The assessment of follicular fluid metabolite profile in poor and high responder patients undergoing intracytoplasmic sperm injection.

Montani, D.A.[1]; Moriyama, D.F.[1]; Braga, D.P.A.F.[1,3];Rodrigues-Oliveira, A.F.[2]; Oliveira-Silva D.[2]; Borges Jr., E.[3]; Fraietta, R.[1]; Lo Turco, E.G.[1]

1 Department of Surgery, Division of Urology, Human Reproduction Section, Sao Paulo Federal University, Sao Paulo, SP, Brazil
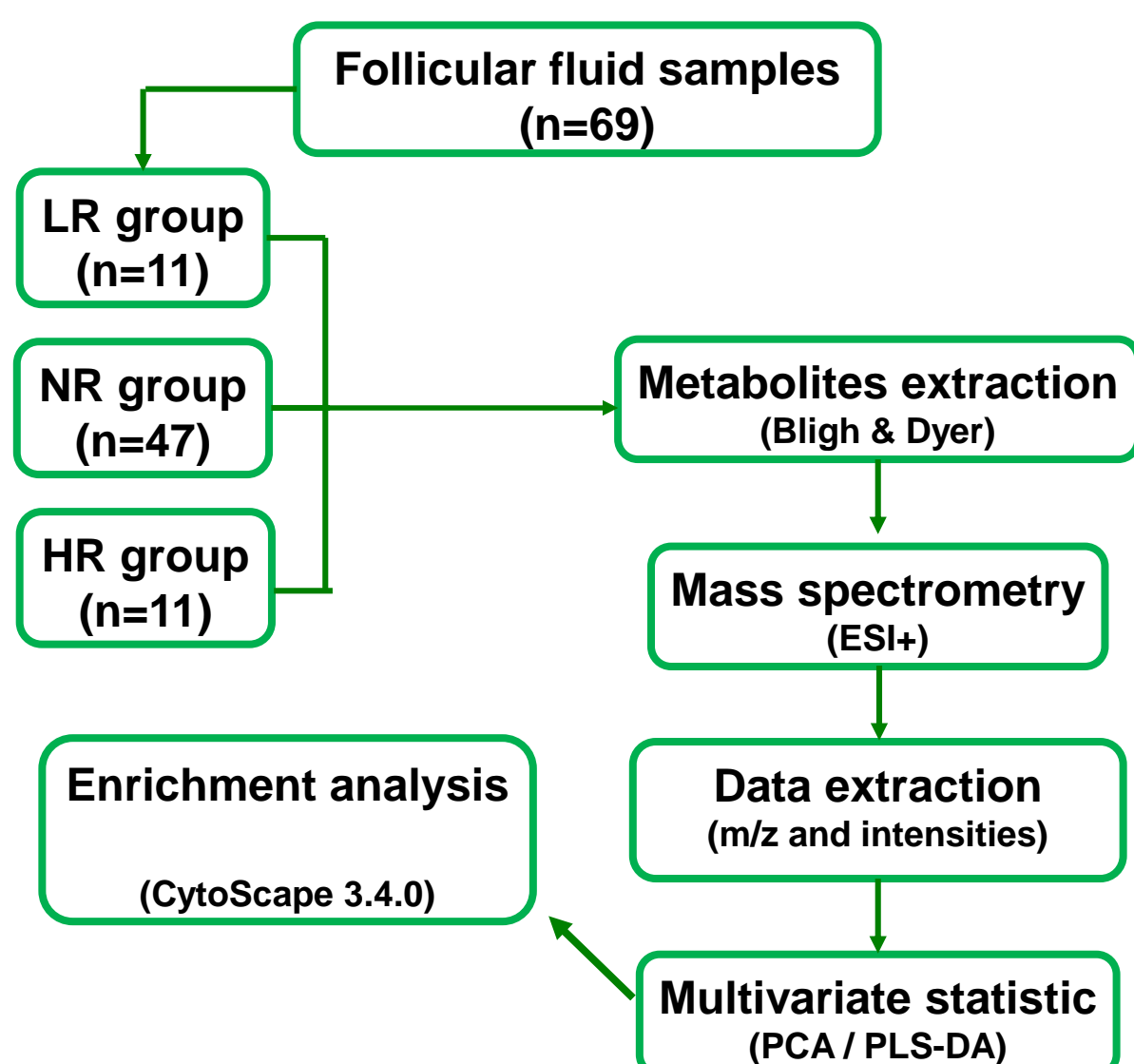2 Institute of Environmental, Chemical and Pharmaceutical Sciences São Paulo Federal University, Diadema, SP, Brazil.
3 Fertility Medical Group, Sao Paulo, SP, Brazil.

INTRODUCTION

Bidirectional communication between the oocyte and surrounding cumulus cells is essential for the acquisition of oocyte competence, and due to their close connection, cumulus cells and FF may retain a footprint of the follicular conditions experienced by the oocyte. Therefore, this may be a valuable tool to understand ovarian physiology. Low-responder young patients have reduced oocyte viability, perhaps as a consequence of altered ovarian microenvironment. On the other hand, the overproduction of oocytes, in high-responders, can cause considerable patient discomfort, and important short-term complications including ovarian hyperstimulation syndrome, high incidence of multiple pregnancies and ethical/legal implications of embryo storage.

MATERIALS AND METHODS

Follicular fluid samples (n=69)

LR group (n=11)

NR group (n=47)

HR group (n=11)

Metabolites extraction (Bligh & Dyer)

Mass spectrometry (ESI+)

Data extraction (m/z and intensities)

Multivariate statistic (PCA / PLS-DA)

Enrichment analysis (CytoScape 3.4.0)

RESULTS

Dithienyl disulphate was hiperrepresented in the LR group, which was associated with the cellular oxidant detoxification, oxidoreductase and glutathione peroxidase activity pathways. Sulfonic acid was increased in the HR group, which was associated with gamma glutamyltransferase activity and glutamate metabolic process
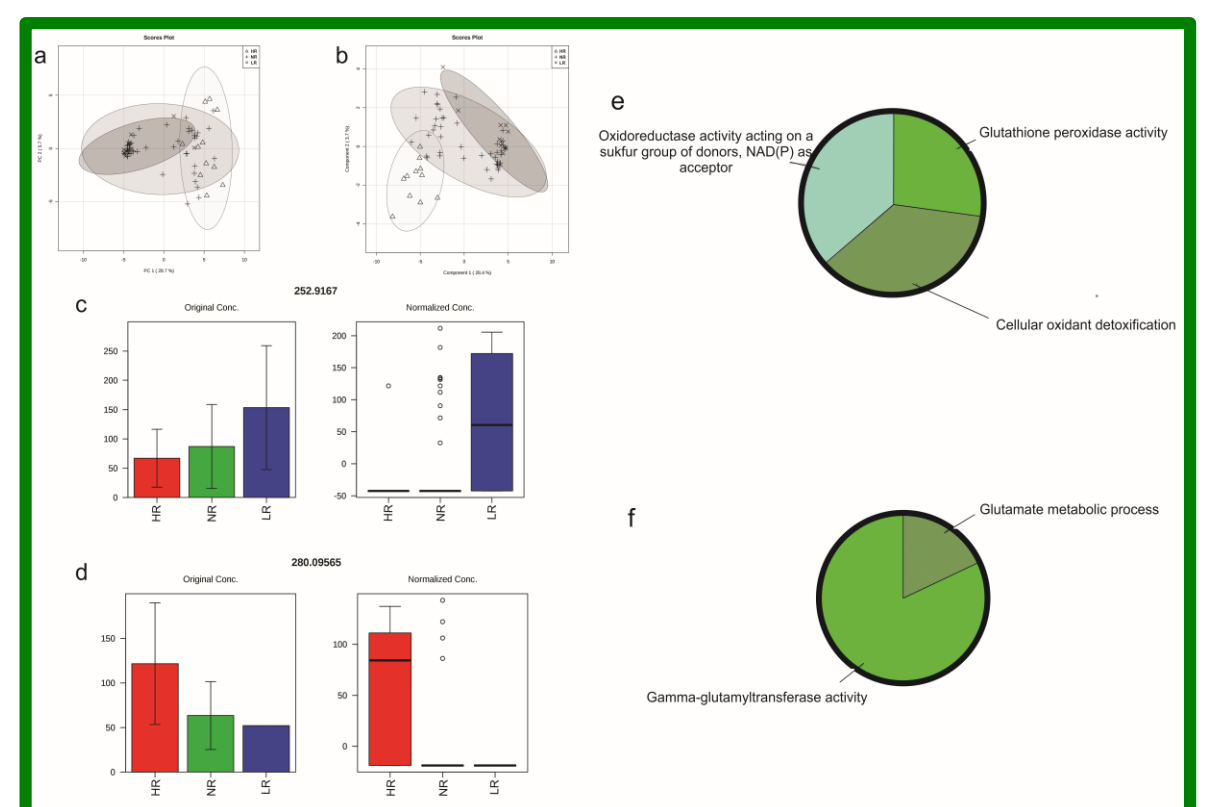
Fig: (a) PCA and **(b)** PLS-DA analysis. The triangle represents the high responder group (HR), cross points represents the normal responder group (NR) and X points represents low responder group. Panel **(c)** ion representative from LR group and panel **(d)** ion representative from HR group. Enrichment functions of the follicular fluid samples of **(e)** low responder and **(f)** high responder. Interactions were inferred using the MetScape plugin and functional enrichment of Gene Ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG) terms were calculated using the ClueGO plugin, both in CytoScape 3.4.0 software.

CONCLUSION

Our data suggest that identification of metabolites correlated with ovarian response to COS may support the implementation of individualized COS protocols, offering a valuable opportunity for achieving the treatment success with reduced discomfort, emotional and financial costs for the patients.