

Routine breast cancer biopsy might predict lymph node cancer spread

18 April 2010

Predicting breast cancer spread from a sentinel lymph node removed during surgery is a hit or miss affair, say researchers: there are still many false negatives, which means the node, when analyzed under a microscope, appears clean of cancer cells, but metastasis can still occur in the patient. The sentinel node is the first lymph node in the axilla that cancer spreads to.

Now, researchers from Georgetown Lombardi Comprehensive Center say that they have clues to molecular markers on breast tumors that may predict which cancers will metastasize to the lymph node system. Details of the study will be presented at the AACR 101st Annual Meeting 2010.

In a pilot study comparing genomic alterations in both [breast cancer](#) cells and sentinel lymph nodes removed from 15 patients whose cancer spread to the lymph nodes, researchers found genes that were altered (amplified or deleted) in both samples. These alterations affected genes that function as either oncogenes or tumor suppressors. The final goal is to be able to identify, at the time of the diagnosis, when a patient has a routine biopsy of their tumor, who is at higher risk for development of lymph node metastasis, says Luciane Cavalli, PhD, an assistant professor of oncology at Lombardi.

"To our knowledge, very few studies have looked specifically for genomic alterations in sentinel nodes in comparison to the primary tumor from the same patient. If we find markers that can be significantly associated with patients that develop axillary metastasis, we can check for these markers at an early stage of the cancer management, before axillary lymph node metastasis develops" says Cavalli. "That will give physicians a chance to treat what is otherwise an unseen metastasis."

Currently, a sentinel lymph node is removed when a patient undergoes surgery to remove breast

tumors, and the node is examined for evidence of cancer cells while the operation is in progress. If these malignant cells are seen, additional nodes in the axilla are removed, Cavalli says. "This procedure is performed during the surgery, and the methods currently used to look for tumor cells in these nodes are not ultra sensitive, and may therefore miss these [malignant cells](#) especially in the case of micrometastasis."

Cavalli and her team first screened the genomes of cells from both tumors and nodes from the same patient using comparative genome hybridization (CGH), and found that most of the genomic regions affected were similar in both of the samples. . They then used microarray technology (array-CGH) to identify the genes altered in these regions and found several that were altered in patient lymph nodes and tumors. Some of these genes are well known, such as the growth promoting gene her2neu, and the tumor suppressor BRCA1.

"It differed between patients - in some, BRCA1 was missing in both samples, in others, Her2neu or other genes were amplified," Cavalli said.

The researchers are now validating their results in other patient samples. "If we can use these genomic markers to identify tumor cells in the [sentinel lymph node](#) to reduce the false negative rates that now exist in sentinel node biopsy, we can advance one step forward in patient care," Cavalli says.

Provided by Georgetown University Medical Center

APA citation: Routine breast cancer biopsy might predict lymph node cancer spread (2010, April 18) retrieved 25 June 2022 from <https://medicalxpress.com/news/2010-04-routine-breast-cancer-biopsy-lymph.html>

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