

Genes set scene for metastasis

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Biologists at Memorial Sloan-Kettering Cancer Center (MSKCC) have identified a set of genes expressed in human breast cancer cells that work together to remodel the network of blood vessels at the site of the primary tumor. These genes were also found to promote the spread of breast cancer to the lungs. The study, conducted in mice and reported in this week's Nature, helps to explain how cancer metastasis can occur and highlights targets for therapeutic treatment.

Metastasis — the leading cause of mortality in cancer patients — entails numerous biological functions that collectively enable cancerous cells from a primary site to disseminate and overtake distant organs. A number of genes are already known to contribute to the spread of breast cancer cells to the lungs.

Using genetic and pharmacological approaches, Joan Massagué, PhD, Chair of MSKCC's Cancer Biology and Genetics Program and a Howard Hughes Medical Institute Investigator, and colleagues showed how four genes facilitate the formation of new tumor blood vessels, the release of cancer cells into the bloodstream, and the penetration of tumor cells from the bloodstream into the lung. The gene set comprises EREG (an epidermal growth factor receptor ligand), the cyclooxygenase COX2, and MMP1 and MMP2 (matrix enzymes that are expressed in human breast cancer cells).

The researchers conclude that drug combinations that target one or more of the proteins encoded by these genes may prove useful for treating metastatic breast cancer.



Source: Memorial Sloan-Kettering Cancer Center

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