ERA PROTEIN NETWORK AS A POTENTIAL BIOMARKER TO IMPROVE PRECISION MEDICINE IN THE ENDOMETRIAL FACTOR (20 WORDS)

P. Díaz-Gimeno¹, M. Ruiz-Alonso², D. Blesa², Ana Conesa³ and C. Simón¹,²,⁴

¹Fundación Instituto Valenciano de Infertilidad (FIVI), Valencia University and Instituto Universitario IVI/INCLIVA, Spain
²IVIOMICS, Parc Científic Valencia University, Paterna, Valencia, Spain
³Principe Felipe Research Center (CIPF), Genomics of gene expression
⁴Department of Ob/Gyn, Stanford University School of Medicine, Stanford University, Ca, USA

The diagnostic genomic signature of receptive endometrium has been developed by us as a predictive method to evaluate endometrial factor (Díaz-Gimeno et al 2011, 2013; Ruiz-Alonso et al 2013). The underlying physiology of the transcriptomic profile remains unclear in the cellular and tissular context. Systems biology approach based on network modeling allows to decipher the personalized subnetworks that are altered specifically in each woman. Systemic approach allows to understand how non coincident genes could be altered in different patients with the same clinical phenotype but could belong to the same function and cause the same dysfunctions. The main objective of this work was to develop a protein interaction network as a model to visualize and analyze the systemic process underlying the diagnosis of ERA test.

The “in silico” and experimental design included the development of ERA protein interaction network and the ERA gene expression network analysis. ERA protein network is a handmade net that has been built using curated protein-protein interactions from Snow (Babelomics platform) and annotated protein functions, tissues, localization and ovarian hormones receptors. Annotated proteins file was obtained from Genecards, Wikigenes, KEGG, UniProt and TRANSFACT databases.

Results: ERA protein network is a highly connected network based on ERA genes composed by 382 genes joined by 497 axis (Figure 1 A). The average connectivity degree of each molecule is from 1 to 3 connections. Subnetworks are a relatively large number in the net composed by 2-4 proteins each one, and two principal subnetworks are underlying ERA transcriptomic signature: Cellular adhesion (Figure 1B1) and signaling subnetwork (Figure 1B2).

The systemic approach provides a holistic understanding that could be used to find similar systemic phenotypes, to define new genes connected in the network as a new potential biomarkers, and to develop personalized treatments.