UNIVERSITY OF MARYLAND MEDICAL News

University of Maryland
School of Medicine
655 West Baltimore Street
Baltimore, Maryland 21201
http://medschool.umaryland.edu

EMBARGOED FOR RELEASE UNTIL: June 24, 2010, 12 p.m. (noon) EDT:

Contact: Karen Buckelew (kbuckelew@som.umaryland.edu)
410-706-7590
Sarah Pick (spick@som.umaryland.edu)
410-706-0866

NEW INSTITUTE FOR GENOME SCIENCES STUDY FINDS MORE VARIATION IN HUMAN GENOME THAN EXPECTED

Surprisingly Common Transposons or 'Jumping Genes' Are Known to Cause Disease

Scientists are finding more variation in the human genome than they had previously expected, now that new technologies are allowing researchers a closer look at the genomes of many individuals, according to a new study led by researchers at the Institute for Genome Sciences at the University of Maryland School of Medicine. The study, to be published in the June 25 issue of the journal *Cell*, is one of the first to take an in-depth look at transposons, known as "jumping genes." Transposons are segments of DNA that can replicate themselves — meaning that each generation of a human family has more transposons in its genome than its ancestors — and move to new sites in each individual person's genome. The researchers examined the genomes of 76 people and found that new occurrences of transposons were surprisingly prevalent. They also found that transposons are very active in lung cancer genomes.

"A key part of this study was that we developed new, next-generation sequencing and informatics technologies that allowed us to look at these variants for the first time in many human genomes," says Scott E. Devine, Ph.D., an associate professor at the University of

Maryland School of Medicine and a research scientist at the school's Institute for Genome Sciences.

"The human genome is a big document full of information, like a blueprint," Dr. Devine explains. "As soon as the human genome was sequenced, it became clear that it was going to vary from one person to the next. Such variation dictates why people look different from one another, why they have different susceptibilities to diseases and different lifespans. In this study, we're looking at transposons that insert themselves in new places in various genomes and disrupt the blueprint."

Dr. Devine continues: "If you think of the human genome as a manual to build a complex machine like an aircraft, imagine what would happen if you copied the page that describes passenger seats and inserted it into the section that describes jet engines. Transposons act something like this: they copy themselves and insert the copies into other areas of the human genome, areas that contain instructions for the complex machine that is the human body. These areas and the instructions they contain may then become corrupted and hard to understand. This, in turn, can alter human traits or even cause human diseases."

Some transposons do not seem to have a serious impact on the genome, but several dozen transposon insertions have been identified that have caused human disease by disrupting genes. "We think this is just the tip of the iceberg," Dr. Devine says. He began the research for this study when he was a faculty member at Emory University School of Medicine in Atlanta.

"We saw for the first time that new transposon insertions are happening at a high frequency in each person's genome," Dr. Devine says. "We found that if you have a child, the child could have one or more new copies of these transposons that you don't have. From these

findings, we predict that there is going to be more variation in human genomes than scientists first believed."

The transposons found in lung cancer tumor genomes had never been seen before, and could have significance for oncology research. "The mutations could possibly be causing cancer or tumor progression," Dr. Devine explains. Technological advances in DNA sequencing have made it possible to examine transposons in greater detail, Dr. Devine adds, and also have cut the cost of sequencing a human genome from millions of dollars just a few years ago to as little as $10,000 now.

Scientists track variation in the human genome to identify specific variants that predict human traits and diseases, says Dr. Devine: "The big picture idea here is personal genomics, a new wave of science where an individual's genome will be sequenced at birth and then used to make predictions about the future health of that person. This will pave the way for a future of personalized medicine, where treatments and preventive techniques will be tailored to each individual based on the information found in that person's genome."

The research was funded by the National Human Genome Research Institute, part of the National Institutes of Health, the American Cancer Society and Sun Microsystems.

"This study is an example of how our world class researchers are leading the field with their innovations at the cutting edge of this emerging sector of personalized genomics and predictive medicine," says E. Albert Reece, M.D., Ph.D., M.B.A., acting president of the University of Maryland, Baltimore and John Z. and Akiko K. Bowers Distinguished Professor and dean, University of Maryland School of Medicine. "They are bringing the field of medicine closer to a future where each person's genome will serve as a map to predict their health over a lifetime. We're proud to be a part of this future."