

“Junk” DNA—Past, Present, and Future, Part 2

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Keywords

junk DNA, genetics, ENCODE, non-coding DNA, neutral DNA

In my previous article on “junk” DNA, I discussed the history of junk DNA and some of the recent findings of the ENCODE Pilot Project. The ENCODE Pilot Project findings have made it clear that junk DNA is not junk and that most of it is functional in the form of RNA or protein. The genome should be viewed as a complex three-dimensional network of millions of interacting parts.

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Great Expectations

The human genome was not the only one studied by ENCODE. Part of the project involved comparing the sequences of the “junk” or non-coding DNA across 23 different mammalian species such as mouse, dog, elephant, rabbit, cow, and chimp. The scientists did this because of their belief in the evolutionary relationships (common ancestry) relating all mammals. Rick Weiss of the *Washington Post* states that Ewan Birney, a coordinator of ENCODE at the European Bioinformatics Institute in England, said that, “The expectation was that many of the most active DNA sequences in humans would be prevalent in other mammals, too, because evolution tends to save and reuse what works best.”¹ Their expectation is that non-coding DNA will be conserved (similar in sequence among species) because it is functional—just as many of the genes (protein-coding regions) are conserved. Rather than believing in a common Designer, God, who used similar parts in different organisms, they believe in common ancestry (no God), where similar parts are “save[d] and reuse[d].”

Surprising Findings

What they found shocked them! The ENCODE Project Consortium states, “Surprisingly, many functional elements [of the non-coding DNA] are seemingly unconstrained [not conserved] across mammalian evolution”.² This means a large portion of the non-coding DNA among the 23 different mammalian species studied was not conserved (or similar). It appears that approximately 50% of the non-coding DNA that was found to be functional was not conserved.³ On the flip side, 40% of the non-coding DNA that was conserved has no known function.⁴ This 40% will be further studied because of their belief that if it is conserved, it is important and does have a function (just not one that is testable yet).⁵ What about the 50% that is not conserved? What explanation may account for this and what further study should be done? While explanations may abound, further study may be inhibited.

Not “Junk” DNA But “Neutral” DNA

While the scientists involved in the ENCODE Pilot Project aren’t ready to call the 50% of non-coding DNA that isn’t conserved really “junk,” they are prepared to say it’s “neutral”. The ENCODE Project Consortium states, “This suggests the possibility of a large pool of neutral elements that are biochemically active but provide no specific benefit to the organism”.⁶ Weiss of the *Washington Post* states that Birney says, “But more than half [non-coding DNA elements] were not found in other creatures, which suggests they may not be important in people, either.”⁷ Birney goes on to say, “I think of them as gate-crashers at a party. They appeared by chance over evolutionary time ... neither to the organism’s benefit nor to its hindrance. That is quite an interesting shift in perspective for many biologists”.⁸ In some ways it seems we may be back to square one when it comes to the importance of “junk” or non-coding DNA. The scientists will admit it has a function, but because of their evolutionary assumptions, they assume that if it’s not conserved it’s not important. If it’s not considered important, it won’t be further funded or studied.

However, a possible role for this “neutral” DNA has been proposed. “This pool may serve as a ‘warehouse’ for natural selection ...” writes the ENCODE Project Consortium.⁹ Another article states, “Thus, it is plausible that many biochemically functional but biologically inert [neutral] elements exist in the human genome and provide evolutionary potential from which new functions may arise”.¹⁰ Basically the scientists are suggesting that over time and with the “help” of mutations, this “neutral” DNA could be altered to perform entirely new functions

that would allow microbes to become monkeys. The problem is that mutations lead to a corruption or a loss of information, not gain, so it is doubtful that time and mutations would allow the DNA to gain a function. Even if the DNA did gain a new function, it would be due to the altering of current genetic information and not new genetic information, which is required for molecules-to-man evolution.

Creationist View

Most biblical creationists would not view the ENCODE Pilot Project findings as surprising but intriguing and further confirmation of what we already know to be true from the Bible. That God created humans and different "kinds" of animals (Genesis 1). We would expect the DNA between humans and the kinds of animals to be similar yet different. For example, the ENCODE Pilot Project found that the protein coding regions of DNA (genes) are more likely to be conserved among mammalian species than the regulatory regions (typically found in the non-coding DNA) controlling the production of the protein.¹¹ It seems reasonable that God would use the same proteins (workhorses of the cell) among organisms but regulate them differently depending on the organism. Much like an artist would use the same paint colors on two different pieces of canvas but use them differently to make completely different paintings. It is also possible that the non-coding DNA among mammals was more similar at one time (part of God's original design) but has since degenerated as a result of the Fall. A future research effort should be made to compare non-coding DNA within a kind (for example, tiger, lion, domestic cat within the cat kind) and between kinds (for example, cat kind versus dog kind). My guess is that non-coding DNA will be more similar within a kind than between kinds.

Conclusion

Speaking of the finding of functional non-coding DNA that is not conserved among mammals, the ENCODE Project Consortium states, "This is perhaps the biggest surprise of the pilot phase of the ENCODE Pilot Project, and suggests that we take a more 'neutral' view of many of the functions conferred by the genome".¹² Again because of their evolutionary assumptions that if it's not conserved (based on the assumption that it should be because all mammals share a common ancestor) it's not important, almost half of the junk DNA is being relegated to a category in which it may not be further studied. Once again we see evolutionary ideas inhibiting science. As creationists, "junk" DNA, whether conserved or not conserved among species, is important and should be studied. Further studies will elucidate more the awesome design of the almighty God.

Footnotes

1. Intricate toiling found in nooks of DNA once believed to stand idle. *Washington Post*.
2. The Encode Project Consortium, 2007. Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. [PDF] *Nature* 447:799–816.
3. The Encode Project Consortium, Ref. 2.
4. The Encode Project Consortium, Ref. 2.
5. The Encode Project Consortium, Ref. 2.
6. The Encode Project Consortium, Ref. 2.
7. Ref. 1.
8. Ref. 1.
9. The Encode Project Consortium, Ref. 2.
10. Margulies, E.H., 2007. Analyses of deep mammalian sequence alignments and constraint predictions for 1% of the human genome. *Genome Research* 17:760–774.
11. Margulies, Ref. 10.
12. The Encode Project Consortium, Ref. 2.