

Research reveals that significantly more genetic mutations lead to colon cancer

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Researchers at UT Southwestern Medical Center say there are at least 70 genetic mutations involved in the formation of colon cancer, far more than scientists previously thought.

Based on the study, published in the July 2011 Cancer Research (Priority Reports), researchers are suggesting a new approach to [colon cancer](#) treatments targeting multiple genes and pathways simultaneously. Current cancer treatments target just one or two known cancer-driver genes believing this would be beneficial to patients. While patients may get transient tumor burden reduction, almost universally tumor growth returns.

The UT Southwestern research contradicts previous thinking that only a few mutated genes are important in the development of [cancerous tumors](#).

"The ways we've been treating patients up to now is to just go after one target when we should be going after three to four different pathways simultaneously," said Dr. Jerry W. Shay, vice chairman and professor of cell biology at UT Southwestern.

Under the old model, scientists believed there were 151 candidate genes and that mutations in just eight to 15 of them would lead to cancer. There were 700 other genes classified as passenger genes whose mutations were incidental to cancer growth.

"Those numbers are dead wrong," Dr. Shay said. According to UT Southwestern's research, there are 65 [candidate genes](#) and at least five passenger genes whose mutations play significant roles in [cancer development](#). Inactivating the function of any of these tumor-suppressing genes led to a key step in cancer development called anchorage-independent growth, meaning cells piled up on top of each other rather than aligning neatly.

The next step is further research to classify more accurately which genes drive cancer and which are merely passengers.

Provided by UT Southwestern Medical Center

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