Researchers develop new method for breast cancer biomarker discovery

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Three researchers from the Virginia Bioinformatics Institute (VBI) at Virginia Tech have developed and evaluated a new one-step bioanalytical approach that allows them to profile in detail complex cellular extracts of proteins. The method has allowed the scientists to look at how the levels of proteins change in breast cancer cells when they are treated with hormones or cancer drugs like tamoxifen.

VBI Assistant Professor Iuliana Lazar, along with VBI Professor Ina Hoeschele and VBI Postdoctoral Associate Jenny Armenta, developed the method*, which uses proteomic technologies for fast biomarker fingerprinting in complex cellular extracts. The goal of biomarker discovery and screening is to identify changes in the levels of key proteins in the cell in response to the onset or development of a disease. The scientific community has invested extensive efforts into the development of methods that would allow for the sensitive screening of large panels of biomarkers, instead of just one at a time. This type of research promises to advance the capabilities of such techniques for early cancer detection, which could significantly reduce the mortality rate from diseases like cancer.

At the heart of the new method are three innovative developments - A data acquisition strategy that permits analysis of different cell states and replicates; an advanced way to filter or process the data; and a novel statistical method that allows the experimental data to be checked and their relevance confirmed. The team used the method for proteomic profiling of MCF-7 breast cancer cells cultured in estradiol, a steroid

hormone, and tamoxifen, a non-steroidal drug commonly prescribed in hormonal breast cancer therapy.

The work resulted in the identification of 16 differentially expressed proteins, which demonstrated the effectiveness of the method for biomarker discovery and also allowed for the establishment of a link between the proteins and certain cancer-related biological processes, such as cell proliferation, cell death, tumor development, and metastasis.

According to Lazar, "Assessing the changes in protein expression levels of these cells will help us better understand the complex biochemical signaling pathways involved in the development of cancer. We hope this will also shed some light on the ways that drugs like tamoxifen work to inhibit cell proliferation and to induce response to stress at the molecular level. This knowledge will help to advance our understanding of how breast cancer cells develop resistance to tamoxifen. In the long term, this should provide opportunities for the development of more effective diagnosis and treatments for cancer patients."

While the current research focuses more on the effectiveness of the method developed, the team plans to pursue more work using complementary techniques on biological replicates to confirm the differential expression of the proteins.

Source: Virginia Tech (news : web)