually identified and its frequency in subjects may be determined, therefore, CCs proteomics may be useful for the identification of patients that should be included in extended embryo culture programs or patients who would benefit from cleavage-stage embryo transfers.

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