Leap forward in cancer research attributed to CRISPR tumor modeling

By sequencing the genomes of tumor cells, thousands of genetic mutations have been linked with cancer.

Sifting through this deluge of information to figure out which of these mutations actually drive cancer growth has proven to be a tedious, time-consuming process but MIT researchers have now developed a new way to model the effects of these genetic mutations in mice. Their approach, based on the genome-editing technique clustered regularly interspaced short palindromic repeats (CRISPR) is much faster than existing strategies, which require genetically engineering mice that carry the cancerous mutations.

“It’s a very rapid and very adaptable approach to make models,” says lead author Thales Papagiannakopoulos, a postdoc at MIT’s Koch Institute for Integrative Cancer Research. “With a lot of these mutations, we have no idea what their role is in tumor progression. If we can actually understand the biology, we can then go in and try targeted therapeutic approaches.”

The team used CRISPR to accurately reproduce the effects of two well-known lung cancer genes and also modeled a gene called APC, whose role in lung cancer was not previously known.

This approach could be used to study nearly any gene in many different types of cancer, the researchers say. “There has to be a functional way of assessing the role of these cancer-gene candidates as they appear in sequencing studies,” said graduate student Francisco Sanchez-Rivera. “The system we developed fills that gap immediately because you can do it very rapidly and very precisely.”

Read full, original article: Fast modeling of cancer mutations