Spread of pancreatic cancer fueled by epigenetic changes

[Editor's note: Excerpts are from an interview with Andrew Feinberg of Johns Hopkins, whose <u>research</u> shows how epigenetics affects the spread of pancreatic cancer.]

Scientists running a genome-wide analysis of pancreatic tumor samples have...discovered that changes in the regulation of genes — not in DNA sequences — seem to be powering the cancer's spread.

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People have simply assumed that metastases are caused by some sort of mutation. We set out to find if epigenetic changes could cause distant metastases, starting with pancreatic tumors.

We found there were large regions of the genome in the tumors that had lost the DNA methylation capability and also had lost what we call heterochromatin, the marks that make the genome squish together. They became sort of unlocked and available for genes to become active.

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We also identified a mechanism for these epigenetic changes, involving activation of genes that protect the cancer cell from oxidative stress. When we blocked that pathway, the epigenetic changes partially reversed and the tumors lost their invasive capacity — at least in the lab. This work opens a new avenue for discovering drugs to block or reverse metastasis.

The GLP aggregated and excerpted this blog/article to reflect the diversity of news, opinion, and analysis. Read full, original post: How epigenetic changes prime pancreatic cancer cells to spread