MASS SPECTROMETRY IN THE WORKFLOW OF PERSONALIZED CANCER TREATMENT: EVALUATION OF PROTEIN EXPRESSION, PTMS AND ACTIVITY

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High sensitivity has firmly established mass spectrometry as the method of choice for identification and analysis of proteins. Clinical challenge of personification of anti-cancer treatment requires analysis of small quantities of proteins. There are more than 300 PTMs which affect functions of proteins, and mass spectrometry is so far the most efficient in their identification. All anti-cancer drugs act on or via proteins. Therefore, proteome analysis is essential for efficient diagnostic and selection of treatment. In my presentation, I will show examples of how we use mass spectrometry in our efforts of personalization of cancer treatment. Expression proteomics, with detection and identification of targets for potential anti-cancer treatment, is one of the examples. Another example is mass spectrometry imaging in combination with magnetic resonance imaging, to monitor responsiveness of cancer cells to treatment. Study of breast and renal cancer cells will be presented as examples. Unbiased detection of >30 PTMs in the same proteins from cancer vs normal cells will also be discussed in the context of tumorigenesis. Have mass spectrometry reached its limits? With a resolution of >0.0001 Da, an impact may have such phenomena as mass vs energy transformation. Isotope distribution in samples is another technical issue which may influence results. These technical aspects will also be discussed.

BIOGRAPHY

Serhiy Souchelnytskyi graduated from Lviv State University (1985) and obtained PhD degree at the Institute of Biochemistry (1992) in Lviv, Ukraine. He worked at the Institute of Biochemistry (Ukraine), INSERM U244 (France), Ludwig Institute for Cancer Research (Uppsala, Sweden), Karolinska Institutet and Karolinska University Hospital (Stockholm, Sweden), before joining Qatar University in 2015. He is involved in commercialization of research by developing diagnostic and personalization of cancer treatment. He has 125 publications, including 5 patents. He is involved in editorial works as an Editor and a member of Editorial boards, works frequently for granting agencies as an expert, and has received awards in the area of proteomics and cancer biology. Current projects are in development of personalized cancer medicine. Proteomics, systems biology and cancer signaling biology are used for individualized profiling of patients, their diagnostic and selection of the most efficient treatment.

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