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The Hitchhiker's Guide to the Genome

Are we still evolving? 'Jumping DNA' could hold the answer.

The human genome is big… very big!

It also has some unexpected features, such as 'jumping DNA' and 'pseudogenes' which 'hitch a lift' from one part of the genome to another. Studies of these elements have given insight into human evolution and genetic disease. Research at the world-renowned Department of Genetics at the University of Leicester is using cutting edge techniques to investigate the continuing role of 'jumping DNA' in human genome evolution.

The human genome is riddled with copies of DNA elements that have in our evolutionary past reproduced and "jumped" to new locations. Sometimes they land inside genes, causing damage to the DNA, or mutations, that result in disease but this is very infrequent.

Contrary to popular belief, most of the human genome does not consist of genes, and this leaves a vast area free for 'jumping DNA' to land in without causing any harm.

Peter Freeman is a Leicester PhD research student working with Dr Richard Badge and Professor Sir Alec Jeffreys FRS, and is funded by the Biotechnology and Biological Sciences Research Council (BBSRC). They are looking directly at human germline DNA (the DNA found in sperm and egg cells) to identify when, where and how often a particular family of jumping DNA (L1s) makes new jumps. This work will indicate the impact that L1s have on human genome evolution and genetic disease.

Peter Freeman commented: "Why should we care about jumping DNA? Well, for example, among the 30-40,000 genes required to make a human, there are a surprising number of extra copies of these genes dispersed throughout the genome. These extra copies are referred to as "pseudogenes" as they contain the genetic information of the parent gene, but are non-functional.

> "Pseudogenes are able to change in ways that the original copies cannot, without affecting vital functions. Although for the most part these changes lead to decay, pseudogenes have the potential to gain new and useful functions, enabling us to evolve.
>
> "But pseudogenes are not themselves 'jumping DNA' so how do they become scattered around the genome? The simple answer is that they 'hitch a lift.'
>
> "L1 is the only human mobile DNA that is known to be still actively moving to new chromosome locations. In addition the 'machinery' made by L1s to move themselves sometimes picks up gene copies, causing them to jump too."

There are approximately 8,000 well-defined pseudogenes of this type scattered throughout the genome, several of which have been identified as having new functions in specific human tissues. So 'jumping' DNA can help genes evolve.

A second class of pseudogene is found within "segmental duplications" where large segments of chromosomes are copied when the process of "crossing over" goes wrong. Crossing over of genetic material between chromosomes frequently happens between very similar DNA sequences. Normally, this is between the two copies of the same chromosome we each have in our cells, resulting in very little change in the chromosome's structure.

But by mobilising itself and other DNA sequences, L1 has generated lots of patches of DNA sequence that are very similar, increasing the chances that crossing over will go wrong. This has probably led to the duplication of large sections of the genome (up to 5% in total) and the generation of many more pseudogenes.

So there is strong evidence that L1s have played an important role in changing human DNA, and also that they are still doing it today. However very little is understood about how this process works during the transmission of DNA from parent to offspring, nor how often these jumps occur. Without knowing the rate at which L1 jumps, it is impossible to determine the effect that L1 is having on the modern genome.

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About BBSRC

This research has been funded by the Biotechnology and Biological Sciences Research Council (BBSRC), the UK funding agency for research in the life sciences. Sponsored by Government, BBSRC annually invests around £336 million in a wide range of research that makes a significant contribution to the quality of life for UK citizens and supports a number of important industrial stakeholders including the agriculture, food, chemical, healthcare and pharmaceutical sectors.

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