

GENES INVOLVED IN OOCYTE PENETRATION ZONA PELLUCIDA (OPZP) PROCESS IN SPERM SAMPLES UNDERGOING IVF

S. Garcia-Herrero¹, M. Meseguer², J.A. Horcajadas¹, M. Ruiz¹, L. Romany², J.A. Matinez-Conejero¹, N. Garrido²

¹ *iGenomix, Paterna, Valencia*

² *IVI Valencia, Valencia Spain*

Introduction: Sperm samples (SS) analysis lacks predictive power on successful fertilization rates in IVF, and microarray analysis of mRNA expression has described the genomic fingerprint related to reproductive success. OPZP is a critical step previous to fertilization, and theoretically, genes involved in this process must be altered in infertile patients (IP).

The aim with this work is to use microarray technology to search for genes involved in OPZP among lists of differentially expressed genes (DEG) between SS achieving or not pregnancy in IVF in order to find success markers in sperm. Material and methods: Cases and controls study with 8 SS obtained from IP undergoing IVF cycle with donated oocytes. SS mRNA was extracted using Trizol protocol, suspended in DEPC-treated water and frozen at -80°C until the microarray experiments were performed. Finally, we identified samples from which pregnancy was achieved (P, n=4) or not (NP, n=4) and compared the gene expression microarray results.

Results: Total number of DEG was 162 and 2 were described among genes belonging to OPZP process by the Gene Ontology: TNP2 NM_005425 Homo sapiens transition protein 2 (during histone to protamine replacement) in the NP group and the HEXB NM_000521 Homo Sapiens hexosaminidase B (beta polypeptide) in the P group.

Conclusions: Differences revealed between expression profiles from samples that achieved pregnancy vs. those unable in IVF could be potentially employed to detect IVF fertility success markers, but to date only a few are related with OPZP, remaining relevant for fertility other processes yet to be determined.