

9th WORLD BIOMARKERS CONGRESS

20th International Conference on

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PHARMACEUTICAL BIOTECHNOLOGY

December 07-09, 2017 | Madrid, Spain

Usage of metabolomics profile as biomarkers itself for diagnostic diseases

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Recently, the researches to find proteins as biomarkers of various diseases have become widespread. Especially these studies are popular in oncology. However, until now proteins specific for cancer cells are not detected. In spite of it, to diagnose cancer diseases biomarkers which are specific for a neoplastic process generally are widely used (such as CA-125, CA 19-9, CA 15-3, PSA, α -fetoprotein etc.). However, they can't discharge the main task: to diagnose the initial stages of disease, because their opportunity is limited by low sensitivity of existing laboratory technologies. The situation is much better in the case of using RNA's as biomarkers, because PCR takes off such restrictions. In the case of metabolomic diagnostics there are the same concentration limits as in proteomics. Therefore, it was decided not to use separate low molecular weight compounds as biomarkers but the whole metabolomic profile of the sick person as a biomarker itself of a disease. With this purpose, at the first stage that profile was clusterized using the method of principle component analysis to detect clusters of metabolites which are different from the clusters of healthy person. At the second stage, the specificity and sensitivity of the proposed technology was evaluated using the SVM and ROC analyses, for diagnostics of lung, prostate and other cancers.

Biography

P G Likhov is the Head of Laboratory for Mass Spectrometry-based Medical Metabolomics in the Department of Proteomic Research and Mass Spectrometry of IBMC, a position he has held since 2012. He is mainly interested in mass spectrometry-based metabolomics and proteomics, and their application for diagnostics. He graduated from the 2nd Moscow Medical Institute, took the post-graduate course and thereafter received a PhD degree in Biochemistry in 2002. During his career Dr. Likhov has received several awards, including the State Prize of the Government of Russia.

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