

New biomarker highly promising for predicting breast cancer outcomes

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A protein named p66ShcA shows promise as a biomarker to identify breast cancers with poor prognoses, according to research published ahead of print in the journal *Molecular and Cellular Biology*.

Cancer is deadly in large part due to its ability to metastasize, to travel from one organ or tissue type to another and malignantly sprout anew. The vast majority of cancer deaths are associated with metastasis.

In breast cancer, a process called "epithelial to mesenchymal transition" aids metastasis. Epithelial cells line surfaces which come into contact with the environment, such as skin and the gastrointestinal tract. Mesenchymal cells are a type of cell in embryonic tissue and in connective tissue, where they form very loose contacts with one-another. Tumor cells lose mature epithelial characteristics, such as the ability to adhere to their neighbors, and gain those of the mesenchymal cells which enable them to move easily through the cellular matrix and into the blood stream. That enables their metastatic migration to distant organs and tissues.

In this study the researchers, led by Josie Ursini-Siegel of McGill University, show that the protein p66ShcA is highly enriched in breast cancers that have undergone epithelial to mesenchymal transition.

"We showed that elevated p66ShcA expression levels are strongly associated with expression of numerous epithelial to mesenchymal transition genes in all <u>breast cancer</u> subtypes," says Ursini-Siegel. "Thus,



p66ShcA may serve as one of the first prognostic biomarkers to identify poor outcome breasts cancers regardless of their molecular subtype."

The ability to predict prognosis is critical to management of treatment. A patient with a good prognosis can be spared aggressive treatment, with its oft-unpleasant side effects. But failure to apply aggressive treatment to an aggressive tumor can lead to death.

Breast cancers stratify into at least five subtypes, each of which is associated with a different outcome. Nonetheless, earlier research showed that there is heterogeneity within the subtypes, which makes predictions of outcome based on subtype less reliable than they might otherwise be.

"By understanding the underlying mechanisms that conribute to tumor heterogeneity and metastatic progression, including the epithelial to mesenchymal transition, we hope to be better able to guide the development of prognostic and therapeutic strategies to improve patient care," says Ursini-Siegel.

More information: The manuscript can be found online at mcb.asm.org/content/early/2014 ... 341-14.full.pdf+html . The final version of the article is scheduled for the October 2014 issue of *Molecular and Cellular Biology*.

Provided by American Society for Microbiology

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