

## Re: Junk DNA: A hypothesis

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**From:** Tim Tyler (*tim\_at\_tt1lock.org*)

**Date:** 01/22/05

Date: Sat, 22 Jan 2005 13:01:45 -0500 (EST)

Larry Moran <lamoran@bioinfo.med.utoronto.ca> wrote or quoted:

> *On Thu, 20 Jan 2005 23:53:54 -0500 (EST),*

> *Tim Tyler <tim@tt1lock.org> wrote:*

> > *jeffp <jeff@brilliantwebsites.com.au> wrote or quoted:*

> > > *Could it be that the junk DNA is a library of spare parts...a warehouse*

> > > *of previously resolved problems awaiting the next eon when its*

> > > *re-expression might be of value?*

> >

> > *[...]*

> >

> > > *Maybe this is something that has been raised and possibly even rejected*

> > > *before...but given that I've never seen it before, I thought I'd come*

> > > *to some people who would know. Any comments or references to*

> > > *pre-existing work?*

> >

> > *There are dozens of theories of possible "functions" of "junk" DNA.*

>

> *Indeed there are. Let's see if any of them make sense ....*

>

> > *Junk DNA affects linkage – and the probability that genes are*

> > *split during meiosis – and if that probability is small it*

> > *can help some deleterious genes form selfish cartels.*

>

> *This one doesn't make any sense.*

>

> > *Another theory is that introns decrease the probability of*

> > *crossovers occurring in the middle of functional genes – and*

> > *turn meiosis into more of a proper shuffle – rather than*

> > *a shuffle that rips cards apart and glues them together again.*

>

> *This one is dead wrong.*

>

> > *Another theory is that "junk" DNA improves evolvability by*

> > *creating "neutral networks".*

>

> *This one is "evo-babble" from people who don't understand evolution.*

>

- > > *Selection for small program size in genetic algorithms can hinder*
- > > *evolvability by eliminating intermediate forms that lie between*
- > > *adaptive peaks.*
- >
- > *More "evo-babble" – in this case it's from computer scientists.*

I don't agree with these assessments – except for the case of the first "linkage" hypothesis – where you might well be correct.

I'd be particularly interested in hearing any evidence against the second hypothesis (that junk DNA allows a less destructive shuffle to take place). I'm relatively new to that idea.

My impression is that the effect is likely to generate a selection pressure favouring spacing out genes – and that it would be worthwhile attempting to quantify the effect.

On what grounds do you describe the idea as "dead wrong"?

- > > *Also, DNA harbours multiple regions such as LINE-1. These*
- > > *act as mutagens – and are likely to be directly deleterious.*
- > >
- > > *However they generate a different pattern of mutations from (say)*
- > > *cosmic rays. They generate patterns of mutations that affect*
- > > *different regions of DNA more frequently than others. That*
- > > *whole set-up could serve some functional purpose.*
- >
- > *There's no way that a population could select for enhanced deleterious*
- > *mutations on the remote chance that some of them will be beneficial every*
- > *million years or so. That sort of thing would require an intelligent*
- > *designer with foresight.*

That was essentially Williams view in 1966 – that organisms could not do anything but attempt to minimise their mutation rate.

IMO, that's not correct.

The issue of to what extent organisms do this is one of the relative strengths of species and individual-level selection – and I don't think anyone can authoritatively answer such questions today.

- > > *We know that some evolution takes the form of duplication and*
- > > *modification. Rapid elimination of unnecessary non-functional*
- > > *genes might significantly hamper this process.*
- >
- > *It might. But once again you are postulating selection for some future*
- > *possibility.*

I wasn't doing that here – or anywhere else.

- > *In this case you suggest that junk DNA has to be kept around*
- > *because it might become useful in the future. How does an individual know*
- > *that it needs to store excess DNA in its genome because there's a small*
- > *chance that one of its descendants might find a use for it at some time*
- > *in the far distant future?*

Modern organisms tend to be products of past events – and are not constructed in anticipation of future ones. They are typically constructed as though the future environment is expected to be like the ancestral one was.

I never suggested that the future in which evolvability might pay off would have to be very distant. Evolvability is needed all the time in populations where pathogens are present.

- > *Note that the genomes of bacteria appear to be under selection for small*
- > *size so they can replicate quickly. That's why they don't have very much*
- > *junk DNA.*

Indeed.

- > *If your speculation is correct then there should have been much less*
- > *gene duplication and divergence in bacterial lineages. Does the data*
- > *lend support to your speculation?*

It's not \*my\* hypothesis – as my reference should illustrate.

I am not aware of any investigation of the issue on the basis of examination of related organisms. It seems to me that there would be many confounding factors if any attempt to compare organisms on very different scales to investigate the point was made. I'm rather sceptical about whether such a study would reach any useful conclusion.

It seems to me that a useful approach would be deliberately excising the "junk" DNA from small organisms and seeing how they fare over an extended period in comparison with wild-types.

- > > *Some references to theories of the "function" of "junk" DNA:*
- > >
- > > *"Inserting introns improves genetic algorithm success rate:*
- > > *Taking a cue from biology"*
- > >
- > > – <http://citeseer.nj.nec.com/context/17647/246003>
- >
- > *This seems to be mostly computer scientists discussing biology. I didn't*
- > *see anything there that's worth remembering. Perhaps you could summarize*
- > *their very best argument for the selective advantage of excess genomic*
- > *DNA?*

I don't know if I'm competent to judge that.

sci.bio.evolution: Re: Junk DNA: A hypothesis

The hypothesis about avoiding breaking genes seems to be a good one – and needs further investigation. That's also true of the "neutral network" theory.

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|im |yler <http://timtyler.org/> tim@ttllock.org Remove lock to reply.