AACR 2016: Sequencing RNA in tumors could help improve cancer care, study finds

In preliminary study findings presented at the American Association for Cancer Research Annual Meeting 2016, UNC Lineberger researchers report they identified changes in RNA based on DNA mutations, and the additional information could be potentially helpful for better management of cancer patients.

April 20, 2016

click to enlarge

Neil Hayes, MD, MPH, is a UNC Lineberger member and an associate professor in the UNC School of Medicine Division of Hematology/Oncology.

After an earlier study determined that genetic sequencing of a patient's tumor could improve care by matching the mutations and genetic abnormalities with targeted treatments, University of North Carolina Lineberger Comprehensive Cancer Center researchers are now studying whether RNA sequencing, in addition to DNA sequencing, can improve patient care further. Their preliminary findings will be presented at the American Association for Cancer Research Annual Meeting 2016, today from 8 a.m. to noon CST.

In the study, researchers selected a subset of 300 patients for RNA sequencing from a group of 2,200 patients who 2 who had been consented as part of a clinical trial for sequencing. The new research looks to build on the findings from the UNCseq program, which was launched in 2011.

In the preliminary study findings, researchers report they identified changes in RNA based on DNA mutations, and the additional information could be potentially helpful for better management of cancer patients.

“With next-generation sequencing and some other advances, we now have the ability to sequencing RNA, which has some advantages over DNA sequencing,” said Neil Hayes, MD, MPH, a UNC Lineberger member and an associate professor in the UNC School of Medicine Division of Hematology/Oncology. “Many of these are technical advances, but there is also a clinical benefit in that we can better characterize many of the mutations found in cancer, especially some of the difficult-to-detect changes in the structure of DNA called ‘fusion oncogenes.’”

Hayes said the use of RNA also could be used to generate gene signatures at the same time they are detecting mutations, providing additional information that could have “broad potential use” for many cancer patients.

Filed under: **2016**