

## Re: Non-Coding DNA preserved by genetic drift?

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- *From:* "rev.goetz" <jimgoetz316@xxxxxxxx>
  - *Date:* Wed, 21 Dec 2005 20:14:00 -0500 (EST)
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whitesickle@xxxxxxx wrote:

- > I don't know if the following is accurate. If so it raises many
- > interesting questions and possibilities:
- >
- > "The data suggest it is genetic drift (an evolutionary force whose main
- > component is randomness), not natural selection, that preserves junk
- > DNA and other extraneous genetic sequences in organisms. When
- > population sizes are large, drift is usually overpowered by natural
- > selection, but when population sizes are small, drift may actually
- > supersede natural selection as the dominant evolutionary force, making
- > it possible for weakly disadvantageous DNA sequences to accumulate.
- > Junk DNA costs energy to duplicate and to carry around as part of each
- > cell. So natural selection operates against it. But if junk DNA gets
- > generated by errors in replication faster than natural selection can
- > select against it then junk DNA can accumulate."
- >
- > A Few questions. If mutations caused by genetic drift are neither
- > harmful or beneficial then what use are they? I get the impression they
- > can be possibly disadvantageous. Secondly, it seems to me natural
- > selection is the most important in evolution, not genetic drift or
- > anything else. I surmise to a biologist this is a simple headed and
- > erroneous way of looking at evolution. Rather the whole picture should
- > be viewed. However, it does seem genetic drift operates the most in
- > small populations and therefore it had more evolutionary importance in
- > the past. Assuming, "The data suggest it is genetic drift (an
- > evolutionary force whose main component is randomness), not natural
- > selection, that preserves junk DNA and other extraneous genetic
- > sequences in organisms" what role does natural selection play in junk
- > DNA? Is it largely decoupled from genetic drift and junk DNA? The
- > article states, "The researchers found that a consistent pattern
- > emerged when genomic characteristics of bacteria and various eukaryotes
- > were plotted against the species' total genome sizes. Bigger species,
- > such as salmon, humans and mice, tended to have small, long-term
- > population sizes, more genes, more junk DNA and longer-lived gene
- > duplications. Almost without exception, the species found to have
- > large, long-term population sizes, fewer genes, less junk DNA and
- > shorter-lived gene duplications were bacteria. The data suggest it is
- > genetic drift (an evolutionary force whose main component is

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- > randomness), not natural selection, that preserves junk DNA and other
- > extraneous genetic sequences in organisms. When population sizes are
- > large, drift is usually overpowered by natural selection, but when
- > population sizes are small, drift may actually supersede natural
- > selection as the dominant evolutionary force, making it possible for
- > weakly disadvantageous DNA sequences to accumulate."
- >
- > So my questions are what role does genetic drift play in "junk" DNA and
- > what role does natural selection (the coding region) play in "junk
- > DNA". And how the two may effect "junk DNA".
- >
- > Michael Ragland
- >
- >
- >
- > November 25, 2003
- > Junk DNA Result Of Slowness Of Natural Selection
- > Species that replicate at a slower rate and that are fewer in number do
- > not experience enough selective pressure to prevent junk DNA from
- > accumulating
- >
- > Genetic mutations occur in all organisms. But since large-scale
- > mutations -- such as the random insertion of large DNA sequences within
- > or between genes -- are almost always bad for an organism, Lynch and
- > University of Oregon computer scientist John Conery suggest the only
- > way junk DNA can survive the streamlining force of natural selection is
- > if natural selection's potency is weakened.
- >
- > When populations get small, Lynch explained, natural selection becomes
- > less efficient, which makes it possible for extraneous genetic
- > sequences to creep into populations by mutation and stay there. In
- > larger populations, disadvantageous mutations vanish quickly.
- >
- > Most experts believe that the first eukaryotes, which were probably
- > single-celled, appeared on Earth about 2.5 billion years ago.
- > Multicellular eukaryotes are generally believed to have evolved about
- > 700 million years ago. If Lynch's and Conery's explanation of why
- > bacterial and eukaryotic genomes are so different is true, it provides
- > new insights into the genomic characteristics of Earth's first
- > single-celled and multicellular eukaryotes.
- >
- > A general rule in nature is that the bigger the species, the less
- > populous it is. With a few exceptions, eukaryotic cells are so big that
- > they make most bacteria look like barnacles on the side of a dinghy. If
- > the first eukaryotes were larger than their bacterial ancestors, as
- > Lynch believes, then their population sizes probably went down. This
- > decrease in eukaryote population sizes is why a burgeoning of
- > large-scale mutations survived natural selection in the first
- > single-celled and multicellular eukaryotes, according to Lynch and
- > Conery.
- >

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- > To estimate long-term population sizes of 50 or so species for which
- > extensive genomic data was available, Lynch and Conery examined
- > "silent-site" mutations. Silent-site mutations are single nucleotide
- > changes within genes that don't affect the gene product, which is a
- > protein. Because of their unique characteristics, silent-site mutations
- > can't be significantly influenced by natural selection. The researchers
- > were able to calculate rough estimates of the species' long-term
- > population sizes by assessing variation in the species' silent-site
- > nucleotides.
- >
- > Of the original group of sampled organisms, Lynch and Conery selected a
- > subset of about 30 and calculated, for each organism, the number of
- > genes per total genome size as well as the longevity of gene
- > duplications per total genome size. They also calculated the
- > approximate amount of each organism's genome taken up by DNA sequences
- > that do not contain genes.
- >
- > The researchers found that a consistent pattern emerged when genomic
- > characteristics of bacteria and various eukaryotes were plotted against
- > the species' total genome sizes. Bigger species, such as salmon, humans
- > and mice, tended to have small, long-term population sizes, more genes,
- > more junk DNA and longer-lived gene duplications. Almost without
- > exception, the species found to have large, long-term population sizes,
- > fewer genes, less junk DNA and shorter-lived gene duplications were
- > bacteria.
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- > The data suggest it is genetic drift (an evolutionary force whose main
- > component is randomness), not natural selection, that preserves junk
- > DNA and other extraneous genetic sequences in organisms. When
- > population sizes are large, drift is usually overpowered by natural
- > selection, but when population sizes are small, drift may actually
- > supersede natural selection as the dominant evolutionary force, making
- > it possible for weakly disadvantageous DNA sequences to accumulate.
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- > Junk DNA costs energy to duplicate and to carry around as part of each
- > cell. So natural selection operates against it. But if junk DNA gets
- > generated by errors in replication faster than natural selection can
- > select against it then junk DNA can accumulate..
- >
- > At some point in the 21st century, barring some natural or human-caused
- > disaster, biotechnology will advance far enough to make it possible to
- > edit out junk sequences from cells. So it should become possible to
- > have offspring that have far fewer junk DNA sequences. Therefore junk
- > DNA may eventually disappear from the human species. Also, replacement
- > organs will eventually be genetically enhanced with more beneficial
- > variants of genes that play important roles in each organ type. It
- > seems reasonable to expect that at least some people will opt to have
- > their DNA edited to eliminate junk DNA sequences from cells that will
- > be used to grow replacement organs. So even some of us who today are
- > walking around with junk DNA will have less of it once we are able to
- > have replacement organs grown for us.

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- > Update: Carl Zimmer raises a number of specific objections against the
- > idea of removing junk DNA but he also sees one point in favor of doing
- > so: some junk DNA sections can hop around the genome and cause
- > mutations when they embed in new locations.
- >
- > There are also arguments for getting rid of junk DNA that Futurepundit
- > doesn't mention. When mobile elements jump around to new homes, they
- > can trigger diseases as they mutate the genome.
- >
- > As for mobile elements that jump around the genome: Yes, note that this
- > reason for removing junk DNA is especially strong in the case of stem
- > cells that are going to be used to grow replacement organs. The cells
- > in those replacement organs (with the exception of testes and ovaries)
- > are not going to have their DNA passed along to progeny and therefore
- > the ability of their junk DNA to mutate to create new environmental
- > adaptations provides no benefit while the junk DNA does pose a
- > mutational threat that can result in cancer and other diseases.
- >
- > The effects of removing various junk sequences will be testable by
- > producing organs without them and then seeing how those organs perform.
- > This will be relatively less risky to experiment with in the case where
- > humans have two of an organ. So, for instance, one could have just one
- > kidney replaced with a junk-free kidney and then, with the other kidney
- > still available as back-up, the functionality of the junk-free kidney
- > could be monitored over time. The same could be done with many muscles.
- > Replace a thigh muscle with a junk-free thigh muscle. If the thigh
- > muscle fails the result is unlikely to be fatal. There would still be
- > risks from such an experiment as one could imagine fatal failure modes
- > where, for instance, an organ releases toxins or clotting factor or
- > something else that damages some other more critical part of the body.
- >
- > Next he raises the point that what seems like junk DNA might not really
- > be junk DNA.
- >
- > Junk-free genomes may indeed become possible in the future, but they're
- > probably not a wise idea. Even if junk DNA doesn't benefit us in any
- > obvious way, that doesn't mean that we can do without it. Many
- > stretches of DNA encode RNA which never become proteins, but that
- > doesn't make the RNA useless--instead, it regulates the production of
- > other proteins. Some broken genes (known as "pseudogenes") may no
- > longer be able to encode for proteins, but they can still help other
- > genes produce more of their proteins
- >
- > Well, my response to this is pretty simple: Yes, it is hard to be
- > certain that some DNA section has no benefit to the cell. But suppose
- > at some point in the future we can assign a really high probability to
- > the idea that some chunk of DNA has no value and that it actually is
- > far more likely to cause disease than benefit? Why not then remove it?
- >
- > This reminds of another point: Some genetic theorists make the argument

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- > that we each have dozens and perhaps hundreds of purely harmful
- > mutations because natural selection can't select out harmful mutations
- > as fast as they are generated by mutations that occur during
- > reproduction. If this argument is correct (and I believe it is) then we
- > should also have junk DNA that is either of no value or harmful.
- > Someone who holds this more pessimistic view of our genomes as full of
- > flaws and parasitic DNA sections is going to tend to be more willing to
- > decide to throw out the suspected junk with the view that the odds are
- > great that the suspected junk really is junk. Of course, there's no
- > rush here and we ought to wait a couple of decades for a lot more
- > evidence to accumulate before acting on this belief.
- >
- > Zimmer also brings up the argument that simply by making the genome
- > bigger that junk DNA may serve a useful function by making cells the
- > correct size. I'm skeptical of this argument mostly because an
- > assortment of different kinds of intracellular components cross-react
- > with each other in undesirable ways and turn into compounds that the
- > cell can not eject or destroy. As a result, cells accumulate junk and
- > this junk accumulation robs the cells of needed space and decreases the
- > efficiency of cells as they age as well. The junk also serves as a
- > source of free radical generation. This problem with junk accumulation
- > has even led Aubrey de Grey to argue for the transfer of lysosomal
- > enzymes from other species into humans as a rejuvenation treatment.
- > Analogously, genomal junk is taking up space that could be used by
- > cells to do useful work. Get rid of it and the cells might become ever
- > so slightly more efficient.
- >
- > Next Zimmer brings up the value of junk DNA and, in particular,
- > pseudogenes, as potential sources of future beneficial mutations:
- >
- > It's on this evolutionary scale where purging junk DNA makes the least
- > sense. The pasting and copying of junk DNA is a major source of new
- > genetic variation. Instead of changing a nucleotide here or there,
- > mobile elements can shuffle big stretches of DNA into new arrangements,
- > taking regulatory switches and other genetic components and attaching
- > them to different genes. While some of this variation may lead to
- > diseases, it also prepares our species to adapt to new environmental
- > challenges. (Similarly, pseudogenes that are truly broken still have
- > the potential to become working genes again. Some scientists have
- > proposed calling them "potogenes.")
- >
- > Here's my problem with that argument: Natural selection is going to
- > cease to be the major source of new beneficial mutations in humans
- > within 20 or 30 years. We are going to have our genomes changed by
- > bioengineering. Therefore junk DNA will have no value to us. Going into
- > future centuries our bioengineering techniques will advance even
- > further and we will be able to simulate the effects of variations
- > orders of magnitude more quickly than mutations occur naturally.
- >
- > There's another point about junk DNA that especially holds for
- > agricultural plants and animals: to the extent that junk DNA can be

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- > removed from crops and livestock a source of variability is removed
- > that essentially serves as noise. If someone develops some ideal dairy
- > cow and wants to clone it he does not want jumping genes creating
- > variations that cause some of them clones to produce less milk.
- > Similarly, jumping genes could create variations in the growth of corn
- > or wheat that would be undesirable.
- >
- > It should be possible to grow up replacement organs in other species
- > first and to try out junk removal in organs and whole genomes in other
- > species before trying it out in humans. This will provide an important
- > way to discover functional purposes served by parts of genomes that are
- > mistakenly thought to be junk. The mechanisms by which those parts
- > serve useful functions will then be able to be searched for in humans
- > as well. In my view, the discovery of which sections of the genome
- > really are junk is a technical challenge that will be solved with time.
- > Once purely junk sections are identified with a fairly high probability
- > of correct classification and techniques for removing it are developed
- > it seems inevitable that more daring individuals will opt to try to
- > have the junk removed from their replacement organs and progeny.
- >
- > By Randall Parker at 2003 November 25 01:39 AM Evolutionary History

This may help to answer your questions.

"Perhaps due to mechanical reasons, the rate of mutational insertions from repeated sequences appears to be significantly more frequent than the rate of mutational deletions. And as long as the mutation rate for the number of neutral nucleotide site insertions exceeds the fixation rate for all nucleotide site deletions, genome sizes will expand over evolutionary time. This appears to be the rule for many multicellular lineages that have little or no constraints concerning genome size, but exceptions include birds because birds may have better fitness when their genome size is compacted."

So this explains how random drift can accumulate DNA with no function.

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• **References:**

◆ **Non-Coding DNA preserved by genetic drift?**

◇ From: whitesickle@xxxxxxx

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