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Systemic properties of proteome profiles of carcinogenesis of human breast epithelial cells, and clinical applications of these profiles

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Proteomics offers unique opportunity to unveil regulatory networks governing transition of normal cells into cancerous. In the author's laboratory, there have been generated proteome profiles representing transitions of human breast epithelial cells from normal to highly proliferative, to tumorigenic, to invasive and to metastatic. These profiles have been analyzed and validated with proteome profiles of clinical samples of human breast cancers of different stages and disease outputs. Combined, all these profiles lead to building proteome-based diagnostic networks which are currently used for personalization of cancer treatment of patients. The proteome-based networks also show functional integration with previously defined hallmarks of cancer. Especially it is pronounced for clinical cases, when individual tumor proteome profiles differ significantly between the cases, but the network analysis shows similarities in functional outputs of the proteome changes, e.g. output on transformation of the cells. Proteome-based networks for carcinogenesis steps of human breast epithelial cells (normal-*in situ*/local-invasive-metastatic disease) and clinical applications of these networks will be presented.

Biography

Serhiy Souchelnytskyi graduated from Lviv State University and obtained a PhD degree at the Institute of Biochemistry in Lviv, Ukraine. His area of interest is personalized medicine since graduation. He worked at the Institute of Biochemistry (Ukraine), INSERM U244 (France), Ludwig Institute for Cancer Research (Sweden), Karolinska Institutet and Karolinska University Hospital (Sweden), before joining Qatar University in 2015. He is involved in commercialization of research by developing diagnostic and personalization of cancer treatment (Ukraine and Sweden).

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