A new approach to analyzing breast cancer

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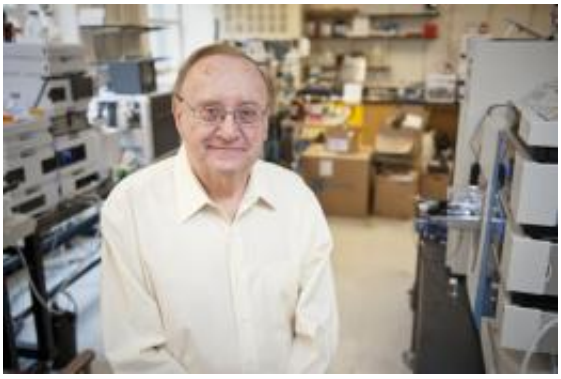

Analytical chemistry professor Barry Karger joined forces with colleagues at the Massachusetts General Hospital Cancer Center to present a new biomarker for breast cancer using a novel method based on multiple data sets. Credit: Mary Knox Merrill.

(Medical Xpress) -- Tumors are complex systems of cells, only some of which may be cancerous. Also, two samples from different areas of a single tumor are rarely identical. To gather important information about tumors, researchers must analyze very small samples because they are more likely homogenous — enriched for either normal cells or cancerous cells.

Barry Karger — the James L. Waters Chair in Analytical Chemistry in Northeastern's College of Science — and colleagues at the Massachusetts General Hospital Cancer Center have identified a network of genetic markers capable of predicting the relapse of estrogen-receptor positive, or ER+, breast cancer. The Susan G. Komen Breast Cancer

Foundation funded the research.

“We have genomics, proteomics, metabolomics,” said Karger, who also directs the Barnett Institute of Chemical and Biological Analysis. Genomics is the study of all of a cell’s genes; proteomics and metabolomics examine a cell’s proteins and metabolites, respectively. “How do you put these different ‘omics’ together to generate meaning?”

Karger and his long-time collaborator, breast-cancer pathologist Dennis Sgroi, had asked this question for a while. But they could not fully address the problem until the duo teamed up with bioinformatics specialist Marcin Imielinski, whose computational know-how proved crucial.

In previous work, Sgroi had isolated highly enriched cancer cell samples by performing microdissection on ER+ tumor tissues. Gene-expression analyses of these samples were compared with those of benign cells to identify a series of genes associated with malignancy.

“We’d been doing gene-expression analyses for years,” said Sgroi. “But analogous proteomic interrogation of limiting amounts of clinical samples was a significant challenge. ”

Karger pointed out that gene expression is only one part of the story: “The protein is where the actual function is,” he explained. “You express a gene that then produces a protein, but the protein does the work.”

If the researchers could perform proteomic analyses on small samples, they could cross-reference those data with the gene-expression data. But it was simply not possible until last year, when Karger presented a new analytical method, which does just that.

By combining genomics and proteomics, the team now had the necessary

tools to generate a network of potentially relevant genes that would be more extensive than networks generated from either genomics or proteomics alone.

To test the significance of the hybrid network, the researchers applied it to the gene profiles of more than 600 ER+ patients. The network had a statistically significant ability to predict which patients relapsed out of remission, making it a prognostic biomarker for ER+ breast cancer.

Many breast cancer biomarkers already exist — but few are very robust, said Sgori. The novel approach gives the work more importance, he explained: “We feel it serves as an important proof-of-concept and stepping stone for future studies.”

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