Researchers find possible link between jumping genes and cancerous tumor growth

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(Medical Xpress) -- Researchers based out of Harvard and Brigham Young Women's Hospital have found compelling evidence that suggests "retrotransposon movement in somatic cells" - DNA sequences that jump (make copies of themselves that make their way to other sequences) might be responsible for the growth of some types of cancerous tumors.

The team, as they describe in their paper published in the journal *Science*, found examples of such jumping genes in samples taken from several different kinds of cancerous tumors in multiple patients.

Jumping genes have been seen in a wide variety of plants and animals but have been thought to be rare in mammals, which of course includes humans. Such jumps are thought to play a role in the evolutionary process because their activity generally results in mutations and thus changes in the plant or animal in which it occurs. The researchers note that the elements necessary for jumping genes are widely known to exist in mammals, including humans, but it was thought that their ability to jump was hampered by physiology.

In this new study, the team looked at five specific kinds of cancer: ovarian, multiple myeloma (a type of white blood cell cancer), colorectal, prostate, and those of the brain. Using a computer software computational method called Tea, for Transposable Element Analysis, they found that the incidence of jumping genes was higher than normal for all of the tumors studied except for those of the brain and blood,

suggesting that jumping genes just might play a role in the development of several types of tumor growth. As part of their findings, they noted that the jumping genes found in cancerous tumors tended to occur in the types of tumors that just happen to mutate in several types of cancers, which include some kinds of genes that are known to be tumor suppressors.

In their research, the team found that some transposable element (TE) insertions seemed to provide a path that led to an environment conducive to tumor growth and that different types of TEs were found in different types of tumors. Specifically, they found that out of 194 insertions, 183 were the so named L1 retrotransposons, 10 were of the Alu variety and just one was an ERV.

Validation testing has shown the Tea software used for testing to be ninety seven percent accurate, though the research team suspects the software likely misses some of the jumping genes due to repeats of the genes that occur in close proximity to one another.

More information: Landscape of Somatic Retrotransposition in Human Cancers, *Science*, DOI: 10.1126/science.1222077 . www.sciencemag.org/content/ear … 6/27/science.1222077