

Re: Article: Different codons, same amino acid

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From: William L Hunt (wlhunt_at_earthlink.net)

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Prokaryotes that have very biased GC or AT genomes will look very different in the codons used (including synonymous codons) and their pool of tRNA species. They are sometimes referred to as using different "dialects" of the genetic code. By weighting the pool of tRNA species, translation will be faster and more efficient. It can be optimized for a particular dialect in prokaryotes with biased genomes.

Since mammals and other vertebrates have an overall genome bias of only about 45% GC, it would seem there is no way to take advantage of using heavily weighted tRNA pools. But because the genome of mammals is composed of GC-rich and AT-rich isochores, it is possible they are using two different dialects to get faster and more efficient translation than would be possible using a single dialect with an unweighted pool of tRNAs. Apparently some tissue cells may be using an AT-rich dialect and others a GC-rich dialect.

I am somewhat dubious that all this is occurring but the possibility is quite interesting.

William L Hunt

On Wed, 18 Aug 2004 14:39:08 +0000 (UTC), "Robert Karl Stonjek" <rstonjek@bigpond.net.au> wrote:

>*Different codons, same amino acid*
>*Study shows that synonymous codon usage varies in human tissues, perhaps due to evolution*
>
>*By Melissa Phillips*
>
>*The genomes of species from bacteria to Drosophila show unique biases for particular synonymous codons—varying triplet base pairs that code for the same amino acids—but it has been unclear if such codon preferences exist in mammals. In a paper published in PNAS this week, a group led by Joshua B. Plotkin of the Bauer Center for Genomic Research at Harvard shows that cell usage of synonymous codons is systematically different between human tissues. In addition, the authors make a case that these codon choices result from evolutionary selection.*
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>Plotkin and his colleagues analyzed genes expressed preferentially in six
>human tissues—brain, liver, uterus, testis, ovary, and vulva—and found
>synonymous codon biases between gene sets. In particular, they compared
>brain-specific genes to liver-specific genes; uterus genes to testis genes;
>and ovary genes to vulva genes. All three pairs differed significantly from
>each other in their synonymous codon usage.
>"We can even predict which genes are turned on in which tissues largely on
>the basis of their synonymous codon usage," Plotkin told *The Scientist*.
>"These codon biases may be partly responsible for determining which genes
>are expressed in which tissues."
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>Previous studies have shown functional selection of codons in simpler
>organisms, Plotkin said. Mammalian genomes, however, are complicated by the
>presence of isochores, long stretches of homogeneous DNA sequence that are
>biased to be either rich or poor in GC content.
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>"Most mammalian genomes have huge variations in GC content from region to
>region, and that controls codon usage to a large degree," Plotkin said.
>"People haven't normally thought that codon usage could have any sort of
>functional importance, because it seems to be controlled by which isochore
>the gene happens to fall in. But the fact that we find such systematic
>differences between tissues is suggestive that there really is some
>functional reason."
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>One possible mechanism linking synonymous codon choice and tissue-specific
>gene expression is local transfer RNA abundance, Plotkin said. "The tRNA
>pools may differ in brain from the pools in liver, and so if the codon usage
>of a gene is calibrated to the tRNA pools that exist in the brain, that gene
>will be translated more efficiently in brain." Other mechanisms could also
>be at work, Plotkin said, such as mRNA modifications or secondary structure.
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>In a second part of the study, Plotkin and his colleagues compared codon
>preference in human tissue genes to orthologous genes in the mouse. Previous
>work has shown that base usage is similar between human and mouse not only
>in coding sequences, but also in untranslated regions, hinting that
>selection is not responsible for codon similarities. Plotkin's team found
>that codon usage for brain-specific genes is significantly more similar
>between the two species than would be expected by chance, even when
>controlling for sequence similarity between the two genomes.
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>Read the rest at *TheScientist*
><http://www.biomedcentral.com/news/20040817/01>
>
>Posted by
>Robert Karl Stonjek
>
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