

Re: Symmetry of DNA replication

Source: <http://sci.tech-archive.net/Archive/sci.bio.evolution/2008-01/msg00100.html>

- *From:* Ron O <rokimoto@xxxxxxx>
 - *Date:* Sat, 26 Jan 2008 23:54:31 -0500 (EST)
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On Jan 26, 12:18 am, "Graham Jones" <x...@xxx> wrote:

"Ron O" <rokim...@xxxxxxx> wrote in message

[news:fnd9kv\\$1kh9\\$1@xxxxxxxxxxxxxxxxxxxxxxxxxxxx](mailto:news:fnd9kv$1kh9$1@xxxxxxxxxxxxxxxxxxxxxxxxxxxx)

On Jan 22, 10:29 pm, "Graham Jones" <x...@xxx> wrote:

"Ron O" <rokim...@xxxxxxx> wrote in message

Why are you using data from this paper. Hall states that his substitution pattern is very different from the usual found and he is only using two genes and two studies to base his frequencies on.

Beats me why they find this substitution pattern. We usually see transitions equalling transversions in a particular sequence after quite a lot of substitutions have occurred (a long divergence time between taxa), and Halls deletion frequency seems to be high too. Transitions occur at a rate of around 2:1, but as double hits start occurring the ratio moves toward 1:1 and can probably go even lower, but by that time you'd have trouble claiming homology for the sequences. The reason for the ratio changes over time is that transversions tend to remain because transitions are more common, and a back transversion is less likely. A transversion tends to stay a transversion because additional transitions at the same site will still identify it as a transversion, while a new transition at a site where a transition occurred will change the site back to the original sequence.

As I said earlier, Hall's figures are for spontaneous mutations of base-pairs, before selection has had an effect, not accepted mutations. The

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usual transition/transversion ratio is more like 2:1 for accepted mutations, because transitions are less likely to cause deleterious mutations. Deletions are very likely to be deleterious, so few will be accepted.

This is only true for a fraction of the nucleotide codon positions (some third position sites), and I guess some similar residue substitutions. You can see the same ratio skew in noncoding DNA sequence. Just think your explanation cannot explain the skew for the simple fact that transversions should be occurring at completely the opposite ratio (1:2). Why would the ratio go flat over time and multiple substitutions at the same site? For some mitochondrial sequences the skew can be over 50:1 in noncoding regions.

Just check out Halls data and what he is considering a substitution. I don't know what he did. If he is looking at the difference between EBG and Lac Z (I think that there is less than 35% amino acid sequence similarity between them) I'd expect the t:v ratio to be flat. If he has sequenced a large number of EBG sequences from the same clonal source and not between species (whatever a bacterial species is) then E. coli might have a different mutational profile.

Ron Okimoto

I wouldn't use Hall's figures directly (except perhaps for non-coding regions of E. Coli DNA). My answer to William L Hunt may give you a hint as to how I might use them, or rather, the symmetry they imply, more generally.

Graham– Hide quoted text –

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