How Scientific Evidence is Changing the Tide of the Evolution vs. Intelligent Design Debate

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Document Revision History

Date	Description
6/17/2007	ENCODE results put the final nail in the "Junk DNA" coffin.
4/28/2007	Added another piece of research showing that transposons play an active role in embryonic development.
1/20/2007	Added another example of perfect DNA sequence conservation between species.
1/11/2007	- New evidence for LTR Retrotransposon function in humans and rodents - Added "Additional Web Resources" section at the end of the essay
1/7/2007	Added research article showing common function of an endogenous retrovirus shared by humans, chimpanzee, gorilla, orangutan, and gibbon
1/1/2007	Added section on the C-Value enigma
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1 Introduction

For the past few years there has been a relatively public battle between Evolution (Darwinism) and Intelligent Design (ID). In courtrooms, classrooms and even at the polls, ID has been mostly losing this battle. Meanwhile, with the completion of the human genome project and the sequencing of many other species, scientific discoveries are upending many long-held assumptions of the pro-evolution community, but they don't seem to realize it yet. The purpose of this article is to illuminate some of these discoveries and give hope to the ID community that steady, patient defense of our position will eventually win the war.

2 Junk DNA - from mostly Non-functional to mostly Functional

Would a Designer create "Junk"? Do most pro-evolution supporters believe that the majority of "non-coding" DNA is "Junk"? Does Junk DNA prove evolution? Let's explore!

What do top evolutionists think about Junk DNA? One of the front-line advocates of Darwinian evolution theory has been Professor Richard Dawkins (Dawkins) of Oxford University. He has published numerous pro-evolution books, one of the earliest of which was "The Selfish Gene" in 1976. In fact, it was in that book that Dawkins made it clear he believed important DNA was in the "genes", and that leftover Junk DNA was a logical consequence of genes striving to maximize themselves. There have been numerous reprints of "The Selfish Gene", including a 30th anniversary edition. Now fast-forward from 1976 to 1999. By 1999 the Intelligent Design movement had been born and many of its advocates as well as others in the scientific community had started questioning the basis of designating non-coding DNA as "Junk". However, Dawkins published an article called "The Information Challenge" that you can find on the "Australian Skeptics" website. I've included this link below as well as a permanent archive in case it is ever changed in the future. I think you can see from the quotes I've highlighted below, that Dawkins views about Junk DNA did not change between 1976 and 1999, in spite of the evidence.

> http://www.skeptics.com.au/articles/dawkins.htm
> http://web.archive.org/web/*/http://www.skeptics.com.au/articles/dawkins.htm
> *"And there's lots more DNA that doesn't even deserve the name pseudogene. It, too, is derived by duplication, but not duplication of functional genes.* ***It consists of multiple copies of junk, "tandem repeats", and other nonsense which may be useful for forensic detectives but which doesn't seem to be used in the body itself."***
>
> ***"Once again, creationists might spend some earnest time speculating on why the Creator should bother to litter genomes with untranslated pseudogenes and junk tandem repeat DNA."***
>
> *"****Can we measure the information capacity of that portion of the genome which is actually used? We can at least estimate it. In the case of the human genome it is about 2%*** *- considerably less than the proportion of my hard disc that I have ever used since I bought it."*

So Dawkins clearly considers 98% of human DNA to be non-functional (non-information carrying) junk. This article has been maintained by "Skeptics" and updated during 2006, so clearly that organization considers these views of Dawkins to be held by him today, and I cannot find any statements of Dawkins that would indicate otherwise.

I've interacted with other pro-evolution individuals who grudgingly admit that some of what used to be considered junk "may not be", but inevitably they will still argue that "the vast majority of non-coding DNA does not have any function". Why does this line of reasoning seem to be so important to evolutionists? I can think of two reasons. For one, if only 2% of human DNA is "functional", then there is a lot less information that had to be produced by random mutations and natural selection. If even 10% of the genome is functional, that would be 5 times more information. If 50% of the genome is functional, that means 25 times more information. Pretty soon the amount of information contained in the genomes of the various species proves to be enormous if it is attributed to evolution. Another reason "junk" appeals to the evolutionists is because it would seem to run counter to the idea of an Intelligent Designer (or Creator). We can see that in Dawkins' statements above. But, more importantly, pro-evolution websites have built major arguments in support of evolution based upon the idea of "shared errors" (shared junk), as proof of evolution.

The Talk Origins Archive, perhaps the number one pro-evolution website (along with "Pandas Thumb"), has two articles that rely on the "shared errors" argument in support of evolution. The Talk Origins authors detail a number of different classes of "Junk DNA" that they claim prove common descent.

> http://www.talkorigins.org/faqs/molgen/
> http://web.archive.org/web/*/http://www.talkorigins.org/faqs/molgen/
>
> http://www.talkorigins.org/faqs/comdesc/section4.html#transposons
> http://web.archive.org/web/*/http://www.talkorigins.org/faqs/comdesc/section4.html

Panda's Thumb also finds it important to argue for "Junk DNA":
> http://www.pandasthumb.org/archives/2005/12/another_example.html

In the rest of this section I will show how those arguments are being obliterated by the evidence pouring in from molecular biology and genetics research.

2.1 Tandem Repeats

Tandem Repeats are a class of repetitive DNA unique in every individual, which is why they are used in DNA forensic evidence, etc. As we saw earlier, Dawkins considers Tandem Repeats to be "junk/nonsense". Similarly, Talk Origins also has this to say about Tandem Repeats:

> *"scientists view tandem repeat sequences as resulting from accidental DNA duplications."*

Now let's look at what the scientific evidence is telling us about Tandem Repeats:

> **They Silence and Activate Genes**
> http://biology.plosjournals.org/perlserv/?request=get-document&doi=10.1371%2Fjournal.pbio.0040363
> *Tandem repeat sequences are frequently associated with gene silencing phenomena.*
>
> http://www.pnas.org/cgi/content/abstract/0602381103v1
> *This region contains the major and minor promoters of the Tsix gene, which runs antisense to Xist, and the* ***DXPas34 tandem repeat*** *lying close to the Tsix major promoter.*
>
> *Our results identify a function for* ***DXPas34*** *in murine XCI and demonstrate the critical role of Tsix transcription in preventing XCI in differentiating male ES cells and in normal functioning of the counting pathway.*
>
> http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?cmd=Retrieve&db=PubMed&list_uids=10649448&dopt=Abstract
> Transfection studies in mouse mesenchymal C3H10T1/2 cells showed that it is the tandem repeat of the C/EBP binding site in PPARgamma2 promoter region that regulates dexamethasone-mediated PPARgamma2 gene activation.
>
> http://www.ionchannels.org/showabstract.php?pmid=7499248
> These observations establish that a dinucleotide tandem repeat sequence, capable of self-association, forms part of a cell-specific silencer element in a mammalian gene.
>
> **They Determine the Length of a Dog's Nose**
> http://bric.postech.ac.kr/biotrend/science/science_view.php?nNum=94147
> *Breeds with collie-like noses had more of a particular tandem repeat, while those with pug-like faces had more of a different tandem. And when the researchers compared bull terrier DNA, they found that terriers have one more repeat unit than they did in the 1950s, which could explain why the nose used to be droopier, the researchers note.*
>
> **They Determine a Cow's Milk Fat Percentage**
> http://physiolgenomics.physiology.org/cgi/content/abstract/25/1/116
> *In addition to this, another polymorphism in the 5'-regulatory region of this gene, the DGAT1 variable number of tandem repeat (VNTR), also showed a strong association with milk fat percentage.*

These research finding show that, far from being junk, Tandem Repeats have important functional roles in the genome. More interestingly, the unique copy number in individuals seems not to be caused by random mutations, but rather by a built-in program that occurs during the combination of male and female DNA. While children will tend to inherit Tandem Repeat numbers similar to those of their parents, this variable component makes every child unique. The fact that Tandem Repeats are so well correlated to racial classifications shows that they have a role in determining what each individual looks like. Tandem repeats appear to be the major factor in what determines the size of your nose, the amount of body fat you have, your height, skin color, etc.

2.2 Transposons/Retrotransposons

Here's what Talk Origins says about Transposons:

> *In many ways, transposons are very similar to viruses. However, they lack genes for viral coat proteins, cannot cross cellular boundaries, and thus they replicate only in the genome of their host. They can be thought of as intragenomic parasites.*
>
> *…finding the same transposon in the same chromosomal location in two different organisms is strong direct evidence of common ancestry, since they insert fairly randomly and generally cannot be transmitted except by inheritance.*

The reason evolutionists consider Transposons as proof of common ancestry is because they believe them to be non-functional junk. If it turns out that they do have a function, then an alternative explanation for the same Transponson being in two separate species could be common design.

So is there evidence that Transposons have function?

> **They are Necessary for Embryonic Development**
> http://www.eurekalert.org/pub_releases/2007-04/sumc-dn041907.php
> http://www.pnas.org/cgi/content/abstract/0701811104v1
> *Many of those snippets were located in gene-free chromosomal expanses once described by geneticists as "gene deserts." These sections are, in fact, **so clogged with useful DNA bits** - including the ones Bejerano and his colleagues describe - that they've been renamed "regulatory jungles*
> …
> *It turns out that most of the segments described in the research paper cluster near genes that play a carefully orchestrated role during an animal's first few weeks after conception. Bejerano and his colleagues think that these sequences help in the intricate choreography of when and where those genes flip on as the animal lays out its body plan.*
> …
> *The 10,402 sequences … are remnants of unusual DNA pieces called **transposons** that duplicate themselves and hop around the genome.*
>
> http://www.medicalnewstoday.com/printerfriendlynews.php?newsid=14812
> *The research, published in the October issue of Developmental Cell, suggests that retrotransposons may not be just the "junk DNA" once thought, but rather appear to be a large repository of start sites for initiating gene expression. Therefore, more than one third of the mouse and human genomes, previously thought to be non-functional, may play some role in the regulation of gene expression and promotion of genetic diversity.*
>
> *Dr. Barbara B. Knowles and colleagues from The Jackson Laboratory in Bar Harbor, Maine, found that distinct retrotransposon types are unexpectedly active in mouse eggs, and others are activated in early embryos. Surprisingly, by acting as alternative promoters, retrotransposon-derived controlling elements drive the coordinated expression of multiple mouse genes.*
>
> *The researchers think that expression of retrotransposons during very early stages may contribute to the reprogramming of the mammalian embryonic genome, a prerequisite for normal development.*
>
> **They Format the Genome File System…**
> http://content.karger.com/ProdukteDB/produkte.asp?Aktion=ShowAbstract&ArtikelNr=84942&Ausgabe=230866&ProduktNr=224037

Generic repeated signals in the DNA format expression of coding sequence files and organize additional functions essential for genome replication and accurate transmission to progeny cells. Retroelements comprise a major fraction of many genomes and contain a surprising diversity of functional signals.

That is just the beginning. Now let's examine specific classes of Transposons mentioned in the two Talk Origins Articles.

2.2.1 SINE/Alu Sequences

The Talk Origins view of SINEs/Alu:

> *…current evidence suggests that only a very few Alu sequences are active sources of transcripts; perhaps transcription from most copies is inhibited by the chromosomal environment of the insertion*
>
> *Further, the excellent health of individuals who lack particular Alu insertions supports the view that these insertions do not serve any important function in human physiology.*

What does the recent scientific evidence say about SINEs/Alu?

> **Alu can turn a single gene into multiple proteins**
> http://www.genomenewsnetwork.org/articles/05_03/junk.shtml
> *Through a process called alternative splicing, humans create multiple versions of a gene and, consequently, multiple proteins. It's a way of constructing a new protein, while keeping a backup copy of the original version.*
>
> *For example, the researchers found that the ADAR2 enzyme contains 40 amino acids in its active site that are derived from an Alu element. The addition changes the activity of the enzyme.*
>
> *http://www.genpromag.com/ShowPR~PUBCODE~018~ACCT~1800000100~ISSUE~0405~RELTYPE~PR~ORIGRELTYPE~GPF~PRODCODE~00000000~PRODLETT~G.html*
> *"The excitement about the exonization of Alu is the ability to explain what is unique in our genome," Ast says. The mouse genome contains 2.5 billion nucleotides, the human genome around 3 billion. "The quarter of a billion nucleotides, [or] the difference between human and mouse, is mostly [due to] retrotransposable elements like Alu ," he says.*
>
> **They affect Micro-RNA processing**
> *http://arrowsmith.psych.uic.edu/arrowsmith_uic/tutorial/smalheiser_tig_preprint_2006.pdf*
> *Although Alu was originally thought to represent 'junk' having no biological functions, the presence of Alu sequences within protein-coding genes can affect the processing of mRNAs at multiple levels*
>
> **Highly Conserved Vertebrate SINEs with unknown function**
> http://www.genome.org/cgi/content/full/12/2/316?ck=nck
> *Extensive conservation of V-SINEs can, however, be more easily explained by the hypothesis that the central conserved domain may somehow "earn its keep" in the genome.*
>
> *http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=1484453*
> *The observed conservation strongly indicates that the central domain of these transposable elements have been exapted, i.e., have become a functional component of the mammalian genomes.*
>
> http://www.eurekalert.org/pub_releases/2006-05/hhmi-mdp050206.php
> *The close copies of the ultraconserved element scattered around vertebrate genomes have changed less than would be expected over evolutionary time, indicating that they are functionally important. But relatively few of the copies contain parts that code for proteins, which suggests they instead are helping to regulate when genes are turned on and off.*
>
> http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?cmd=Retrieve&db=PubMed&list_uids=16717141&dopt=Abstract
> *"Thus, AmnSINE1 appears to be the best example of a transposable element of which a significant fraction of the copies have acquired genomic functionality."*

So many SINES have been shown to be FUNCTIONAL, counter to the Talk Origins claims. Alu sequences are unique to primates and seems to be particularly active in the human brain.

2.2.2 LINES

Talk Origins has this to say of LINES:

> *LINEs thus have several properties expected of "selfish" DNA sequences that can spread in the host DNA simply because they encode their own machinery for spreading.*

In other words, they don't serve a purpose other than to copy themselves, according to Talk Origins.

Here's what some recent scientific evidence says about LINES:

> **Human LINE-1 sequences being investigated for function**
> http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=539998&tools=bot
> *Long interspersed elements (LINE-1, L1s) are the only active autonomous retrotransposons in mammals, covering as much as 18% of their genomes. L1s' activity results in a great repertoire of actions, such as gene disruption, transcriptional regulation, alternative splicing, creation of exons and gene coding regions and amplification of the processed pseudogenes and the Alu SINE family.*
>
> **A LINE-2 sequence which functions as a potent T-cell-specific silencer**
> http://hmg.oxfordjournals.org/cgi/content/full/8/9/1723
> *In summary, we have identified a LINE-2 fragment named ALF that is a potent T-cell-specific silencer. We also show that agonists that down-regulate ALF-containing genes in T cells induce a factor that binds to a sequence within ALF. These findings are in contrast to other reports associating enhancer or promoter activities with repetitive elements (16,17), because ALF has the potential to function as a cell-type-specific silencer. We favour the hypothesis that this is not an arbitrary activity, and that ALF contributes to gene regulation in vivo.*
>
> **LINE-1 sequences modify RNA expression**
> http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?cmd=Retrieve&db=pubmed&dopt=Abstract&list_uids=15152245
> *Because L1 is an abundant and broadly distributed mobile element, the inhibition of transcriptional elongation by L1 might profoundly affect expression of endogenous human genes. We propose a model in which L1 affects gene expression genome-wide by acting as a 'molecular rheostat' of target genes. Bioinformatic data are consistent with the hypothesis that L1 can serve as an evolutionary fine-tuner of the human transcriptome.*
>
> **LINE-1 may have a role in DNA Repair**
> http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?cmd=Retrieve&db=pubmed&dopt=Abstract&list_uids=12006980
> *Thus, our results suggest that LINE-1s can integrate into DNA lesions, resulting in retrotransposon-mediated DNA repair in mammalian cells.*
>
> http://www.genome.org/cgi/content/abstract/10/4/411
> *Extrapolating these findings to the 600,000 copies of L1 in the genome, we predict that the amount of DNA transduced by L1 represents ~1% of the genome, a fraction comparable with that occupied by exons*

So again, there are plenty of examples now of functional LINES.

2.2.3 Endogenous Retroviruses and LTR retrotransposons

Talk Origins has this to say of Endogenous Retroviruses:

> *Endogenous retroviruses are molecular remnants of a past parasitic viral infection. Occasionally, copies of a retrovirus genome are found in its host's genome, and these retroviral gene copies are called endogenous retroviral sequences.*

Essentially all of these endogenous retroviruses contain mutations that would disrupt the function of their genes, as would be expected if they inserted millions of years ago with no selective pressure to maintain the function of the genes.

Here's what some recent scientific evidence says about Endogenous Retroviruses:

They show up expressed in many cell tissues
http://jvi.asm.org/cgi/content/full/79/1/341
*Human tissues that lack HERV transcription **could not be found**, confirming that human endogenous retroviruses are permanent components of the human transcriptome. Distinct activity patterns may reflect the characteristics of the regulatory machinery in these cells, e.g., cell type-dependent occurrence of transcriptional regulatory factors.*

ERVWE1 provirus necessary for placental development in humans, chimpanzee, gorilla, orangutan, and gibbon (common function – not shared error)
http://www.pnas.org/cgi/content/full/101/6/1731
We show in this article that the ERVWE1 locus is functionally preserved in the human population and in the identified orthologous locus of chimpanzee, gorilla, orangutan, and gibbon.

Functional LTR promoters for Neuronal apoptosis inhibitory protein (NAIP) in Humans and in Rodents
http://genetics.plosjournals.org/perlserv/?request=get-document&doi=10.1371/journal.pgen.0030010
*In human, an LTR serves as a tissue-specific promoter, active primarily in testis. However, in rodents, our evidence indicates that an ancestral LTR common to all rodent genes is the major, constitutive promoter for these genes, and that a second LTR found in two of the mouse genes is a minor promoter. Thus, independently acquired LTRs have assumed regulatory roles for orthologous genes**, a remarkable evolutionary scenario**.*
…
We offer a number of potential explanations, including the intriguing possibility that it may be advantageous for anti-cell death genes like NAIP to use ERVs to control their expression. These results support the view that not all retroviral remnants in our genome are simply junk DNA.

They are required for placental development in sheep
http://agnews.tamu.edu/dailynews/stories/ANSC/Sep1106b.htm
In particular, a class of endogenous retroviruses, known as endogenous retroviruses related to Jaagsiekte sheep retrovirus or enJSRVs, are critical during the early phase of pregnancy when the placenta begins to develop.

LTR is the dominant promoter in the colon
http://www.pnas.org/cgi/content/abstract/100/22/12841
Indeed, the LTR is the dominant promoter in the colon, indicating that this ancient retroviral element has a major impact on gene expression

Two examples where LTR sequences contribute to increased transcription of human genes
http://www.jbc.org/cgi/content/abstract/jbc;276/3/1896
EBR LTR promotes a significant proportion of the total EBR transcripts, and transient transfection results indicate that the LTR acts as a strong promoter and enhancer in a placental cell line.

They are highly conserved between the mouse and distantly related species …
http://genomebiology.com/2004/5/3/R14
On account of their abundance, LTR retrotransposons are believed to hold major significance for genome structure and function.
…
High sequence similarity between several LTR retrotransposons identified in this study and those found in distantly-related species suggests that horizontal transfer has been a significant factor in the evolution of mouse LTR retrotransposons.

Did they cause the human/chimp split or are they simply one more indicator that humans are unique?

http://www.uga.edu/news/newsbureau/releases/2002releases/0208/020801herv.html
The discovery that human-specific retroviruses emerged at the same time other researchers believe humans and chimps diverged was startling.
…
McDonald said it is increasingly clear that organisms need the viral elements and that their apparent continual backdoor assaults on normal genes may, in truth, be more like a vast, sophisticated chess game on an enormously complex board.

Admittedly, most of the scientists involved in the above studies of Endogenous Retroviruses still assume that they were parasites that somehow were incorporated into the genome with functional roles. However, since many of these perform similar functions in different species, one cannot prove common descent based upon the idea that shared retroviruses are shared errors.

2.3 Pseudogenes

Finally, Pseudogenes really are the poster child for the "Shared Error"/"Junk DNA" argument of the pro-evolution camps. Both the Talk Origins and Panda's Thumb websites spend a lot of time on Pseudogenes. In fact, when a particular Pseudogene that one set of researches concluded was functional was later disputed by different researchers, Panda's Thumb appeared to take great joy in ripping the Intelligent Design community over this:

http://www.pandasthumb.org/archives/2006/08/rumors_of_pseud.html
Thus, pseudogenes - and especially retrotransposed pseudogenes - are generally considered to be non-functional relics and, together with other sorts of repetitive and "selfish" DNA elements, as well as other unique DNA sequences, form the so-called "junk DNA". (For a more general discussion of "junk DNA", see Ian Musgrave's discussion here at PT.) Indeed, when the pseudogenes can be followed over evolutionary lineages, they appear to evolve neutrally, accumulating mutations progressively and freely until they become almost unrecognizable, or disappear from the genome altogether. Note that the number of pseudogenes in the human genome (20,000 or so at the latest count, many of them crippled viral elements) is comparable to that of our functional genes - an impressive amount

Where does this leave us with regard to pseudogenes? Actually, pretty much where we were before the Gray paper came out. If you take away the hype and ignore the wishful thinking of ID supporters, the evidence still overwhelmingly supports the notion that many, likely most pseudogenes are functionless, and it does so regardless of the validity of Hirotsune's findings. Indeed, if one assumes that evolutionary conservation of DNA sequences is a strong hallmark of potential function, then a recent study by a Swedish group shows that at best a few dozens of the thousands of pseudogenes in the human and mouse genomes are under sufficient selective pressure to be highly conserved between the two lineages, suggesting they may be functional [8]. Still, there is ample room for potential interesting mechanisms by which pseudogenes can on occasion be recruited into regulatory and structural functions.

So is the case really closed regarding pseudogenes? Based upon the review of the available literature I've done, it appears that the folks at Panda's Thumb and Talk Origins are spending all of their time gloating over past victories and missing the forest of evidence showing that many Pseudogenes are functional, or that the term Pseudogene is incorrectly applied to a large portion of the DNA. Here is what I was able to find just spending a few hours of searching the Internet.

In evolutionary conserved regions, 90% of pseudogenes appear to be under regulation. Note also that the Panda's Thumb article assumes that Methylation means "inactivity"/non-function, while these researchers conclude it implies regulatory function.
http://ec.europa.eu/research/headlines/news/article_06_11_21_en.html
They discovered that regions called evolutionary conserved regions (ECRs), lying distant from genes, out in the 'junk' DNA, had high concentrations of methylation. This may indicate that these regions have an undiscovered role to play in gene or chromosome activity, according to the scientists.

In addition, analysis of methylation led the team to portions of DNA previous thought to be relatively inactive. Some portions of DNA, known as pseudogenes, appear to have lost function or their exact function is unknown because they have not yet been experimentally studied. Researchers found that these regions were approximately 90 percent methylated, leading them to suspect that methylation might contribute to the inactivity of such genes.

Functional Small nucleolar RNAs (snoRNA) were previously mistaken as pseudogenes
http://genetics.plosjournals.org/perlserv/?request=get-document&doi=10.1371/journal.pgen.0020205
Although four examples of Type-1 retroposons were previously reported [25,43], types 2 and 3 are characterized here for the first time. Several Type-3 snoRTs originating from ribosomal protein genes were previously annotated as processed pseudogenes, but their intronic parts (snoRNA sequence and downstream intron) were overlooked since the pseudogenes were identified by alignment of cDNA or peptide sequences with genomic sequences

The NANOG Pseudogene family is touted by evolutionists as an example of common descent between Humans & Chimps. Meanwhile research has shown that the NANOG Pseudogenes 1 & 8 appear to have regulatory roles (for starters)
http://stemcells.alphamedpress.org/cgi/content/full/23/8/1035
The most effective short double-stranded RNA corresponded to a sequence shared by NANOG and the duplication pseudogene, NANOGP1. This would suggest that NANOGP1 transcript, despite not being translated into a protein, would be downregulated as result of the RNAi approach.

http://content.febsjournal.org/cgi/content/abstract/273/8/1723
*The expression of NANOGP8 in cancer cell lines and cancer tissues suggests that NANOGP8 may play important roles in tumorigenesis. This work not only has potential significance in stem cell and cancer research**, but it also raises the possibility that some of the human pseudogenes may have regulatory function**s.*

Alpha globin pseudogene discovered to be functional gene
http://www.bloodjournal.org/cgi/reprint/2005-03-0948v1.pdf
Surprisingly, we also identified transcription from the genomic region previously thought to encode the pseudo-alpha2 gene. The source of that transcription is characterized in this report as a previously unrecognized globin gene.

Unprocessed KLK pseudogene expressed abundantly in prostate tissues
http://www3.interscience.wiley.com/cgi-bin/abstract/112492090
KLK31P is a novel androgen regulated and transcribed pseudogene of kallikreins that may play a role in prostate carcinogenesis or maintenance… KLK31P is expressed abundantly in prostate tissues and is androgen regulated. KLK31P is expressed at lower levels in localized and metastatic prostate cancer cells than in normal prostate cells.

Pseudogene inhibits tumor growth – may have other roles
http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?cmd=Retrieve&db=PubMed&list_uids=15122329&dopt=Abstract
Based on our findings, PsiCx43 joins and enlarges the thus far restricted group of functionally transcribed and translated pseudogenes.

Two examples of Micro-RNA arising from within processed pseudogenes
http://jhered.oxfordjournals.org/cgi/content/abstract/97/2/186
A survey of the genomic context of more than 300 human miRNA loci revealed that two primate-specific miRNAs, miR-220 and miR-492, each lie within a processed pseudogene.

41% of pseudogenes have match to small RNAs, while only 1 in 6 genes do…
http://forest.mtu.edu/faculty/tsai/FW5085_files/5085_14_sRNAs.pdf

Oct4 pseudogene - functional relevance and indicative of epigenetic regulation
http://www.jbc.org/cgi/content/full/280/8/6265
Through analysis of the mouse genome, we also found that an Oct4 pseudogene was located in the same locus as Nanog, Stella, and GDF3 on chromosome 6. Moreover, the relative positional order of these genes was conserved between the mouse and human genomes. By BLASTing the EST data base we found that this mouse pseudogene is likely transcribed, as an exact sequence hit was generated (data not shown). This suggests that the mouse oct4 pseudogene, which colocalizes with Nanog, Stella, and GDF3 is transcriptionally functional.

Pseudogenes are often evolutionary conserved and transcriptionally active, implying function
http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?cmd=Retrieve&db=PubMed&list_uids=15490577&dopt=Abstract

The above evidence has clearly shown that biologists' assumptions about pseudogenes have been largely mistaken. Even when pseudogene sequences are different in different species (not conserved), this doesn't necessarily prove that they are non-functional. Instead, these could be regulatory sequences where the differences are part of the explanation of why species are unique in the first place.

Does this mean that truly non-functional Pseudogenes don't exist? No. I would expect them to, but it doesn't prove that the Intelligent Designer created junk. If a gene is no longer needed for something it used to do as part of original design, then it is likely to become non-functional. For example, when fish species move into caves, they lose the ability to see and lose their skin pigmentation in a relatively small number of generations, since neither of those features are necessary to survive in a dark cave. It is no surprise that the genes and/or regulatory DNA associated with those become non-functional as well over time. Sean Pitman has further information about Pseudogenes at is excellent website "The Emperor Has No Clothes" at:
http://www.detectingdesign.com/pseudogenes.html

2.4 C-Value Enigma

If there is any good reason why biologists were under the assumption that much DNA must be Junk, it would be the C-Value Enigma (or C-Value Paradox), which is mentioned briefly in the Talk Origins "shared errors" article. Basically, the Enigma is that "genome size does not correlate with organismal complexity" as discussed in the following Wikipedia article: http://en.wikipedia.org/wiki/C-value_enigma

At first blush, the C-Value Enigma would seem to imply that much DNA in some eukaryotic species is redundant at best. However, there is now evidence for correlation between C-Value and organismal complexity, and also valid reasons for extra copies of DNA in certain species, as discussed in the following scientific research:

> **Positive correlation between genome size and the number of cell parts and cell size.**
> http://bioweb.wku.edu/faculty/Marcus/LNBI_2005.pdf
> *For all of the data sets examined here, there are significant positive correlations between genome size or numbers of open reading frames and numbers of cell types and numbers of types of cell parts.* ***These results suggest that the greatest irony about the C-value paradox may very well be that there is no paradox at all and that genome complexity and morphological complexity actually do significantly positively correlate with one another, at least for the organisms with sequenced genomes in this data set****.*
>
> **Correlation between genome size and red blood cell size**
> http://www.genomesize.com/rgregory/reprints/BCMD.pdf
> *As is apparent from the brief review given above, the relationship between genome size and erythrocyte size is detectable in each of the vertebrate classes, even in the uniquely enucleate case of mammals.*
>
> *There are many ways in which erythrocytesize is of relevance to organismal biology. Larger RBCs contain more hemoglobin, but they also require larger blood vessels. Species with large cells also typically have fewer cells. Blood viscosity, total hemoglobin content, and other such parameters are of obvious significance to organismal physiology, but no other parameter has received more attention in regards to genome size/cell size interactions than erythrocyte surface area to volume (SA:V) ratios.*
>
> **Correlation between ribosomal DNA copy number and genome size**
> http://www.genomesize.com/rgregory/reprints/rDNA.pdf
> *It is not clear based on the present dataset whether or not the stronger association in animals is of any functional significance, but it is nevertheless obvious that rDNA copy number and genome size are strongly related in these organisms.*
>
> *The necessity for this abundance of rDNA has been attributed to the fact that, unlike protein-coding genes, it cannot undergo secondary rounds of amplification via translation when organisms require more rRNA transcripts.*
>
> **Large genomes protect cells from mutation**
> http://www.innovations-report.de/html/berichte/biowissenschaften_chemie/bericht-76099.html

The researchers have determined that the injury frequency depends on the size of genome: the larger the size it, the lower the frequency is. So, large genome serves protection from injuries.

2.5 "Junk DNA" becomes "The Transcriptome"

So now that we've shown that all of the classes of Junk DNA touted by Talk Origins can have functional roles, let's conclude this discussion with some of the latest findings regarding non-coding DNA including the complexity that is expected by proponents of Intelligent Design.

The findings of the FANTOM3/Genome Network project
http://genetics.plosjournals.org/perlserv/?request=get-document&doi=10.1371/journal.pgen.0020063
This issue of PLoS Genetics includes a special collection of articles that explore the transcriptome complexity being revealed by work on the FANTOM3 dataset. ***Besides revealing staggering complexity, analysis of this collection is providing an increasing number of novel mRNA classes, expressed pseudogenes, and bona fide noncoding variants of protein-coding genes****.*

These studies force a paradigm shift in the understanding of the transcriptome. First, the studies find that 63% of the genome is transcribed from at least one strand (in contrast to the earlier belief that only 2% of the genome is transcribed into protein-coding mRNAs*). Second, an unexpected amount of variation was found in alternative splice forms (65% of all transcriptional units [TUs] contain alternatively splicing variants), TSSs (which identify promoters), and polyadenylation sites.*

Frith and colleagues have extended the analysis of noncoding transcript expression and have identified 10,000 full-length cDNAs derived from expressed pseudogenes—constituting approximately 10% of the known transcriptome—half of which are promoted by retrotransposons, or otherwise characterized promoters, and are likely to participate in various regulatory mechanisms.

http://genetics.plosjournals.org/perlserv/?request=get-document&doi=10.1371/journal.pgen.0020023
This study provides an unprejudiced survey of "pathological" RNA molecules, which resemble protein-coding RNA except that they contain violations of the genetic code. These pseudo–messenger RNAs constitute a surprisingly large fraction of all transcripts, as much as 10%. ***These ghostly molecules have always been present in RNA surveys, but have stayed below the radar because they do not cleanly correspond to annotated elements in DNA, i.e., "genes".*** *Their prevalence demonstrates that RNA is a distinct continent that cannot be fully understood as a mirror of DNA or proteins.*

http://genetics.plosjournals.org/perlserv/?request=get-document&doi=10.1371/journal.pgen.0020037
Non-protein-coding RNAs (ncRNAs) are increasingly being recognized as having important regulatory roles. Although much recent attention has focused on tiny 22- to 25-nucleotide microRNAs, several functional ncRNAs are orders of magnitude larger in size. Examples of such macro ncRNAs include Xist and Air, which in mouse are 18 and 108 kilobases (Kb), respectively.

As stated earlier – it is the Non-Coding DNA that makes species unique
http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=395773
As discussed in this article, the non-coding transcribed part of the genome increases dramatically in size with the complexity of organisms, culminating in an estimated 1.2 billion nucleotides in humans

http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=1557810
It is clear that much of what was once termed 'junk' DNA represents highly evolved, functional sequence containing amongst other things, numerous transcriptional regulatory motifs.

Non-Coding RNA represents a set of Refined Control Switches
http://www.eurekalert.org/pub_releases/2006-11/uoi-uis111306.php
"Not so many years ago our understanding was that DNA was transcribed to RNA, which was then translated to protein. Now we know that the levels of control are much more varied and that many RNAs don't make protein, but instead regulate the expression of proteins," Davidson explained. "Non-coding RNA like microRNAs represent a set of refined control switches, and understanding how microRNAs work and how they are themselves controlled is likely to be very important in many areas of biology and medicine."

2.6 Junk DNA – the biggest mistake in the history of biology

Even as many scientists are finding function in the "junk", their logic is still clouded by evolutionary reasoning. For example, rather than just accepting Transposons as functional, this article concludes that RNA editing sites are trying to protect the genome from Transposons.

> http://www.eurekalert.org/pub_releases/2006-12/twi-pit120406.php
> *"We used to believe there were only a limited number of RNA editing sites," she says, "but now we think there may be as many as 20,000 sites involving perhaps 3,000 genes. Interestingly, most of the editing sites correlate with non-coding regions of DNA, the so-called junk DNA."*
>
> *"Transposons occupy as much as half of our entire genome, and they can be dangerous," Nishikura says. "As a result, mechanisms have arisen through evolution to suppress their activity. This is particularly true in the egg and sperm, where maintenance of the genome's integrity is critical."*

I believe such reasoning will eventually be squashed as the evidence of the Transcriptome is revealed. Unlike the arrogant statements of Richard Dawkins, Talk Origins, and PT, at least some biologists are able to honestly admit what has been happening in biology for the past 30 years:

> http://www.abc.net.au/catalyst/stories/s898887.htm
> http://www.imb.uq.edu.au/download/large/TheUnseenGenome.pdf
> *"I think this will come to be a **classic story of orthodoxy derailing objective analysis** of the facts, in this case for a quarter of a century," Mattick says. **"The failure to recognize the full implications of this—particularly the possibility that the intervening noncoding sequences may be transmitting parallel information in the form of RNA molecules—may well go down as one of the biggest mistakes in the history of molecular biology."***

2.7 Junk DNA – Thanks for the Memories

Six months after this paper was originally written, the initial "ENCODE" project results were reported in Nature and discussed extensively by science news sites and in the "blogosphere". The final demise of "Junk DNA" is now complete.

> http://www.sciencedaily.com/releases/2007/06/070613131932.htm
> http://www.nature.com/nature/journal/v447/n7146/full/nature05874.html#Integrated%20Analysis%20and%20Manuscript%20Preparation
> http://www.genome.gov/Pages/Research/ENCODE/nature05874.pdf
> *The ENCODE consortium's major findings include **the discovery that the majority of DNA in the human genome is transcribed into functional molecules, called RNA**, and that these transcripts extensively overlap one another. This broad pattern of transcription **challenges the long-standing view that the human genome consists of a relatively small set of discrete genes, along with a vast amount of so-called junk DNA that is not biologically active**.*
>
> *At the outset of the ENCODE Project, many believed that the broad collection of experimental data would nicely dovetail with the detailed evolutionary information derived from comparing multiple mammalian sequences to provide a neat 'dictionary' of conserved genomic elements, each with a growing annotation about their biochemical function(s). In one sense, this was achieved; the majority of constrained bases in the ENCODE regions are now associated with at least some experimentally derived information about function. **However, we have also encountered a remarkable excess of experimentally identified functional elements lacking evolutionary constraint, and these cannot be dismissed for technical reasons. This is perhaps the biggest surprise of the pilot phase of the ENCODE Project, and suggests that we take a more 'neutral' view of many of the functions conferred by the genome.***

3 EVOLUTIONARY CONSERVATION

Shared "Junk DNA" was supposed to be something that could only be explained by evolution. Now that that argument is gone, let's build our case further by showing some things about the genome that are better explained by Intelligent Design than by evolution.

First up are highly conserved areas of the DNA between all species. While evolutionists may argue that this shows common descent, it is just as easily argued that a common designer would use the same components. More telling, there are many examples where higher species (e.g. humans) share identical DNA with single-celled organisms. If evolution is constantly improving on things over time, why would species that have been separated by hundreds of millions of years (per the evolutionary timeline) still share identical DNA? A better answer is that these critical systems are so highly specified, they must have been optimal from the start, and so evolution has no answer for how they could have arisen from some sub-optimal precursor. There are thousands of examples of highly conserved DNA, and we offer a few examples below:

An accuracy center in the ribosome conserved over 2 billion years.
http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=47604
Thus, the interplay of these three proteins to provide the optimal level of accuracy of translation has been conserved during the 2 billion years of evolution that separate E. coli from S. cerevisiae.

Cytoplasmic proteins that are identical between species
http://biology.plosjournals.org/perlserv/?request=get-document&doi=10.1371/journal.pbio.0040330
Sec1/Munc18 (SM) proteins comprise a small family of cytoplasmic proteins that play a pivotal role in intracellular membrane fusion. They are structurally highly conserved in evolution, and each SM protein is specialized for a single or a small group of trafficking steps. ***SM proteins of evolutionarily distant species that are involved in the same trafficking steps are capable of replacing each other*** *whereas within one organism, different SM proteins show no functional redundancy*

Cell Cycle Promoter regulatory elements perfectly conserved between Chimpanzee, Orangutan, Mouse and Human
http://mbe.oxfordjournals.org/cgi/content/abstract/msl210v1
A tandem repressor site named cell cycle-dependent element (CDE) and cell cycle genes homology region (CHR) is responsible for the correct expression during the cell cycle. Another feature of these G2/M-specific promoters is the activation through two or three CCAAT-boxes binding the transcription factor NF-Y. ***These major activating sites have to be spaced 32 bp or 33 bp apart to be fully functional.***
…
CHR and CCAAT-boxes stand out in that they are perfectly conserved in all promoters tested.

Highly conserved protein kinases involved in the regulation of carbon and amino acid metabolism
http://jxb.oxfordjournals.org/cgi/content/abstract/55/394/35
These protein kinases show an extraordinary level of conservation with their fungal and animal homologues given the span of time since they diverged from them.

Thousands of more examples…
http://www.google.com/search?hl=en&lr=&rls=GGGL%2CGGGL%3A2006-46%2CGGGL%3Aen&q=highly+conserved+protein&btnG=Search

http://www.google.com/search?sourceid=navclient-ff&ie=UTF-8&rls=GGGL,GGGL:2006-46,GGGL:en&q=highly+conserved+dna

4 Human Accelerated Regions (HARs)

As compelling as DNA sequences are that are identical between all species, showing how critical their exact sequence is for function, an even more compelling argument for Intelligent Design are those sequences that make us uniquely human.

http://genetics.plosjournals.org/perlserv/?request=get-document&doi=10.1371%2Fjournal.pgen.0020168
We found 202 genomic elements that are highly conserved in vertebrates but show evidence of significantly accelerated substitution rates in human. These are mostly in non-coding DNA, often near genes associated with transcription and DNA binding. Resequencing confirmed that the five most accelerated elements are dramatically changed in human but not in other primates, with seven times more substitutions in human than in chimp.

To identify changes that may be functional, we focus on the set of regions of the human genome of at least 100 base pairs (bp) that appear to have been under strong negative selection up to the common ancestor of human and chimp (as evidenced ***by high sequence identity between chimp and rodents****), but exhibit a* ***cluster of changes in human compared to chimp****. Our expectation is that the selective constraint* ***on the most extremely accelerated regions of the human genome may have switched from negative to positive (and possibly back to negative) some time in the last 5−6 million years****.*

http://www.medicalnewstoday.com/medicalnews.php?newsid=49868
HAR1 has only two changes in its 118 letters of DNA code between chimpanzees and chickens. But in the roughly five million years since we shared an ancestor with the chimpanzees, 18 of the 118 letters that make up HAR1 in the human genome have changed.

http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=pubmed&list_uids=16915236&cmd=Retrieve&indexed=google
HAR1, is part of a novel RNA gene (HAR1F) that is expressed specifically in Cajal-Retzius neurons in the developing human neocortex from 7 to 19 gestational weeks, a crucial period for cortical neuron specification and migration. HAR1F is co-expressed with reelin, a product of Cajal-Retzius neurons that is of fundamental importance in specifying the six-layer structure of the human cortex.

http://www.eurekalert.org/pub_releases/2006-11/uoc--uwc110906.php
The scientists identified networks of genes that correspond to specific brain regions. When they compared these networks between humans and chimps, they found that the gene networks differed the most widely in the cerebral cortex -- the brain's most highly evolved region, which is three times larger in humans than chimps.

Secondly, the researchers discovered that many of the genes that play a central role in cerebral cortex networks in humans, but not in the chimpanzee, also show significant changes at the DNA level.

http://brainethics.wordpress.com/2006/08/17/the-non-coding-dna-that-makes-us-human/
One thing is becoming clear: proteincoding genes may not be the movers and shakers of human evolution scientists once thought. "We should stop looking at proteins and start looking at noncoding DNA," says Lunter. "Everything points in that direction."

So, here we have DNA that is so important in brain development that it is nearly identical in all other animals tested, but radically different in humans. In this particular area, chimps are much more closely "related" to chickens and rodents than to humans. Look at the ridiculous statements this forces those committed to evolution to make – *"the most extremely accelerated regions of the human genome may have switched from negative to positive (and possibly back to negative) some time in the last 5−6 million years."* Said another way, the only evolutionary explanation is that there was DNA so important to the brain that any change in it was not tolerated in any other species, but somehow in the line leading to humans change was beneficial. Then, once it reached a certain point, the changes to humans stopped again. A much more straightforward interpretation of the evidence is that the DNA code that specifies the human brain was uniquely created.

For additional accumulating evidence that humans are unique compared to other species, read on:

http://www.the-scientist.com/news/home/25713/
"The idea that microRNAs can contribute to species identity has been bandied about for some time, and this is nice confirmation of that," said Zamore. "We're beginning to home in on what makes us, us.

http://www.newscientist.com/channel/being-human/human-evolution/mg19225764.700-humans-left-chimps-behind-in-evolutions-playground.html
Now, researchers at the Hubrecht Laboratory in Utrecht, the Netherlands, have combed painstakingly through the RNA in human and chimp brains, and found 447 new micro-RNAs, more than doubling the number discovered so far (Nature Genetics, DOI: 10.1038/ng1914). Some were expressed very rarely.

"The brain has 10,000 cell types," says team member Edwin Cuppen. "Perhaps that is because of all these micro-RNAs." ***Many were unique to chimps and humans, and some only to humans. So even though we share most of our DNA with chimps, small genetic changes that fine-tune its expression might account for the radical differences in our brains****.*

http://www.sciencedaily.com/releases/2005/01/050111170714.htm
*"We've proven that there is a big distinction. Human evolution is, in fact, a privileged process because it involves a large number of mutations in a large number of genes," Lahn said. "****To accomplish so much in so little evolutionary time a few tens of millions of years requires a selective process that is perhaps categorically different from the typical processes of acquiring new biological traits.****"*

The making of the large human brain is not just the neurological equivalent of making a large antler*. Rather, it required a level of selection that's unprecedented," Lahn said. "****Our study offers the first genetic evidence that humans occupy a unique position in the tree of life.****"*

http://biology.plosjournals.org/perlserv?request=get-document&doi=10.1371/journal.pbio.0030050
The human brain is not just a scaled-up version of a mammal brain or even of an ape brain. *"All told,* ***it seems that the human brain may be more dynamic than ape or monkey brains"****, says Preuss. "The human brain seems to be running hot in all sorts of ways."*

http://www.sciam.com/article.cfm?chanID=sa003&articleID=9D0DAC2B-E7F2-99DF-3AA795436FEF8039
*A lot more genes may separate humans from their chimp relatives than earlier studies let on. Researchers studying changes in the number of copies of genes in the two species found that their mix of genes is only 94 percent identical****. The 6 percent difference is considerably larger than the commonly cited figure of 1.5 percent.***

5 Conclusion

What can we conclude from the evidence presented in this essay:

- Every type of "Junk DNA" presented by pro-evolution websites has been found to have functional roles in organisms, which severely undermines the "shared errors" argument;
- A large percentage of the human genome previously assumed to be non-functional is now believed to be functional (from 2% to 60% or more);
- Extra DNA that may not provide direct function still likely serves other structural/protective roles (C-value enigma);
- Many DNA regions are identical across species (highly conserved), undermining the notion that they evolved slowly over time;
- Human DNA contains unique regions that are fundamentally different from chimps or any other species, and this correlates with the unique structure of the human brain.

I hope this essay shows that Intelligent Design supporters shouldn't be discouraged by the losses in the courts, or the arguments contained on the pro-evolution websites that seem convincing at face value. The mounting genetic evidence since the sequencing of the human genome is about to upend the scientific world, and Intelligent Design supporters won't have to work very hard for it to happen.

6 Additional Web Resources

http://crev.info/
http://www.newcreationism.org/DesignWatch.html
http://www.evolutionnews.org/
http://www.detectingdesign.com/
http://www.arn.org/
http://www.researchintelligentdesign.org/wiki/Main_Page