Aging contributes to rapid rates of genomic change, signaling challenges for personalized medicine

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(Medical Xpress)—Exploiting individual genomes for personalized medicine may be more complicated than medical scientists have suspected, researchers at Virginia Bioinformatics Institute have discovered.

In a paper published in June in the journal *Aging*, scientists from the institute's Medical Informatics and Systems Division found that spontaneous mutations occur in our bodies constantly, but the rate of change differed dramatically among various people.

The study has implications for personalized medicine, which will make use of genomic information to predict future diseases and treatments. With genomes continually shifting over time, the monitoring of genomic health will require more frequent measurement of patients' genomes.

"We have long known that there were mutations acquired in cancerous tumors, but this study confirms that our genome is constantly changing even in healthy tissues," said Harold "Skip" Garner, a professor of biological sciences and computer science at Virginia Tech and a professor of medicine at the Virginia Tech Carilion School of Medicine. "The implications on using genomic information for medicine and medical research in the future are tremendous. Things are not as simple as we once thought."

DNA in our cells changes from exposure to various environmental stressors. This can cause mutations in up to 13,000 genes that raise the risk of diabetes, kidney failure, cancer, rheumatoid arthritis, and Alzheimer's disease—conditions usually associated with aging.

The research may help scientists better understand how individuals tolerate environmental exposure and why some people seem to age faster or slower than others.

"We observed that certain portions of our genome age 100 times faster than others," Garner said. "Microsatellites, once considered 'junk DNA,' are known to be associated with many diseases. They change much faster than individual DNA bases (known as single nucleotide polymorphisms, or SNPs), so it is important that future studies look at this very dynamic

part of the human genome."

The researchers used the latest DNA sequencing technology to study the genetic makeup of three individuals at different times in their lives, spanning nine to 16 years. One of the individuals had almost 10 times as many variations as the others, and was found to be at risk for many more potential diseases.

"We observed that the variation rate is specific to the individual and also varies even within an individual's genome," said Jasmin Bavarva, a geneticist at the institute and lead scientist on the project. "Understanding the dynamics of the genome is the key to the success of personalized genomics and this is a major step forward."

More information: The research paper is available online: www.impactaging.com/papers/v6/n6/full/100674.html

Provided by Virginia Tech

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