

Study shows new 'driver' to assess cancer patient survival and drug sensitivity

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Cancer specialists have long looked at genetic mutations and DNA copy changes to help predict patient survival and drug sensitivity. A study led by The University of Texas MD Anderson Cancer Center has opened up yet another avenue for understanding the biological reasons why some people live longer or respond better to treatment - RNA editing events.

An assessment of 6,226 samples from patients with 17 different [cancer](#) types taken from The Cancer Genome Atlas has revealed new information about RNA editing events in tumors versus normal tissue, and provided evidence that RNA editing could selectively affect [drug sensitivity](#). RNA editing is the process where genetic information is altered in the RNA molecule. Once thought rare in humans and other vertebrates, RNA editing is now recognized as widespread in the human genome.

Results from the study are published in the Oct. 1 online edition of *Cancer Cell*.

"These results highlight RNA editing as an exciting theme for investigating cancer mechanisms, biomarkers and treatments," said Han Liang, Ph.D., associate professor of Bioinformatics and Computational Biology. "In this study, we identified an appreciable number of clinically relevant editing events, many of which are in non-coding regions."

Liang said that specific RNA editing processes, adenosine-to-inosine (A-to-I), are plentiful in the [human genome](#) but have not been investigated

in depth. The study provided new detail on this little understood biological phenomenon that may have significant clinical relevance.

"If a protein is only highly edited in the tumor proteins, but not in normal proteins, then it's possible that a specific drug could be designed to inhibit the edited mutant protein," said Liang. "Previous studies have focused on DNA mutations and mainly focused on RNA editing in normal tissues. The role of RNA editing in human cancers is only beginning to emerge from those early studies of individual patient samples in a few cancer types."

The larger scale Cancer Genome Atlas study provided the information needed to alter proteins or RNA sequences that may act as "drivers" for prognostic biomarkers or therapeutic targets. RNA editing adds another layer of complexity in the quest to predict patient survivability and suggest new therapies, said Liang.

Provided by University of Texas M. D. Anderson Cancer Center

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