New sequencing technique reveals genetic clues to rare breast tumors

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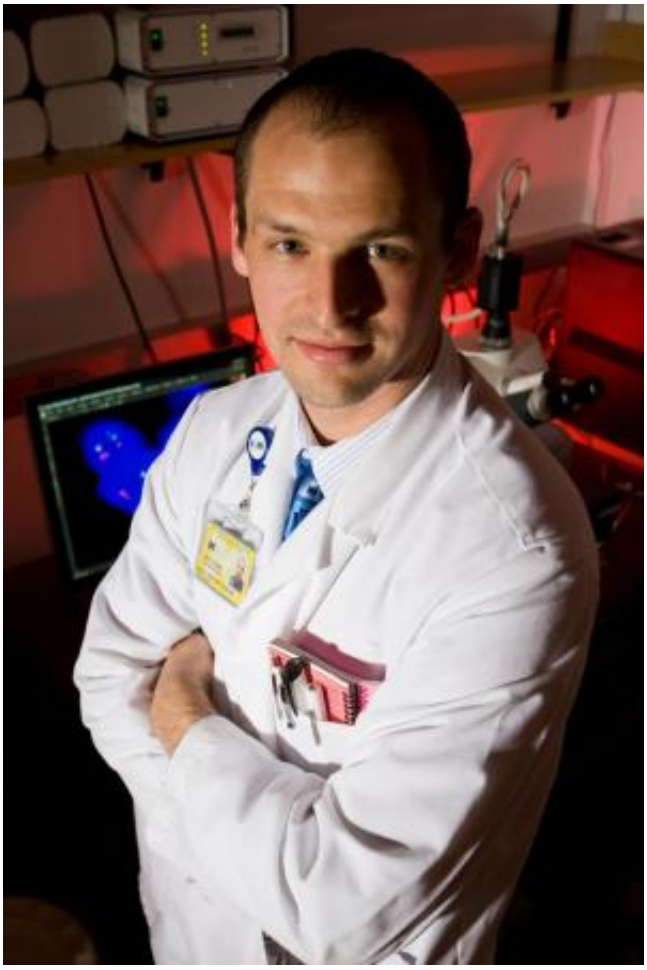

Scott Tomlins, M.D., Ph.D. Credit: University of Michigan Health System

A new study from researchers at the University of Michigan Comprehensive Cancer Center characterizes the genetic underpinnings

of a rare type of breast tumor called phyllodes tumors, offering the first comprehensive analysis of the molecular alterations at work in these tumors.

The analysis uses next-generation sequencing techniques that allow researchers to identify alterations in more than 100 genes from archived tissue samples.

"We know little about the biology of phyllodes tumors. In part, they have not been studied much because it's difficult to accumulate a large number of samples. Using these new sequencing techniques, we were able to study archived tissue samples, which allowed us to identify enough samples to perform a meaningful analysis," says study author Scott A. Tomlins, M.D., Ph.D., assistant professor of pathology and urology at the University of Michigan Medical School.

Phyllodes tumors represent about 1 percent of all types of breast tumors. Most are benign but they do have the potential to become metastatic. Currently, there are no good ways to reliably predict which tumors are likely to recur or spread after initial treatment. Once phyllodes tumors become metastatic, there are few effective treatments.

Researchers looked at 15 samples of phyllodes tumors, pulled from archived tissue samples at the University of Michigan. The samples were equally divided according to their classification, with five considered benign, five borderline and five malignant. While still a small sample, it can be sufficient with a rare tumor to identify genetic clues to the tumor's biology. The researchers sequenced the samples against a panel of genes known to have some function or role in cancer.

They found two genes, EGFR and IGF1R, that were amplified in multiple malignant phyllodes tumors. Therapies have already been developed against EGFR and IGF1R proteins and tested in other

cancers. Results from this study support evaluating these therapies in phyllodes tumors as well.

In addition, the researchers found the gene MED12 was frequently mutated in all classifications of phyllodes tumors. This gene also plays a role in some rare gynecological tumors that are related to phyllodes tumors. The researchers believe MED12 could be involved with tumor initiation.

Results of the study appear in *Molecular Cancer Research*.

"Even though phyllodes tumors are rare, it's important to have good treatment options for the aggressive cases. The first step is understanding the underlying biology of these tumors," Tomlins says. "Further study and validation is needed, but our work has identified several promising targets involved in phyllodes tumors."

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