Medical Xpress

New subsets of lung cancer with KRAS gene mutations identified

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Mutations of the KRAS gene are commonly known to lead to cancer. However, deeper understanding of exactly how they do this continues to be explored by cancer researchers.

Scientists at The University of Texas MD Anderson Cancer Center have gained further insight about the processes behind KRAS [mutations](#) through a study that identified three subsets of [lung cancer](#) with mutations in this gene. This line of research has the potential to open up new approaches for treatment of [lung adenocarcinoma](#) (LUAC), the most common form of lung [cancer](#).

The data was presented on April 19 at the 2015 American Association for Cancer Research (AACR) Annual Meeting in Philadelphia.

"The development of more effective treatments for LUAC-bearing activating mutations in KRAS has been hampered by the biological heterogeneity of KRAS-mutant tumors," said John Heymach, M.D., Ph.D., chair of Thoracic/Head & Neck Medical Oncology. "The molecular underpinnings that drive this process are poorly characterized."

Heymach and his study team adopted an integrated approach to the discovery of biologically distinct subsets of KRAS-mutant LUAC and explored their molecular vulnerabilities.

"Our work revealed three major subsets of KRAS-mutant LUAC, which

were dominated by co-occurring genetic events, each biologically distinct and susceptible to different therapeutic strategies," said Ferdinandos Skoulidis, M.D., Ph.D., instructor of Thoracic/Head & Neck Medical Oncology.

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