MedicalXpress

Aging impacts epigenome in human skeletal muscle

November 20 2013

Our epigenome is a set of chemical switches that turn parts of our genome off and on at strategic times and locations. These switches help alter the way our cells act and are impacted by environmental factors including diet, exercise and stress. Research at the Buck Institute reveals that aging also effects the epigenome in human skeletal muscle. The study, appearing on line in *Aging Cell*, provides a method to study sarcopenia, the degenerative loss of muscle mass that begins in middle age.

The results came from the first genome-wide DNA methylation study in disease-free individuals. DNA methylation involves the addition of a methyl group to the DNA and is involved in a particular layer of epigenetic regulation and genome maintenance. In this study researchers compared DNA methylation in samples of skeletal muscle taken from healthy young (18 - 27 years of age) and older (68 – 89 years of age) males. Buck faculty and lead scientist Simon Melov, PhD, said researchers looked at more than 480,000 sites throughout the genome. "We identified a suite of epigenetic markers that completely separated the younger from the older individuals – there was a change in the epigenetic fingerprint," said Melov. "Our findings were statistically significant; the chances of that happening are infinitesimal."

Melov said scientists identified about six-thousand sites throughout the genome that were differentially methylated with age and that some of those sites are associated with genes that regulate activity at the neuromuscular junction which connects the nervous system to our

muscles. "It's long been suspected that atrophy at this junction is a weak link in sarcopenia, the loss of muscle mass we get with age," said Melov. "Maybe this differential methylation causes it. We don't know."

Studying the root causes and development of sarcopenia in humans is problematic; the research would require repeated muscle biopsies taken over time, something that would be hard to collect. Melov says now that the epigenetic markers have been identified in humans, the goal would be to manipulate those sites in laboratory animals. "We would be able to observe function over time and potentially use drugs to alter the rate of DNA methylation at those sites," he said. Melov says changes in DNA methylation are very common in cancer and that the process is more tightly controlled in younger people.

More information: "Genome-wide DNA methylation changes with age in disease-free human skeletal muscle," *Aging Cell*, 2013.

Provided by Buck Institute for Age Research