Team investigates function of 'junk DNA' in human genes

February 28 2011

Part of the answer to how and why primates differ from other mammals, and humans differ from other primates, may lie in the repetitive stretches of the genome that were once considered "junk."

A new study by researchers at the University of Iowa Carver College of Medicine finds that when a particular type of repetitive DNA segment, known as an Alu element, is inserted into existing genes, they can alter the rate at which proteins are produced -- a mechanism that could contribute to the evolution of different biological characteristics in different species. The study was published in the Feb. 15 issue of the journal Proceedings of the National Academy of Sciences (*PNAS*).

"Repetitive elements of the genome can provide a playground for the creation of new evolutionary characteristics," Xing said. "By understanding how these elements function, we can learn more about genetic mechanisms that might contribute to uniquely human traits."

Alu elements are a specific class of repetitive DNA that first appeared about 60 to 70 million years ago during primate evolution. They do not exist in genomes of other mammals. Alu elements are the most common form of mobile DNA in the human genome, and are able to transpose, or jump, to different positions in the genome sequence. When they jump into regions of the genome containing existing genes, these elements can become new exons -- pieces of messenger RNAs that carry the genetic information.

Although scientists have known for more than a decade that these Alu elements are an important source of new exons in the human genome, it has been more difficult to determine if these new exons are biologically important.

"It's been hard to say whether these Alu-derived exons actually do anything on a genome-wide level," said senior study author Yi Xing, Ph.D., assistant professor of internal medicine and biomedical engineering, who holds a joint appointment in the UI Carver College of Medicine and the UI College of Engineering. "Our new study says they do - they affect protein production by altering the efficiency with which messenger RNA is translated into protein."

Xing noted that in other circumstances, altering the rate of protein production can cause disease, meaning that a mechanism that can affect protein production can have a real impact on the characteristics of an organism.

"This would not be the only mechanism that might differentiate humans from other primates, but our study suggests that the creation of new exons from Alu elements is an important process that contributes to those differences," Xing said.

The UI team, including co-first authors Shihao Shen, doctoral student in the Department of Biostatistics; and Lan Lin, Ph.D., associate in the Department of Internal Medicine, made use of data from a new technology called high throughput RNA sequencing to analyze more than 120 million RNA sequences from human cerebellum. Using this data, the team was able to quantify how often Alu-derived exons were included in the mature RNA sequences, which provide the final blueprint for protein production, and where they were inserted in the genes.

"What we found is that these exons tend to avoid protein-coding regions of the genes and rather they end up in the non-coding region that precedes the protein-coding region, called the five prime untranslated region or 5' UTR," Xing explained. "This is the part of the gene that usually contains regions that help control the stability of the messenger RNA and the efficiency at which the messenger RNA is translated into protein."

Experiments to probe the function of these newly inserted elements proved that Alu exons in this region are able to alter the efficiency of messenger RNA translation, which means they affect how fast protein is produced from the altered genes.

The study also suggests that the effect of the newly created exons might be amplified because of which genes were "targeted" by the Alu exons. The researchers found that Alu exons are highly enriched in genes that code for zinc-finger transcription factors -- proteins that act as master regulators of gene expression and that previously have been linked to human and primate evolution. Because these transcription factors control the expression of thousands of other genes, any changes to the amount of transcription factor available would likely have a cascade effect on the downstream genes.

Provided by University of Iowa

Citation: Team investigates function of 'junk DNA' in human genes (2011, February 28) retrieved 2 May 2024 from https://phys.org/news/2011-02-team-function-junk-dna-human.html