

of categories.

My thanks go to Dr Batten for taking the time to review my work, for pointing out an error (my use of 'polyploidy'), and for *not* pointing out a number of other genuine errors that might have sidetracked the review. I am aware that revisions and improvements must eventually come. I do hope, however, that rather than to be skeptical of a Biblical classification scheme's usefulness to biology, Batten and others will remain open to the possibility that this is a logical extension of baraminology, providing a framework for an origins-based sorting of the Kinds. If Kinds, or holobaramin, are indeed discontinuous biological units of Creation (not ancestrally related to each other), then we should reconsider our practice of grouping these discontinuous units according to anatomical continuities, rather than according to the discrete groupings laid out in Scripture. My exhortation in this area was echoed by Richard Sternberg at the Discontinuity Conference, which I attended.² He challenged creationists to avoid evolutionary terms, and advocated the development of an alternate vocabulary.

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References

1. Batten, D., A rose by any other name, *TJ* 15(3):27-28, 2001.
2. Wood, T.C., The future looks bright, *TJ* 15(3):75, 2001.

The crimes of Galileo

I found Dr Schirmmacher's article in *CEN Tech. J.* 14(1) most interesting and enlightening. However, I am perplexed by a statement he made regarding the charges brought against Galileo. He writes (p. 97, para. 3):

'The Court of Inquisition did not accuse Galileo of teaching

against the Bible, but of disobeying a papal decree.'

However, the actual charges brought against Galileo say otherwise:¹

'We say, pronounce, sentence and declare that you, Galileo, by reason of these things which have been detailed in the trial and which you have confessed already, have rendered yourself according to this Holy Office vehemently suspect of heresy, namely of having held and believed a doctrine that is false and contrary to the divine and Holy Scripture: namely that Sun is the centre of the world and does not move from east to west, and that one may hold and defend as probable an opinion after it has been declared and defined contrary to Holy Scripture. Consequently, you have incurred all the censures and penalties enjoined and promulgated by the sacred Canons and all particular and general laws against such delinquents. We are willing to absolve you from them provided that first, with a sincere heart and unfeigned faith, in our presence you abjure, curse and detest the said errors and heresies, and every other error and heresy contrary to the Catholic and Apostolic Church in the manner and form we will prescribe to you. Furthermore, so that this grievous and pernicious error and transgression of yours may not go altogether unpunished, and so that you will be more cautious in future, and an example for others to abstain from delinquencies of this sort, we order that the book Dialogue of Galileo Galilei be prohibited by public edict. We condemn you to formal imprisonment in this Holy Office at our pleasure. As a salutary penance we impose on you to recite the seven penitential psalms once a week for the next three years. And we reserve to ourselves the power of moderating, commuting, or taking off, the whole or part of the said penalties and penances. This we say, pronounce, sentence, declare,

order and reserve by this or any other better manner or form that we reasonably can or shall think of. So we the undersigned Cardinals pronounce:

F. Cardinal of Ascoli
B. Cardinal Gessi
G. Cardinal Bentivoglio
F. Cardinal Verospi
Fr. D. Cardinal of Cremona
M. Cardinal Ginetti
Fr. Ant. s Cardinal of. S. Onofrio.'

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1. See <galileo.imss.firenze.it/museo/a/esenten.html>.

Protein families

As a molecular biologist, I read with interest Truman and Heisig's recent article.¹ I had been pondering over this type of study a number of months ago, but had no idea of how I would even begin to estimate constraints related to function and correct protein folding. I wanted to estimate how unlikely it would have been for the proposed evolutionary bacteria to have spontaneously arisen based on DNA polymerase, RNA polymerase, some sort of tRNA loading enzyme, plus DNA encoding these components. If one imagined this floating in a nutrient rich pool, one could even forgo metabolic enzymes and packaging and just call the pool itself a life form if it could make more of each component. However according to this reported cytochrome c model, there would be more than enough problems even getting the DNA right for one of the enzymes, let alone spontaneous generation of the first proteins to transcribe/translate the DNA. This paper is an elegant demonstration of how, if the earth were treated as a giant test tube, sporting paranormal organism growth and mutation rates,

and if it was allowed one billion years worth of attempts, it would still not be capable of generating a small functional gene product by chance.

There are three matters I would like to address. Some readers might mistakenly believe that the reported probabilities of cytochrome *c* generation are based solely on the 7 entries shown in Table 2. I had initially made this oversight myself, though clearly this cannot be the case. The very low probability of 6.88×10^{-45} was indeed generated using all 110 codons, as was originally reported in Dr Yockey's book, and alluded to in footnote 32. Footnote 32 also indicates that 16 of the 110 codons are highly conserved residues, being constrained to a single amino acid.

Secondly, I have noticed that the authors only treat the 110 codons encoding the various amino acids, but that the stop codon has not been accounted for in the statistics. Every translated polypeptide requires a stop codon in order to terminate the translation process, though the various forms of cytochrome *c* examined may not all be exactly 110 amino acids long. However, if greater than 95% of all sequences are conserved to exactly 110 aa's, then wouldn't that be a significant reason to also include a 111th codon as a stop codon?

The final matter I would like to address is the calculation of probabilities based on 61 of the 64 codons. The premise is made in this paper that a number of conditions must be met before Darwinian natural selection can come into effect, and I agree that this is the best way to approach the model. Based on this premise, random mutagenesis of the 110 (or 111) codons will occur, generating any one of the 64 possible triplet arrangements of A, C, G and T. This process will undoubtedly include the occurrence of stop codons throughout the multitude of generations of organisms predeceasing the organism harboring a functional gene for cytochrome *c*. However, the final functional product must not encode for a premature stop codon, and therefore this should be statistically

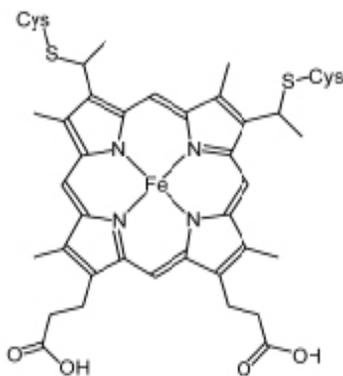
selected against.

I would presume that the 3 codons encoding stop codons have not been treated statistically because a truncated version of cytochrome *c* would be selected against. My argument against this treatment is that this model, by definition, cannot allow for selection until a functional protein has finally been achieved. Progeny will not be selected for or against if the molecule is initially truncated, any more than if a key amino acid is missing. Only when functionality is reached does one have to worry about avoiding a truncated protein. My general feeling is that stop codons are as likely to arrive by chance (3 of 64 codons) as any one of the 20 amino acids (61 of 64 codons between 20 aa's = avg 3.05 of 64 codons per aa), and need to be treated with equal weight in the unbiased world of statistics. Also, treating with 64 rather than 61 would further decrease to probability of finding the first cytochrome *c* gene with minimal functionality for natural selection to act on.

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References

1. Truman, R. and Heisig, M., Protein families: chance or design? *TJ* 15(3):115-127.



A heme group (above) is associated with the protein backbone of cytochrome *c*.

Royal Truman replies:

Dr Warawa identified some legitimate statistical issues which we should consider. Dr Yockey's analysis

dealt with a *functional* cytochrome *c* protein. He denied the 3 *Stop* codons the opportunity of appearing in the coding region, reasoning that an evolutionary starting point might be a duplicated gene or gene transferred from another organism. Thus, a biologically useful protein would possess only 61 different codons in the coding region, which mutations must convert into codons for acceptable amino acids at that position.

Warawa is surely correct in pointing out that our statistics¹ deal with generating a *first* minimally functional ancestral gene which natural selection could sense. It seems reasonable, whether the evolving gene would be expressed or not, that the non-functional sequence could use all 64 codons during the initial trial-and-error period. For this scenario, both I and Yockey agree our correspondent's observation is correct.

A refinement to this observation considers the case where a new gene would express worthless polypeptides during much of its putative evolution. This would waste cellular material and energy and increase the risk of interference with useful proteins. Any accidentally generated *Stop* codons would minimize the damage and actually be selected *for!* Mutations which removed such *Stop* codons would be disadvantageous and (re)introduction anywhere in the coding sequence would be favoured. One would expect *Stop* codons to be represented in higher than statistically expected proportions (3/64), especially near transcription initiation (to truncate the worthless polypeptide as much as possible). This scenario would then demand additional evolutionary trials and error to remove such useful *Stop* codons until the first minimally functional protein would be stumbled upon.²

The number of tolerated amino acids predicted to be permitted³ is shown in Figure 1. Dr Heisig and I had printed only a few residues to illustrate how the calculations are performed. Notice that no less than 16 of the 110 residues of cytochrome

(not published) suggest that the chance of the whole path, including pre-selection and fine-tuning afterwards actually be executed, appears to be *less* than that the highly refined final gene should arise by trail and error in one leap. Not only are the chances of fixing each mutation having positive selection small, but extinction of each evolutionary ‘experiment’ to generate new genes requires starting all over again multiple times.

Is Cudi Dagh an *impossible* location?

I am writing in response to Bill Crouse’s article in which he espouses an alternative resting-place for Noah’s Ark. While I would agree that the *primary* reason for searching on Mount Ararat is the wealth of eyewitness accounts that place the Ark there, I would heartily disagree that other reasons are invalid. The very fact that physical conditions on Ararat make it *possible* for the Ark to both be preserved, as well as hidden most of the time (which thus lends credence to the eyewitness accounts), make Ararat a leading candidate, whereas Cudi Dagh is an *impossible* location for the Ark’s preservation from a physical standpoint alone. If it had indeed landed there, it would hardly have been preserved to be the subject of eyewitness reports several millennia later. I would furthermore take issue with Crouse’s rather flippant dismissal of the eyewitnesses as either mistaken or crackpots. He admits that *one* example of a credible witness would suffice to undermine his entire thesis. Has he spoken with Vince Will? Vince is a Christian pastor who saw the Ark *both* in photographs *and* from the pilot’s seat of a plane during WWII. He examined the photos closely and then verified his sightings from the air. He is adamant that it was no rock, since it was broken open and he was able to see inside a portion of it (ever seen a *rock* with cages inside it?). He is so certain of what he saw that he has stated he would ‘stake his salvation upon it being the Ark’. If Vince Will

is a crackpot or mistaken, Mr. Crouse at least owes us an explanation of how he—a *non-witness*—is better able to determine what Vince saw than Vince himself.

Crouse also contends that Ararat has been thoroughly searched and fully documented. I doubt that *anyone* actually involved in climbing Ararat believes that to be the case—myself included. Two of my friends and partners at different times, John McIntosh and Richard Bright, were with James Irwin at various times and both have attested to the fact that even Irwin’s teams searched very little of the upper reaches of the Ahora Gorge. They were thwarted at different times by the military, by the conditions, and even by Irwin himself (falling and being injured and thereby aborting that year’s mission). The mountain is vast, treacherous, and difficult to access—physically, politically *and* spiritually—and *fully capable of continuing to hide the Ark*, especially given the year-round snow cover.

Crouse, in lieu of eyewitnesses, uses the Koran and several other Muslim sources to bolster his theory that the Ark came to rest on Cudi Dagh. Of course, it stands to reason that since the Koran mentions Cudi Dagh as the resting-place of the Ark, other Muslim sources would scarcely dare publicly contradict Mohammed. Even the existence of a stone ‘mock-up’ of the Ark on Cudi Dagh is *not* evidence of the Ark having once been there, but evidence of the Islamic faithful paying tribute to their belief in the Koran.

Crouse has an interesting pattern of determining the reliability of a witness: Everyone who claims to have seen Noah’s Ark on *Mount Ararat* is ‘unreliable’ because, according to Crouse, it is not there; on the other hand, those eyewitnesses who were either lost or *liars* are deemed reliable when Crouse—a *non-eyewitness*—believes their testimony can be *altered* to bolster his theory. It’s easy to claim that there are no reliable eyewitnesses when you simply change the testimony of those you disagree with, or better

yet, call them liars.

But going one step further, for the sake of argument, suppose Crouse is right that the Turkish soldiers *did* see the Ark (and they were wrong about their own location) after WWI. That would have to mean that the Ark was still extant *at least* until WWI. Yet, elsewhere in the same article is a photo of a stone structure on the mountain, called ‘the Ship of Noah’ by the locals. According to Crouse, Gertrude Bell took this photo after ‘exploring the summit’ in 1910 many years *prior* to WWI.

Where is the Ark of Noah purportedly seen by the Turkish soldiers seven years later? Is it possible Gertrude would ‘explore the summit,’ take a photo of a crumbling stone corral, and *ignore* a 150-m long ship? Hardly. Which means that *photographic evidence* in Crouse’s own article *preclude* him from using the Turkish soldiers, or Prince Nouri, or ‘two Turkish journalists in 1949’ to somehow add credibility to a theory which otherwise is completely devoid of *any* credible eyewitness support.

To put it simply, if Crouse’s theory had *any* merit, we would have to accept the following: the Ark lasted for well over 4,000 years on a mountain *not* covered in ice, a mountain readily accessible, but it was never photographed or properly documented, and the only people who saw it and told about it, either did not even know where they were or they *lied* about where they were in order to make their story more acceptable to other Christians, and *then* the Ark completely disappeared within the last 80 years. *Or*, the Ark can disappear and reappear, even though, as the photo shows, there is no snow to hide it.

Maybe, the Ark no longer exists in recognizable form, but *if* it does, the only credible evidence for it is on Mt. Ararat. I would, however, concur with Crouse on one additional point, namely that finding Noah’s Ark will most certainly require God’s intervention and timing, *as well as the prayers and efforts of His people*.