New research gives hope to women with deadliest breast cancer

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Women with the deadliest and rarest form of breast cancer now have a chance of treatment where once their options were severely limited, thanks to a new discovery by George Mason University researchers.

This aggressive cancer, called "inflammatory breast cancer," kills about half the women who have it within five years; patients live on average a mere 18 months after diagnosis. About 10,000 women are diagnosed each year with inflammatory breast cancer, according to U.S. government statistics.

In a recent study, Mason scientists pinpointed a key driver in the cancer that is leading to new ways to treat it. This study is not only a success for cancer patients but for a pioneering research method that discovered the finding as well, says Emanuel "Chip" Petricoin, co-director of Mason's Center for Applied Proteomics and Molecular Medicine (CAPMM) along with Lance Liotta.

This summer, doctors at Philadelphia's Fox Chase Cancer Center under the direction of Massimo Cristofanilli, the center's chair of medical oncology, began treating inflammatory breast cancer patients with a drug originally developed for non-small cell lung cancer because Mason research revealed a commonality between the two cancers. Prior to the research, these breast cancer patients had limited treatment options, Petricoin says.

Discovering how the cancer works using proteomics, an approach that

looks at the proteins on the genes, was essential to the finding. If researchers had stuck with traditional genome analysis, they would have missed the protein that can be targeted to treat this particularly dangerous form of breast cancer, Petricoin says. The proteins on the genes are the key for successful treatment.

"It is the proteins that the drug targets, not the genes," he says.

Petricoin and Liotta invented a technology called the reverse phase protein array a decade ago, which Mason exclusively licensed to Theranostics Health, Inc, a company the two co-founded over 5 years ago. It's a way of physically arranging proteins to reveal how they work on individual cells, such as cancer cells.

"DNA is the information archive, but it is the proteins that do the work," Petricoin explains. "Proteins are the software of the cell. They basically direct the cell to die, grow, divide and metastasize. While many think of cancer as a genomic disease, it's actually a proteomic disease. What is actually deranged in the cancer cells are protein pathways. These protein pathways form a linked network of interaction, talking to each other."

And not everyone has the same network of activated proteins. If a patient's cancer doesn't have a particular protein turned on that the drug targets, then the drug fails.

"Now we know that's why the one-size-fits-all approach doesn't work," Petricoin says.

When Petricoin, and CAPMM researchers Julie Wulfkuhle and Rita Circo began to study the cells from inflammatory breast cancer patients, they were surprised. They used the array platform and found that a protein called anaplastic lymphoma kinase (ALK), which was previously unconnected to breast cancer, is highly activated in nearly all the samples

they looked at.

"When we looked at these breast cancer samples, we saw ALK and the entire ALK pathway lit up like a string of lights," Petricoin says.

The best news is that there's already a drug on the market for treating patients with activated ALK, and it can be used for inflammatory breast cancer, too, Petricoin says. If the results of their work are validated in further patients, more people stand to benefit because ALK activation appears much more often in inflammatory breast cancer patients than in lung cancer patients.

Petricoin and his team worked with Fredika M. Robertson, a professor in the department of experimental therapeutics at the University of Texas MD Anderson Cancer Center, who led the study.

More research is on the way. Working with Robertson, the Mason team plans to find better drugs or a new combination of drugs to treat the cancer as patients build resistance to existing treatments. They're also searching for new ways to use current drugs that are already in the pipeline or have been cleared by FDA.

"The technology has graduated to the point where we can do this at the bedside, and we hope that through Theranostics Health it can benefit many patients in the future" Petricoin says.

The Mason team also is applying its know-how to breast cancer in general, colorectal cancer, multiple myeloma and cancers of the prostate, brain, lung and ovaries.

While Petricoin doesn't expect a complete shift from genomic research, the study boosts the role of proteomics.

"It really highlights that you can't put all your eggs in one basket," he says. "You can't just invest in genomic analysis. At the very least, proteomic analysis should be done simultaneously with the genomic analysis. This finding basically validates the philosophical approach we're taking and the power that the array platform provides"

Provided by George Mason University