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Beating advanced cancers: New epigenomic block for advanced cancer

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An international research team led by Mayo Clinic oncologists has found a new way to identify and possibly stop the progression of many late-stage cancers, including bladder, blood, bone, brain, lung and kidney.

The precision medicine study appears online in *Oncogene* and focuses on kidney cancer and its metastases. Recent studies of the same epigenomic fingerprint in other cancers suggest a common pathway that could help improve the diagnosis and treatment of advanced disease across a wide variety of cancer types.

"If you think of late-stage cancer as a runaway car, most of our drugs take a shot at a tire here and there, but sometimes they miss and often they can't stop it entirely," says Thai Ho, M.D., Ph.D., a Mayo Clinic oncologist and lead author of the study. "We believe we have identified a mechanism that seizes the cancer's biological engine and could potentially stop it in its tracks."

The new approach zeroes in on an epigenomic fingerprint in metastatic disease, in which the body often misinterprets a healthy genetic blueprint, producing toxic cells that run afoul of the body's normal functions.

Dr. Ho and his colleagues are currently validating a test based on the newly identified epigenomic fingerprint, called H3K36me3 loss, which could help providers identify more aggressive cancers or find the best drug for the individual patient to further personalize medical care.

"This paper is the first report we know of translating this fingerprint into patient tissues, and efforts are ongoing to expand this to tumors beyond kidney cancer," says Dr. Ho.

The test and a potential treatment are based on an emerging discipline of medical research called epigenomics, the complex biological process through which individual cells read their genetic blueprints and then determine what type of tissue to become.

Dr. Ho offers the example of honeybees as among the starkest examples of how epigenomics affects cellular function and an organism's fate.

Throughout their life spans, all bees in a hive share the same DNA sequence. But some bees become drones, others sterile female workers, and still others the queen. Much of this differentiation can be attributed to epigenomics, says Dr. Ho.

In feeding a larval honeybee with copious amounts of a richly nutritious secretion called royal jelly, the larva will eventually develop into a queen. Chemicals present in the royal jelly, but absent in nectar and pollen, are thought to activate entirely different parts of the same bee genome—converting one larva into the queen while others, such as workers and drones, are much smaller and have shorter life spans. Similarly, cancers often subvert a cell's normal epigenomic mechanisms to become more aggressive.

Provided by Mayo Clinic