DIFFERENTIAL GENE EXPRESSION ANALYSIS OF KPNA GENES IN HUMAN EMBRYOGENESIS

Takeda, A. A. S.¹, Rybarczyk-Filho, J. L.¹, Lemke, N.¹

¹Departamento de Física e Biofísica, Instituto de Biociências de Botucatu, Universidade Estadual Paulista Júlio de Mesquita Filho - UNESP, São Paulo, Brasil.

The Importin-alpha (ImpA) is the protein responsible for the recognition of the proteins that need to be transported to the nucleus through the classical nuclear import pathway. Several studies have shown that the nuclear machinery is an important regulator of development, organogenesis and tissue maintenance. The *Homo sapiens* has seven ImpA genes (KPNA1-7) and their differential expression during the embryogenesis suggests that ImpA can play an important role on cellular differentiation. In this work we analysed KPNA expression in a dataset of *H. sapiens* embryonary stages. The gene expression data were obtained from Gene Expression Omnibus (GSE18290), which includes one cell, 2-cells, 4-cells, 8-cells, morula and blastocyst datasets. To evaluate differential gene expression the datasets were normalized using the software Limma, and we only considered results with p-value<0.001. Differential expression levels can be observed after the 2-cell stage. The KPNA1, 4 and 6 are up regulated in morula and blastocyst when compared to the stages 1-8 cells, while the KPNA3 is down regulated in blastocyst suggesting that these proteins play specific roles during embryogenesis. The expression of KPNA2 remained constant in all stages, in accordance with previous studies. We also constructed an integrated network including protein-protein interaction, transcription regulation and metabolic associations for the KPNA genes. The network maps the genes that are directly influenced by KPNAs differential expression. The first neighboring proteins present in the network of KPNAs comprise transcription factors, ubiquitins, DNA repair proteins, epigenetic-related proteins and transport proteins. We are currently investigating the role played by these genes to understand which biological functions are affected by KNPAs differential expression.

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