CONSTRUCTION OF LARGE SCALE BOOLEAN LOGIC BASED PATHWAYS OF COLORECTAL CANCER STEM CELLS

D. A. Abetov*, Z. N. Mustapova, D. A. Begimbetova, D. S. Bulanin

Center for Life Sciences, Nazarbayev University, Astana, Kazakhstan; *danysh.abetov@nu.edu.kz

Introduction Despite advances in the post-genomic era, which allowed for generation of an impressive amount of biological data, representing the whole network of biological interactions, gene regulating networks and signaling pathways in a unified temple and coherent way is still a challenging task. Here we performed analysis of upregulated molecular networks found in colorectal cancer stem cells (CCSC).

Materials and methods. The scheme was created based on published articles, pathway datasets (Reactome, KEGG, Ingenuity), as well as protein interaction databases (BIND, STRING). The accuracy of the interacting components, nature of reactions was confirmed in three or more independent studies. Data was organized into pathways according to the modified Edinburgh Pathway Notation (mEPN) using official Entrez ID and HUGO nomenclature. The scheme was created using yED program. In order to optimize and validate the depicted information, pathways were subjected to the second round of layout optimization and validation.

Results. The diagram represents signaling pathways of the Wnt, Notch, NF-kappa-B, Hedgehog (Hh) and tumor growth factor (TGF) and PI3K/Akt/mTOR growth cascades including selected transcriptional networks, found to be upregulated in colorectal cancer stem cells. The scheme contains 317 proteins and protein complexes producing a network of 817 nodes connected by 754 edges.

Conclusions, to our knowledge this large scale model of signaling networks representing upregulated pathways found in CCSC is the most comprehensive to date. The pathway diagram may be ofvalue for those who interested in CCSC biology. The diagram may be used for mathematical modelling of dependencies and relationships between components of the network, interpretation of functional genomics data and ultimately empirically tested to aid interpretation of the consensus account of the CSC biology.