NEW HOT PAPERS - 2008

September 2008

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Kerstin Lindblad-Toh talks with *ScienceWatch.com* and answers a few questions about this month's New Hot Paper in the field of Molecular Biology & Genetics.

Field: Molecular Biology & Genetics
Article Title: Genome of the marsupial Monodelphis domestica reveals innovation in non-coding sequences
Authors: Mikkelsen, TS, et al.
Journal: NATURE
Volume: 447
Issue: 7141
Page: 167-U1
Year: MAY 10 2007
* MIT, Broad Inst, 7 Cambridge Ctr, Cambridge, MA 02142 USA.
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(Addresses have been truncated)

SW: Why do you think your paper is highly cited?

There are two primary reasons why the paper is highly cited: it described the first marsupial genome sequence and a comparison between this genome and those of placental mammals. Secondly, it provided major insights on how vertebrate genomes evolve. It showed that regulatory elements account for a large portion of the novel innovation within the placental lineage and that many of these novel elements appear to have arisen from transposable elements.

SW: Does it describe a new discovery, methodology, or synthesis of knowledge?

It describes a new discovery that roughly one-fifth of the conserved non-coding elements (regulatory elements) in placental mammals are novel innovations since the common ancestor of the marsupial and placental mammals and that the origin of these elements is commonly from repetitive elements. Thus it appears that innovation occurs largely by new regulation rather than by the introduction of new genes.

"I want to continue to understand both the function and evolution of the human genome so that we can identify genomic changes

SW: Would you summarize the significance of your paper in layman's terms?

This paper has important information about how mammals evolve. It suggested that the major changes in the genome that lead to evolutionary changes in body plans and development of mammals are caused by changes that regulate when and how much of a protein is produced rather than by the addition of novel proteins.

SW: In this paper we also discovered that these novel signals of regulation often arise from repeat sequences, the portion of the genome that is often called "junk-

DNA." Our discovery therefore could suggest that mammalian genomes contain such a lot of junk DNA because it has been useful for allowing us to evolve and develop.

that underlie human disease."

How did you become involved in this research, and were there any problems along the way?

SW: I became involved in this project by writing a proposal to the National Human Genome Research Institute (NHGRI) together with several members of the genetics and genomics community. Our goal was to be able to study the genome of the opossum and compare marsupial and placental mammals to better understand the human genome through this comparison. Like all genome projects this was a large collaborative project requiring the expertise and hard work of a few hundred people, so coordinating these efforts was a critical part.

SW: Where do you see your research leading in the future?

I want to continue to understand both the function and evolution of the human genome so that we can identify genomic changes that underlie human disease.

SW: Do you foresee any social or political implications for your research?

There should be no specific social or political implications of this research, other than that it reinforces the importance of natural evolution.

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Keywords: marsupial genome sequence, monodelphis domestica, how vertebrate genomes evolve, placental lineage, mammalian genomes, genomic changes, junk DNA.

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