'Jumping genes' may drive esophageal cancer

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Cancer Research UK scientists have found that 'jumping genes' may add to the genetic chaos behind more than three-quarters of oesophageal cancer cases, according to research published in *BMC Genomics* today.

The scientists, from the University of Cambridge, used cutting-edge technology that can read DNA to study the genes of 43 oesophageal tumour and blood samples to discover how much these mobile genetic sequences travel.

'Jumping genes', called L1 elements, can uproot themselves and move to new areas in the DNA, sometimes accidentally moving into genes that control the cell's growth.

They found evidence that this happened around 100 times in each tumour sample, and in some tumours it happened 700 times.

If a jumping gene lands in or near an important gene that controls cell growth, it can wreak havoc, changing how the gene works so that it inadvertently tells the cell to grow and divide out of control - which could lead to cancer.

Study author Dr Paul Edwards, at the Cancer Research UK Cambridge Institute, said: "These jumping genes play hopscotch across our genetic code in cancer cells more than in normal cells. When one of these mobile genetic sequences plants itself in the middle of a gene that controls the cell's growth it radically alters how the cell behaves, which can sometimes cause cancer.

"Research has shown that this might also happen in lung and bowel cancers. So it's vital we find out more about how the cells do this in a bid to find ways to treat these cancers."

The research is part of the International Cancer Genome Consortium (ICGC) - a global project using the latest gene sequencing technology to reveal the genetic changes behind cancer. The oesophageal cancer project is funded by Cancer Research UK's Catalyst Club.

Dr Kat Arney, Cancer Research UK's science information manager, said: "Oesophageal cancer is one of the hardest cancers to treat, and we are committed to funding more research to find out its underlying causes. These new findings reveal more about the genetic chaos that underpins oesophageal tumours, and could one day help us develop better ways to diagnose, treat and monitor the disease."

More information: Paterson et al. Mobile element insertions are frequent in oesophageal adenocarcinomas and can mislead paired end sequencing analysis. *BMC Genomics*. DOI: 10.1186/s12864-015-1685-z. Research article will appear online at dx.doi.org/10.1186/s12864-015-1685-z

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