$\Delta a/a = (0.1 \pm 1.7) \times 10^{-6}$. The much larger variation ($\Delta a/a = (-5.7 \pm 1.0) \times 10^{-6}$) for the previous study presented by Murphy *et al*.,[5] from a sample of 143 complex metal systems using the same many-multiplet (MM) analysis, has a significance level of only 12%.

An MM analysis performed by Srianand *et al*., on a new, very high-quality sample of 23 systems with Mg II absorption lines, measured over the redshift range of $0.4 \le z \le 2.3$, confirms the latest results of small variation, with $\Delta a/a = (-0.6 \pm 0.6) \times 10^{-6}$. (For a detailed explanation of the methods used, see ref. 16.) The variations of the fine-structure constant are constrained tightly about zero, irrespective of the distances of the quasar sources.

Figure 3 of Srianand *et al*.[13] is reproduced here (figure 1) and strongly supports the news headlines. The horizontal dashed lines are the previous results (weighted mean and 1s range presented by Murphy *et al*.). The filled circles are the new results of Srianand *et al*. Clearly most of these new measurements are inconsistent with the range of the previous (Murphy *et al*.) data.

Recent research on the Oklo natural uranium reactor (Gabon, Africa) claims a historical variation in $\Delta\alpha/\alpha \ge 4.5 \times 10^{-8}$ with 6 σ confidence.[17] This earth-based calculation involves certain model dependent assumptions and remains controversial. Recently reported astrophysical observations have consistently indicated an invariant α.[18,19]

References

1. <www.spacedaily.com/yesterday/spacedaily-2004–04–01.html>, 1 April 2004.
2. <www.answersingenesis.org/fine_structure>, 22 August 2001.
3. Webb, J.K., Flambaum, V.V., Churchill, C.W., Drinkwater, M.J. and Barrow, J.D., Search for time variation of the fine structure constant, *Phys. Rev. Lett.* **82**(5):884–887, 1999.
4. Webb, J.K. *et al*., Further evidence for cosmological evolution of the fine structure constant, *Phys. Rev. Lett.* **87**(9):091301, 2001.
5. Murphy, M.T., Webb, J.K. and Flambaum, V.V., Further evidence for a variable fine-structure constant from Keck/HIRES QSO absorption spectra, *M.N.R.A.S.* **345**(2):609–638, 2003.
6. Davies, P.C.W., Davis, T.M. and Lineweaver, C.H., Black holes constrain varying constants, *Nature* **418**(6898):603–603, 2002; Comment by Wieland, C., Speed of light slowing down after all, *TJ* **16(3)**:7–10, 2002.
7. Cho, A., Light may have slowed down, <www.newscientist.com/news/print.jsp?id=ns99991158>, 2001.
8. Duff, M.J., Comment on time-variation of fundamental constants, <arxiv.org/abs/hep-th/0208093>, 13 August 2002.
9. Forum on Speed of Light, *TJ* **1**:71–139, 1984.
10. Moffat, J.W., Variable speed of light cosmology: an alternative to inflation, <www.arXiv.org/abs/hep-th/0208122 v2>, 22 August 2002.
11. Hartnett, J.G., Is there any evidence for a change in c? Implications for creationist cosmology, *TJ* **16**(3):89–94, 2002.
12. Cowie, L.L. and Songaila, A., The inconstant constant? *Nature* **428**:132–133, 2004.
13. Srianand, R., Chand, H., Petitjean, P. and Aracil, B., Limits on the time variation of the electromagnetic fine-structure constant in the low energy limit from absorption lines in the spectra of distant quasars, *Phys. Rev. Lett.* **92**, 121302, 2004. (Also at <www.arXiv.org/abs/astro-ph/0402177>, 8 February 2004.)
14. Chand, H., Srianand, R., Petitjean, P. and Aracil, B., Probing the cosmological variation of the fine-structure constant: Results based on VLT-UVES sample, *Astron. Astrophys.* **417**, 853–871, 2004. (Also at <www.arxiv.org/abs/astro-ph/0401094>, 16 April 2004.)
15. Quast, R., Riemers, D. and Levshakov, S.A., Probing the variability of the fine-structure constant with the VLT-UVES, *Astron. Astrophys*. **415**, L7–L11, 2004. (Also at <www.arXiv.org/abs/astro-ph/0311280>, 8 January 2004.)
16. Murphy, M.T., Webb, J.K., Flambaum, V.V. and Curran, S.J.; in: *Physics in Collision*, Stanford, CA, 20–22 June 2002. (Also at <arxiv.org/PS_cache/astro-ph/pdf/0209/0209488.pdf>, 24 September 2002.)
17. Lamoreaux, S.K. and Torgerson, J.R., Neutron moderation in the Oklo natural reactor and the time variation of α, *Phys. Rev. D* **69**:121701, 2004.
18. Olive, K.A. *et al*., Reexamination of the ^{187}Re bound on the variation of fundamental couplings, *Phys. Rev. D* **69**:027701, 2004.
19. Darling, J., A Laboratory for constraining cosmic evolution of the fine-structure constant: Conjugate 18 centimeter OH lines toward PKS 1413+135 at Z = 0.24671, *Astrophys. J.*, **612**: 58–63, 1 September 2004

Design in the genome? A matter of bias

C. W. Nelson

Error-proof information

In Vancouver, in 1998, evolutionists gathered to discuss evidence that the genetic code is not the result of pure chance, but was shaped by natural selection over time.

> 'Experiments with RNA have shown that chemical attractions between the genetic material and the components of proteins may have helped shape the original code, reported one speaker. Another researcher, using powerful computer analyses, suggested that the modern code is the product of evolution because it is so error-proof: Only one in a million other possible codes is better at producing a workable protein even when the DNA carries mistakes.'[1]

Amazing design in the DNA molecule[2] has also been affirmed more recently. For example, Donall Mac Donaill of Trinity College Dublin believes that the nitrogen bases which comprise DNA—adenine, thymine, guanine and cytosine—must be a product of evolution due to the fact that this choice of bases

> 'incorporates a tactic for minimizing the occurrence of errors in the pairing of bases, in the same way that error-coding systems are incorporated into ISBNs on books, credit card numbers, bank accounts, and airline tickets'.[3]

Just how such an error-checking system could indeed evolve has not been stated, but authors recognize that mere chance is not a sufficient explanation for the complexity that is observed.

In addition to DNA's amazing error-proof tactics, the genome (the entire DNA content of a cell) also contains a vast amount of information. Richard Dawkins is

well known for stating that 'there is enough information capacity in a single human cell to store the *Encyclopaedia Britannica*, all 30 volumes of it, three or four times over'.[4] In fact, geneticist Gary Zweiger believes that 'Although most biology textbooks fail to mention it, information is as fundamental and unique to life as either metabolism or reproduction.'[5]

Some, however, may think the idea of DNA as a book which contains actual information is strictly metaphorical. Contrary to this opinion, Matt Ridley writes that

> 'The idea of the genome as a book is not, strictly speaking, even a metaphor. It is literally true. A book is a piece of digital information, written in linear, one-dimensional and one-directional form and defined by a code that transliterates a small alphabet of signs into a large lexicon of meanings through the order of their groupings. So is a genome. The only complication is that all English books read from left to right, whereas some parts of the genome read from left to right, and some from right to left, though never both at the same time.'[6]

No junk in the genome

Despite this evidence, the majesty of DNA has lately fallen under attack. For example, it has been claimed that most of the human genome is merely junk, having no influence on the coding of proteins. Pseudogenes, one type of this so-called 'junk DNA', are thought to be functionless genes that once had a function but have since lost it. This assertion has not proven true, however. In a recent study by Woodmorappe, it was found that pseudogenes have many possible functions, including gene regulation: 'a processed pseudogene located near a suitable promoter could produce antisense RNA, thus potentially regulating its parent gene.'[7] Of course, a very small amount of junk DNA would be expected in a creation model (resulting from harmful mutations after the Fall), but nothing near the magnitude that is claimed.

Another example of junk DNA includes introns within DNA. During transcription, mRNA (messenger RNA) is made from the DNA in the nucleus of the cell (this sequence is later matched with transfer RNA anticodons in order to form a protein). However, the parts of DNA called introns interrupt the stretches of DNA that actually code for protein, which are called exons. In transcription, these introns are deleted and exons combined to form the mRNA copy in a process known as splicing.

Since introns do not code for proteins (presumably), they are thought to be useless junk left over from evolution. But this isn't exactly true, either; for example, introns can allow alternative splicing,[8] possibly resulting in a splice variant that differs from the original protein only slightly but has an entirely different function.[9] Additionally,

> 'researchers have found that an intron mutation causes the disease *ataxia-telegiecstasia*. Deletion of just four nucleotide "letters" from the middle of a 69-nucleotide intron disrupts the splicing process. The intron is not spliced out, so the final, edited, mRNA has the extra sequence incorporated, resulting in the manufacture of a defective protein.'[10]

Because a mutation in the intron is actually harmful, the intron cannot only be junk. Woodmorappe[11] mentions a number of other possible functions, including the idea that introns may act as 'islands' of DNA that are used for the encoding of non-coding RNA (that is, RNA which is not translated into protein, but instead performs various regulatory roles; for example, rendering other RNA useless). Introns can function as binding sites for proteins, or simply as space needed between exons—they are certainly *not* without function.[12]

Molecular complexity

New discoveries broaden our knowledge about life's complexity all of the time. For example, it is known that the cell uses an extremely efficient repair system to correct nearly all its copying mistakes in DNA, without which life would be threatened.[13] It has recently been discovered that the protein AlkB in *E. coli* actually repairs *both* DNA *and* RNA. It seems that

> '… repairing RNA may be more efficient than destroying it and starting again. Ribosome assembly is a complex, energy-intensive process, and it is not hard to imagine that the thrifty repair of damaged rRNA [ribosomal RNA] would be preferable to disassembling or discarding an entire ribosomal particle. Likewise, it takes several hours to produce full-length mRNA copies of large genes, so the repair of damaged copies might make energetic sense.'[14]

The complexity and elegance of life becomes increasingly more amazing, especially when the seemingly less-complex bacteria are considered. Dr Kim M. Risley points out that coupled transcription and translation add weight to the case for design:

> 'Many bacteria live in environments that are constantly changing. Because of their small genome size and the need to rapidly adapt to their metabolic and environmental needs, many types of bacteria, including the well studied *E. coli*, use a process called coupled transcription and translation. Coupled transcription and translation is a mechanism that allows for rapid bacterial gene expression by allowing ribosomes to attach to the mRNA before its synthesis is totally complete. This is in direct contrast to multicultural organisms, such as humans, where mRNA synthesis is completed prior to ribosome binding. Bacteria use coupled transcription and translation to synthesize proteins that are needed immediately, without having to wait until the entire mRNA message is completely synthesized. This event saves the bacterial cell crucial time when major shifts in

protein expression must occur, and thus are a way to insure the survival of the species.'[15]

Life is incredibly complex at every level.

Chance or design?

Evidence of DNA's efficiency caused the evolutionists at the Vancouver meeting to evaluate their interpretation of its existence. Two possibilities were considered: (i) that the genetic code is merely a result of chance, and (ii) that the genetic code has evolved over time, being perfected by natural selection. This was all that the participants allowed—but is there a third option? One person commented, 'What really astounds me is the architecture of life. It's like it was designed.'[16] If life *seems* designed, why not consider a third option: that the genetic code, in all its greatness, indeed *has* been designed? Richard Dawkins describes biology as 'the study of complicated things that give the appearance of having been designed for a purpose.'[17] He attributes this appearance to natural selection. But why not allow another option? The reason it is dismissed *a priori* is simple: design, as an explanation, is considered unscientific.

> 'Even if all the data point to an intelligent designer, such a hypothesis is excluded from science because it is not naturalistic. Of course the scientist, as an individual, is free to embrace a reality that transcends naturalism.'[18]

So design, no matter how plausible or well-supported by empirical evidence, *cannot* be accepted as a possible explanation. This same criterion was not used for the SETI project, however. 'If we should receive a radio message from an extraterrestrial civilization, [Carl] Sagan suggested that such an intelligent message would be: 1) elegant, 2) complex, 3) internally consistent, and 4) utterly alien.'[19] Contemplating these standards, does DNA not perfectly fulfil each? It is elegant in the sense that the genetic code is amazingly efficient. Steve Olson comments,

> 'Electronic engineers often congratulate themselves on the amount of data they can cram into a semiconductor chip. They have a long way to go to catch up with the information density of DNA.'[20]

DNA is also complex due to its incredible information content, and internally consistent in that, overall, the same three-base code is used for the same amino acid in organisms (with possible evidence to the contrary,[21] but this is not a direct prediction of the evolutionary model and fits quite well in the creation one). The only possible point which DNA does not mesh well with is that of being 'utterly alien', but this depends on Sagan's meaning. It's certainly alien to anything one would expect to arise from natural processes (chemistry alone).

Conclusion

It is clear that one's premise determines the conclusion reached regarding empirical evidence. Evolutionists exclude an intelligent designer from the very definition of possible scientific alternatives. Swindell truly states that

> 'man's way of defining words has no jurisdiction in the dominion of objective reality. Truth is sublimely indifferent to our definition of words, even to our definition of science.'[22]

Rather than ruling out an evolutionary explanation of life's complexity, the creationist instead contends that the Bible explains life *better* than evolution—indeed it has *predicted* what is today observed.

The fact that scientists would use such as double standard as to infer intelligence in the SETI project but not in DNA, despite DNA's compliance with the same criterion, illuminates a great philosophical bias in the arena of origins favouring naturalism. Both paradigms—evolution and creation—offer an explanation of DNA. However, one is ruled out simply because it is not naturalistic. So-called 'objective science' already has its mind made up, and a Divine Creator is not in the picture.

References

1. Vogel, G., Tracking the history of the genetic code, *Science* **281**(5375):329–331, 1998.
2. Sarfati, J., DNA: marvellous messages or mostly mess? *Creation* **25**(2):26–31, 2003.
3. Bradley, D., The genome chose its alphabet with care, *Science* **297**(5588):1789–1791, 2002.
4. Dawkins, R., *The Blind Watchmaker*, W.W. Norton & Company, New York, pp. 115–116, 1996.
5. Zweiger, G., *Transducing the Genome*, McGraw-Hill, New York, p. 13, 2001.
6. Ridley, M., *Genome*, Perennial, New York, pp. 7–8, 1999.
7. Woodmorappe, J., Pseudogene function: regulation of gene expression, *TJ* **17**(1):47–52, 2003.
8. Walkup, L.K., Junk DNA: evolutionary discards or God's tools? *TJ* **14**(2):18–30, 2000.
9. Zweiger, ref. 5, p. 48.
10. Batten, D., More junk reclaimed, *TJ* **16**(2):8, 2002.
11. Woodmorappe, J., Junk DNA indicted, *TJ* **18**(1):27–33, 2004.
12. DeWitt, D., 'Junk' DNA is not 'junk', lecture given at Creation Conference 2003, West Harrison, 25 May 2003.
13. Weaver, R.F. and Hedrick, P.W., *Genetics, Second Edition,* Wm. C. Brown Publishers, Dubuque, IA, p. 332, 1992.
14. Begley, T.J. and Samson, L.D., A fix for RNA, *Nature* **421**(6925):795–796, 2003.
15. Risley, K.M., personal correspondence, 2 June 2003.
16. Abate, T., quoted in: Batten, D., Catchpoole, D. and Wieland, C., Message mania, *Creation* **23**(3):16–19, 2001.
17. Dawkins, ref. 4, p. 1.
18. Todd, S.C., A view from Kansas on that evolution debate, *Nature* **401**(6752):423, 1999.
19. Sivertsen, W.I., SETI and DNA, *CRSQ* **39**(3): 190–193, 2002.
20. Olson, S. *Mapping Human History*, Houghton Mifflin Company, Boston, p. 17, 2002.
21. Atkins, J.F. and Gesteland, R., The 22nd amino acid, *Science* **296**(5572):1409–1410, 2002.
22. Swindell, S., Shining light on the evolution of photosynthesis, *TJ* **17**(3):74–84, 2003.