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*****Researchers discover patterns of genetic changes in cancer cells.

DALLAS--Genetic researchers at The University of Texas Health Science Center at Dallas have discovered patterns of gene alteration that seem to be common within certain types of cancer. By identifying these changes, scientists move closer toward an understanding of which genes are involved in the formation of cancer.

Further investigation of these altered patterns, in which certain genes make increased numbers of copies of themselves or fail to copy themselves at normal levels, may allow scientists to identify persons with a predisposition to develop cancer. Among people who do develop cancer, it may help identify those who have a better prognosis than others.

The UTHSCD team, led by genetic researchers Dr. Fred Baskin and Dr. Roger Rosenberg, who is also chairman of the university's Department of Neurology, used a special DNA separation technique on tissue from 12 tumor samples. Tumors included cancers of the brain, colon, lung and uterus. In each case, the cancer tissue was compared to normal tissue from that same individual.

Other members of the team included Drs. Abraham Grossman, Sumedha Bhagat, Dennis Burns, Richard Davis and Larry Warmoth. Their findings are slated for publication in Cancer Genetics and Cytogenetics later in the year.

Applying the DNA separation technique, invented by Dr. I.B. Roninson of the University of Illinois, to the tumor DNA, the health science center team has been able to identify and quantitate genes that are replicated more than 25 times. The results of those tests reveal patterns of gene sequences that had not been disclosed before, the scientists say. Some of the repeated gene sequences seen with the tests were unique to particular individuals, but some seemed common among a particular cancer type, says Rosenberg.

DNA in normal cells is composed largely of single copies of genes -- each gene with its own purpose and function, Baskin explains. Certain genes that promote the development of cancer are found to be reproduced in larger numbers in some cancers. The so-called "oncogenes" are often replicated in many types of cancer.

This replication occurs through a process known as "gene amplification." Genes may be reproduced, or amplified, hundreds or thousands of times. Chromosomes containing amplified genes are sometimes greatly expanded beyond their normal lengths, and staining techniques reveal elongated regions on these chromosomes.

(More)

The researchers found one sequence specific to colon cancer and not present in normal tissue of the hosts. They also found other new amplified sequences that seemed specific to brain cancers, specifically gliomas and neuroblastomas -- the two most common forms of nervous system tumors.

Baskin says, "The approach was a way to ask, 'What is the complete list of genes that this cancer wants to amplify or delete?'

"We had a chance to find any amplified gene, where before we had no means of identifying them." The team believes that genes other than known oncogenes were amplified.

By finding these new DNA sequences "we are beginning to understand the biology of cancer," says Baskin. "There is more going on in cancer than the amplification of oncogenes. Eventually we will have a list of all the genes that each cancer needs to promote its own growth," he says.

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Distribution: AA,AB,AC,AF,AF1,AG,AG1,AH,AI,AK,AK1,AM,SC

NOTE: The University of Texas Health Science Center at Dallas comprises Southwestern Medical School, Southwestern Graduate School of Biomedical Sciences and the School of Allied Health Sciences.