

CREATION RESEARCH SOCIETY



QUARTERLY

Volume 58 Fall 2021 Number 2

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Number 2

Fall 2021

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Haec Credimus

For in six days the Lord made heaven and earth, the sea, and all that in them is, and rested on the seventh. —Exodus 20:11

Creation Research Society Quarterly

Volume 58

Number 2

Fall 2021

Cover by Michael E. Erkel, Afton, Virginia

Design services by Cindy Blandon, cblandon@aol.com

The *Creation Research Society Quarterly* is published by the Creation Research Society, 1 W. Firestorm Way #145, Glendale, AZ 85306, and it is indexed in the *Christian Periodical Index* and the *Zoological Record*.

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ISSN 0092-9166

Printed in the United States of America

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Classification of the Enigmatic Red Panda (*Ailurus fulgens*) Based on Molecular Baraminology-Based Analysis

Matthew Cserhati

Abstract

The red panda is a curiosity of biological classification. Taxonomists have come to different conclusions on its placement depending on which characteristics are considered. It was once considered closely related to bears (ursids), other times to raccoons (procyonids), or animals such as skunks (mephitids), badgers, otters, or martens (mustelids). Perhaps the red panda belongs to its own group.

Since the whole genome sequence was available for this organism, the Whole Genome k-mer Signature algorithm was used to classify the red panda. Mitochondrial DNA and cytochrome-b protein sequence similarity was also measured to help determine the baraminic status of the red panda.

According to the whole genome analysis, the red panda groups with the mustelids, apart from ursids. The placement of mephitids is uncertain. According to the mitochondrial DNA analysis, the red panda is part of a cluster discontinuous with mustelids and all other groups. However, when the sequence identity of the cytochrome-b protein is assessed, it appears that the red panda again shows continuity with mustelids, and discontinuity with ursids. Mephitids also show discontinuity with mustelids. The difference between the whole genome and mitochondrial results could be due to nucleo-mitochondrial discordance, a common phenomenon. A higher number of four-fold degenerate sites in the mitochondrial cyt-b compared to the first exon of the nuclear RAG1 gene support this.

Based on these results, it is likely that the red panda belongs to the mustelid holobaramin, although further baraminology studies are warranted, both morphological and molecular.

Key Words: Red panda, whole genome, mitochondrion, mephitid, mustelid, ursid

Introduction

Genesis 1:20–25 describes how God created fish, birds, and land-animals each according to their kinds. Species within a kind were originally capable of breeding with one another but are incapable of breeding with species from another kind. Hence, there is continuity between species within a kind, and discontinuity between two separate kinds. In technical terms, a kind is called a ‘baramin,’ which is a compound of two Hebrew words, ‘bara’ meaning ‘he created,’ and ‘min’ meaning kind. Thus, molecular baraminology is the study of the created kinds from a molecular biology perspective. A ‘holobaramin’ denotes all species which constitute a single baramin. A ‘monobaramin’ denotes either part of, or the entire holobaramin. This means it can also denote a specific lineage or subgroup within a holobaramin. For example, domesticated cats are a monobaramin within the cat holobaramin.

Most baraminology studies classify an entire set of species. However, there are many individual species that defy classification. These organisms do not resemble any other known organism, and as such are enigmatic. Such organisms include the duck-billed platypus, the tuatara (Cserhati, 2021a), and the echidna. These organisms could either belong to their own holobaramin, with all other related species within its group dying out, or they could possibly be related to other contemporary species, albeit in an unapparent way. Or it may even be that a holobaramin consists of but a single species, for example the human holobaramin, since only man was made in the image of God (Genesis 1:26–27). God probably created holobaramins with only one single species, but some kinds diversified more than others over time.

Looks can deceive, the saying goes, so alongside morphological analysis, a molecular baraminology analysis may unveil true baraminic relationships—an



Figure 1. The red panda (*Ailurus fulgens*, upper left), the giant panda (*Ailuropoda melanoleuca*, lower left) raccoon (*Procyon lotor*, upper right), American marten (*Martes americana*, lower right). Copyright of images: red panda: en.wikipedia.org/wiki/Red_panda, giant panda: en.wikipedia.org/wiki/Giant_panda, raccoon: en.wikipedia.org/wiki/Raccoon, American marten: inaturalist.org/guide_taxa/335813.

other advantage of molecular methods augmenting with morphological ones. Whereas morphology studies may not detect variation within a species, the genome is more static, and thus its analysis may uncover the presence of more cryptically related species.

One such hard-to-classify animal is the red panda (*Ailurus fulgens*). Distinguished by its bushy tail and red-white coloration, it is found in parts of Nepal, India, and China (Figure 1, upper left). Whereas *A. fulgens* denotes the Himalayan red panda, another subspecies exists, called the Chinese red panda (*Ailurus fulgens styani*). The two subspecies have been differentiated based on geographic isolation and genomic differences (Hu et al., 2020). According to Su et al. (2001) the genetic diversity of the mtDNA of the red panda shows that there are two major populations of the red panda in the provinces of Sichuan and Yunnan in China.

Theories about the exact position of the red panda abound. Geoffroy-Saint-Hilare and Cuvier originally classified the red panda as a member of the raccoon family (Procyonidae), although they ended up calling it *Ailurus*, because of its somewhat feline appearance (though this is subjective) (Slattery and O'Brien, 1995; Flynn et al., 2000). Some think that the red panda is related to the giant panda (*Ailuropoda melanoleuca*), because of its sesamoid bone, an enlarged toe-like structure, produced by an enlarged carpal bone (Hennigan, 2009; Abella et al., 2015). This modified bone is used to process bamboo, which makes up 99% of their diets. Still others place the red panda into its own family (Ailuridae) (Ledje and Arnason, 1999). More recent molecular-based studies of the red panda are somewhat divided, with some associating it with mustelids, procyonids, and mephitids (Fulton, 2007; Sato, 2009). Dragoo and Honeycutt (1997)

place *A. fulgens* within Procyonidae based on total evidence from the 12S, 16S rRNA and cytochrome-b genes, combined with morphological data.

Biblical considerations

The red panda is not mentioned anywhere in the Bible, so we must classify it based on genetic and genomic data.

Previous baraminology studies

Previous baraminology studies have not addressed the baraminic statuses of the red panda in much depth. Hennigan (2010), for example, does not classify the red panda as a member of the bear holobaramin, despite mentioning several shared features with the giant panda (*A. melanoleuca*). Both types of pandas have a diet consisting almost exclusively of bamboo (both species eat meat on occasion), and an enlarged radial sesamoid bone, which they use to process bamboo. Genetic evidence classifies *A. melanoleuca* as a member of the family Ursidae. This includes analysis of the mtDNA analysis, chromosome banding patterns, and serological and immunological evidence (Yu et al., 2007; Krause et al., 2008).

Thompson and Wood studied craniodental characteristics of ‘Cenozoic’ mammal baramins but did not find any continuity or discontinuity between *A. fulgens* and Procyonidae (Thompson and Wood, 2018). *A. fulgens* also has some unique characteristics: a large zygomatic arch, a powerful jaw, and complex cheek teeth, following a P2–3 pattern, uncommon in carnivores. These evidences would support placing the red panda into its own group.

Materials and Methods

Sequence data

The whole genome sequences of 28 mammals were downloaded from NCBI, including organisms that are classified near *A. fulgens*, namely, species from

the families Ursidae (bears), Procyonidae (raccoons), Mephitidae (skunks and stink badgers), Mustelidae (weasels, badgers, otters, ferrets, minks, martens, wolverines, etc.), and Felidae (cats). A list of these species and the link to their WGS can be found in Supplementary file 1 online. The WGS were analyzed using the Whole Genome K-mer Signature (WGKS) algorithm (Cserhati, 2020).

The mtDNA sequences of 52 mammals from these families were also downloaded from NCBI for analysis. The species and the accession number of their mtDNA sequences can be found online in Supplementary file 2.

A study focused on the sequence identity of the cytochrome-b protein sequence was also done for 51 species. These results are in Supplementary file 3. The cytochrome-b sequences were all downloaded from the NCBI Nucleotide database for these species. The mtDNA and cytochrome-b sequences were analyzed by looking at their sequence similarity.

To examine mito-nuclear discordance, both a mitochondrial gene and a nuclear gene of approximately the same length from *A. fulgens* and the closely related *A. fulgens styani* were aligned and examined for four-fold degeneracy in the third position of triplets in the mRNA sequence. These two genes were cytochrome-b (1,130 bp) and the first exon of RAG1 (1,095 bp). They can be seen in Table 4.

Software

Supplementary files 1, 2, and 3, and supplementary Figures 1 and 2 are available online at github.com/csmaty/redpanda. The *Kalign* multiple alignment program was used with default parameters to create a multiple alignment of mtDNA sequences on the EBI website at [ebi.ac.uk/Tools/msa/kalign](https://www.ebi.ac.uk/Tools/msa/kalign) (Lassmann, 2006). The alignment of the 51 cytochrome-b sequences were done using the *MUSCLE* algorithm (Edgar, 2004) using the MEGA-X software (Ku-

mar et al., 2018). Using this software, the distance matrix was transformed into a similarity matrix by subtracting the distance values from 1. Heatmaps were created using the heatmap command in R, version 3.6.0. The ‘ward.D,’ ‘single,’ and ‘mcquitty’ algorithms were used to cluster organisms in the heatmaps for the WGKS, mtDNA and cyt-b analyses, respectively.

Results

Whole Genome K-mer Signature analysis

According to the protocol of the WGKS algorithm, the octamer signature for the WGS of 28 mammals was calculated and compared to one another to generate Pearson Correlation Coefficient (PCC) values. This PCC matrix was then visualized in a heatmap, in Figure 2. The Hopkins clustering statistic is 0.9, which denotes excellent clustering.

In Figure 2 we can see three groups, with the western spotted skunk (*Spilogale gracilis*) possibly as a singleton species in its own group. A silhouette plot was constructed for either three or four clusters. The average silhouette width is 0.82 in the case of three clusters (Supplementary Figure 1) and 0.8 for four clusters (Supplementary Figure 2). The difference is very slight. Based on this result, three putative baramins can be defined: felids covering the family Felidae (eleven species), ursids covering the family Ursidae (five species), and musteloids, a superfamily including Mephitidae and Mustelidae (twelve species). All three of these groups show statistically significant continuity within themselves and discontinuity with all other species in this study. Table 1 lists the results of the WGKS clustering, showing the species according to the cluster to which they belong.

A. fulgens has a mean PCC value of 0.877 ± 0.011 (mean $\pm$ standard error of the mean, SEM) with all other members

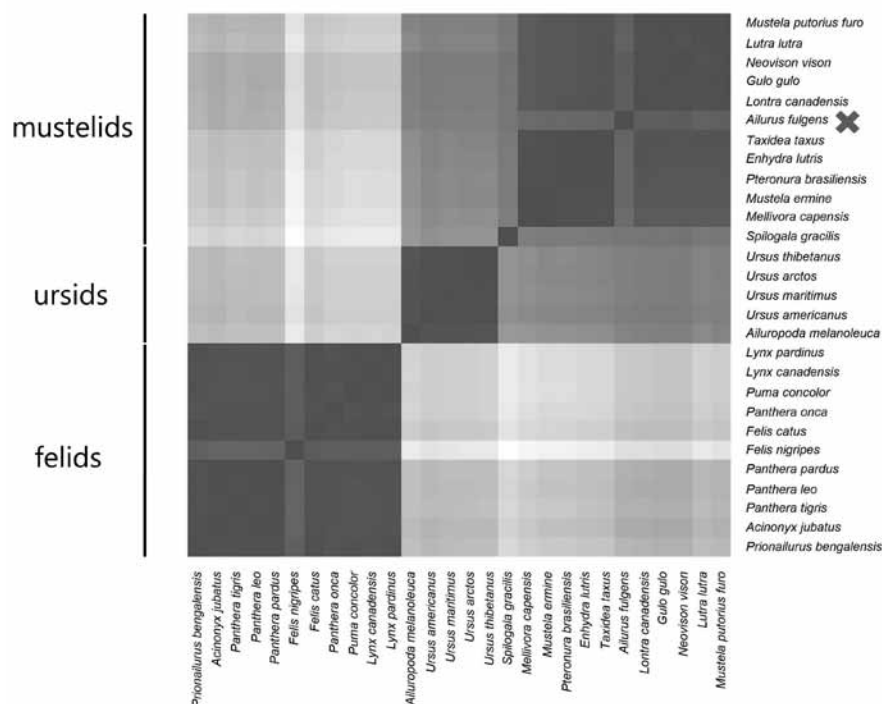


Figure 2. Heatmap showing baraminic relationships between *A. fulgens* (indicated by an X) and several ursid, mustelid, mephitid, and felid species. Each pixel in the heatmap represents the PCC value between the WGKS of two given species in the study. Species with high continuity have a high PCC value, which corresponds to darker colors. Species with high discontinuity have lower PCC values, represented by a lighter pixel. *A. fulgens* clusters nicely within Musteloidea, apart from felids and ursids, although with a lesser than average PCC value.

of the Musteloidea baramin. However, all other mustelids have a mean PCC value of 0.93 ± 0.024 , which is somewhat higher. The reason for the low mean PCC value between *A. fulgens* and all other mustelids might be its geographic isolation in the mountainous areas of Nepal, India, and China. This could have allowed for greater genetic change to take place.

This difference in PCC values does not seem significant if we look at the fact that the black-footed cat (*Felis nigripes*) has a mean PCC value of 0.9 ± 0.005 with all other felids, whereas all other felids have a mean PCC of 0.98 ± 0.003 among themselves. The black-footed cat definitely belongs to the cat holobaramin. *F. nigripes* is also an isolated species, found

in South Africa, Namibia, Botswana, and Zimbabwe. It has been listed as a vulnerable species on the IUCN Red List since 2002, and in vitro fertilization and cryopreservation efforts are being undertaken to help preserve this species (Herrick et al., 2010).

A. fulgens has a mean PCC value of 0.73 ± 0.004 with the five members of the ursid holobaramin, suggesting it is unrelated to bears. It has a mean PCC value of only 0.58 ± 0.01 with the members of the felid baramin, meaning that it is also neither a cat, nor a 'bear-cat.'

Analysis of the alignment of mtDNA sequences

Besides WGS, the mtDNA sequences of 15 ursids, 30 mustelids, 3 mephitids,

Table 1. Classification of 28 mammalian species based on the WGKS method. Group 1 consists of Mustelidae+Mephitidae, plus the red panda; Group 2 is all the species from Ursidae, and in Group 3 are all the species from Felidae from this study.

Species	Group
<i>Ailurus fulgens</i>	1
<i>Enhydra lutris</i>	1
<i>Gulo gulo</i>	1
<i>Lontra canadensis</i>	1
<i>Lutra lutra</i>	1
<i>Mellivora capensis</i>	1
<i>Mustela ermine</i>	1
<i>Mustela putorius furo</i>	1
<i>Neovison vison</i>	1
<i>Pteronura brasiliensis</i>	1
<i>Taxidea taxus</i>	1
<i>Ailuropoda melanoleuca</i>	2
<i>Ursus americanus</i>	2
<i>Ursus arctos</i>	2
<i>Ursus maritimus</i>	2
<i>Ursus thibetanus</i>	2
<i>Acinonyx jubatus</i>	3
<i>Felis catus</i>	3
<i>Felis nigripes</i>	3
<i>Lynx canadensis</i>	3
<i>Lynx pardinus</i>	3
<i>Panthera leo</i>	3
<i>Panthera onca</i>	3
<i>Panthera pardus</i>	3
<i>Panthera tigris</i>	3
<i>Prionailurus bengalensis</i>	3
<i>Puma concolor</i>	3
<i>Spilogala gracilis</i>	3

and 2 procyonids as well as the two sub-species of the red panda were available at NCBI. These 52 mtDNA sequences

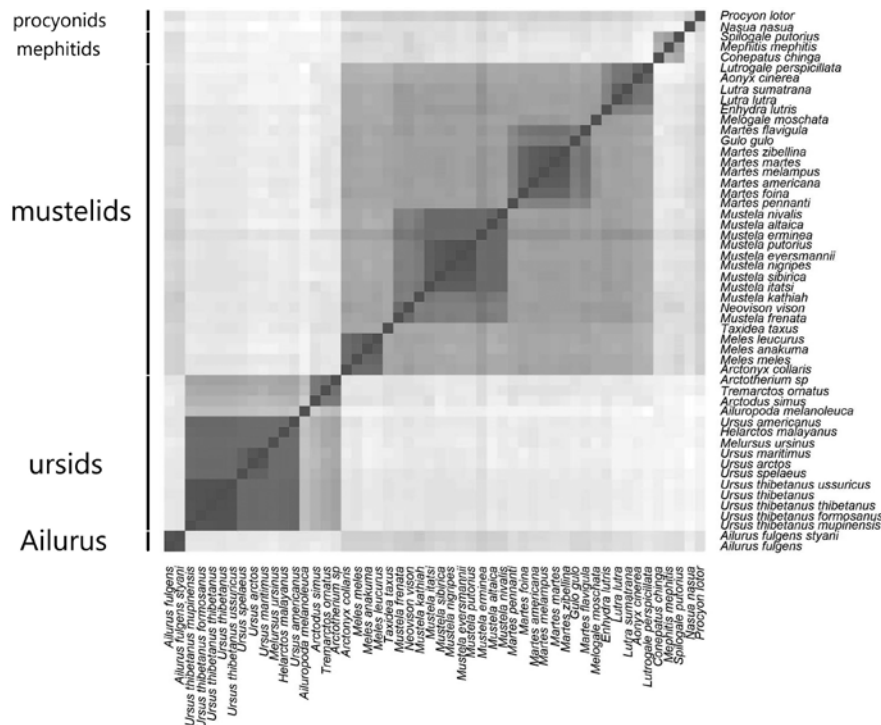


Figure 3. Heatmap showing baraminic relationships between two *Ailurus* species and several procyonid, mephitid, mustelid, and ursid species based on sequence similarity between their mtDNA sequences. Species with high continuity have a high PCC value, which corresponds to darker colors. Species with high discontinuity have lower PCC values, represented by a lighter pixel. The two *Ailurus* species and the three mephitids both form clusters separate from mustelids.

were aligned with the MUSCLE aligner software (Edgar, 2004). The resulting identity matrix showing global sequence similarity was visualized in a heat map (Figure 3). The list of species, their mtDNA accession numbers, the sequence identity matrix, the clusters and the baraminic classification statistics can be found in Supplementary file 2. The Hopkins clustering statistic is 0.841, which corresponds to good clustering. The list of species and their corresponding clusters can be seen in Table 2.

In this heatmap we can see two main, large clusters as well as three smaller ones. All five groups show statistically significant continuity among themselves and discontinuity with all other groups. Two small groups can be

seen in the upper right, the first one being two procyonid species, *Procyon lotor* (the common raccoon), and *Nasua nasua* (the South American coati). Next are three mephitid species, *Spilogale putorius* (the eastern spotted skunk), *Mephitis mephitis* (the striped skunk), and *Conepatus chinga* (Molina's hog-nosed skunk). Thirty mustelid species make up the largest cluster, with species from the genera *Aonyx*, *Arctonyx*, *Enhydra*, *Gulo*, *Lutra*, *Lutrogale*, *Martes*, *Meles*, *Mustela*, *Neovison*, and *Taxidea*. Another large cluster with 15 ursid species can be seen to its lower left. This group is made up of the species *Arctodus simus*, *Arctotherium sp.*, *Ailuropoda melanoleuca*, *Helarctos malayanus*, *Melursus ursinus*, *Tremarctos ornatus*, and nine species of

Ursus. In the lower left corner, we have the two red panda species, *A. fulgens*, and *A. fulgens styani*.

The findings of the mtDNA study contradict those of the whole genome analysis. It is true that the mtDNA is only a small fraction of the whole genome, so more weight should be given to the results of the WGKS analysis. However, some authors have found that *A. fulgens* is related to mustelid species. For example, Peng et al. (2017) placed *A. fulgens* next to *Martes americana*, the American marten in an analysis of 13 concatenated mtDNA proteins. Based on a study of the 12S rRNA, the 16S rRNA, and cytochrome-b, Flynn et al. (2000) also classified *A. fulgens* as a mustelid.

Protein sequence analysis of cytochrome-b

Cytochrome-b is a structurally conservative protein which does not mutate freely. It is often used to infer phylogenetic relationships between organisms (Meyer, 1994), and can so be used in baraminology studies as well. The cytochrome-b sequences of 51 felids, ursids, mustelids, procyonids and mephitids were aligned and the similarity matrix was determined using the MEGA-X software. The Hopkins clustering statistic is 0.8, which denotes good clustering. In Figure 4 we can see the heatmap which depicts the baraminic relationships between the 51 species. The species list, the identity matrix, the clusters, and the clustering statistics are available online in Supplementary file 3. The clustering results are available in Table 3.

In the heatmap (Figure 4) we can see three main clusters and two species by themselves, *N. nasua* and *M. mephitis*. In the lower left there is a tight cluster of 25 felids. In the upper right there is a cluster of five ursid species, and another with 19 mustelid species. All three larger clusters show statistically significant continuity among themselves and discontinuity with all other clusters.

Table 2. Classification of 52 mammalian species based on sequence identity calculated from the alignment of their mtDNA sequences. The numbers correspond to the following groups: 1: Ursidae, 2: Mephitidae, 3: Procyonidae, 4: Ailurus, 5: Mustelidae.

Species	Group	Species	Group
<i>Ailuropoda melanoleuca</i>	1	<i>Meles leucurus</i>	5
<i>Melursus ursinus</i>	1	<i>Melogale moschata</i>	5
<i>Ursus spelaeus</i>	1	<i>Martes pennanti</i>	5
<i>Ursus arctos</i>	1	<i>Gulo gulo</i>	5
<i>Ursus maritimus</i>	1	<i>Martes flavigula</i>	5
<i>Helarctos malayanus</i>	1	<i>Martes foina</i>	5
<i>Ursus americanus</i>	1	<i>Martes americana</i>	5
<i>Ursus thibetanus mupinensis</i>	1	<i>Martes melampus</i>	5
<i>Ursus thibetanus formosanus</i>	1	<i>Martes martes</i>	5
<i>Ursus thibetanus thibetanus</i>	1	<i>Martes zibellina</i>	5
<i>Ursus thibetanus</i>	1	<i>Mustela frenata</i>	5
<i>Ursus thibetanus ussuricus</i>	1	<i>Neovison vison</i>	5
<i>Arctodus simus</i>	1	<i>Mustela kathiah</i>	5
<i>Tremarctos ornatus</i>	1	<i>Mustela erminea</i>	5
<i>Arctotherium sp.</i>	1	<i>Mustela itatsi</i>	5
<i>Conepatus chinga</i>	2	<i>Mustela sibirica</i>	5
<i>Mephitis mephitis</i>	2	<i>Mustela nigripes</i>	5
<i>Spilogale putorius</i>	2	<i>Mustela eversmannii</i>	5
<i>Nasua nasua</i>	3	<i>Mustela putorius</i>	5
<i>Procyon lotor</i>	3	<i>Mustela nivalis</i>	5
<i>Ailurus fulgens</i>	4	<i>Mustela altaica</i>	5
<i>Ailurus fulgens styani</i>	4	<i>Enhydra lutris</i>	5
<i>Taxidea taxus</i>	5	<i>Lutra lutra</i>	5
<i>Arctonyx collaris</i>	5	<i>Lutra sumatrana</i>	5
<i>Meles meles</i>	5	<i>Aonyx cinerea</i>	5
<i>Meles anakuma</i>	5	<i>Lutrogale perspicillata</i>	5

The heatmap shows that *A. fulgens* and *A. fulgens styani* clustering together with mustelids. However, *M. mephitis* clusters away from the mustelids indicating that the skunk might possibly be from a separate holobaramin. This was

also indicated in the WGKS analysis, where the average silhouette width was 0.8 for classifying *M. mephitis* by itself as opposed to the average silhouette width of 0.82 (a mere difference of 0.02) for putting them together with mustelids.

Degenerate sites between a nuclear and a mitochondrial gene in the two *A. fulgens* species

The accession number and the number of four-fold degenerate triplet third positions of the mitochondrial gene cytochrome-b and the first exon of the nuclear gene RAG1 between *A. fulgens* and *A. fulgens styani* are shown in Table 4. For the mitochondrial gene cytochrome-b there are nine degenerate positions, whereas for exon 1 of the nuclear gene RAG1, there are none. The mitochondrial gene has undergone more mutations, and thus is more degenerate. Therefore, it makes sense that its mtDNA sequence has also diverged more than the nuclear genome.

Other studies have found similar results. For example, Su et al. (2001) found 25 haplotypes in 17 polymorphic positions in an analysis of a 236-bp region of the D-loop region of the mtDNA in 53 red pandas. This is another indication that mtDNA mutates faster than nuclear DNA.

This can explain why the WGS, mtDNA, and cytochrome-b results are divergent. It also shows the importance of performing multiple analyses using different data sets on the same group of organisms. A faster mutation rate means larger differences in the mtDNA sequence in contrast with the nuclear genome. This may reveal lineages within a kind, which might appear to be separate baramins.

Discussion

Based on all this evidence, how do we then classify *A. fulgens*? Based on the somewhat differing results between the WGKS and the cytochrome-b analysis compared to the results of the mtDNA analysis, can we say anything definitive about which holobaramin *A. fulgens* belongs to?

The WGKS analysis seems to bring the strongest results, since it is a global analysis of the entire genome. Accord-

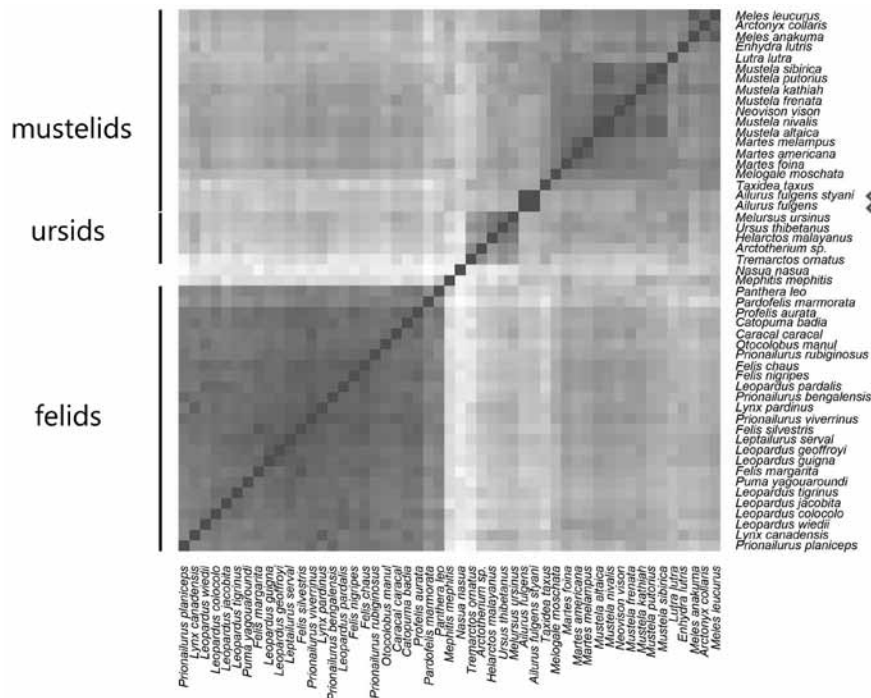


Figure 4. Heatmap showing baraminic relationships between two *Ailurus* species (indicated by the X) and several felid, ursid, mustelid, mephitid and procyonid species based on sequence similarity of the cytochrome-b protein. Species with high continuity have a high sequence similarity, which corresponds to darker colors. Species with low discontinuity have lower sequence similarity, represented by a lighter pixel. The two *Ailurus* species cluster with mustelids. *M. mephitis* does not cluster with mustelids + *Ailurus*

ing to this analysis, *A. fulgens* belongs to the mustelid holobaramin. Also, *M. mephitis* could either belong to the mustelid holobaramin, or it could either belong to another holobaramin, due to the minimal differences in average silhouette width values. Genomically, *A. fulgens* shares several apomorphic chromosome fusions with mustelids, namely F2+C1p and Alp+C1q (Nie, 2002). However, *A. fulgens* differs in several other chromosomal rearrangements indicating that it diverged early from the mustelids. In contrast, the mtDNA is only a small fraction of the entire genome and contains only a handful of genes. According to the mtDNA results, *A. fulgens* seems to cluster away from mustelids and to belong to its own group.

Mephitids also form another cluster. But when we look at the heat map in Figure 4 on cytochrome-b sequence similarity it appears that *A. fulgens* clusters together with mustelids, with mephitids again forming their own holobaramin.

What could be causing the difference? A possibility could be something called mito-nuclear discordance, which entails differences between selective and mutational pressures between nuclear and mitochondrial DNA. This is a common phenomenon and can be caused by migration of organisms (Toews and Brelsford, 2012; Morales et al., 2015; Bernardo et al., 2019).

Alternatively, *A. fulgens* could be the only known member of its own holobaramin, as mentioned in the Introduction

and supported by the mtDNA results. Such a phenomenon is not uncommon. When a taxon, as in this case, a holobaramin loses a large portion of its constituent species, during a mass extinction, such as the Genesis Flood, it loses its capability to re-diversify after the extinction. Such taxa include the bi-valve genera *Permophorus* and *Linearia* (Jablonski, 2002), bellerophonitid snails, prolecanitid ammonoids (Jablonski, 2001) the tuatara (*Sphenodon punctatus*) (Cserhati, 2021a), and parareptiles (MacDougall, 2019). Taxa that find physical refuge can also exist for long periods of time without going extinct. *A. fulgens* may be the sole survivor of its own holobaramin, living in geographic isolation in mountainous habitats of India, China, and Nepal.

Summary and Conclusion

Based on all of these considerations, it is likely that *A. fulgens* belongs to the mustelid holobaramin, and not the ursid holobaramin. Mephitids also very likely form a separate holobaramin apart from mustelids. This is a result similar to the one found by Cserhati (2021b) in a similar analysis.

Acknowledgements

This paper is a part of Creation Research Society Grant #62 and part of the analysis was performed on the new CRS server based at Arizona Christian University.

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Table 3. Baraminic classification of 51 mammals based on their sequence identity of the cytochrome-b protein. The numbers correspond to the following groups: 1: Mustelidae+Ailurus, 2: Felidae, 3: Mephitidae, 4: Procyonidae, 5: Ursidae.

Species	Group	Species	Group
<i>Ailurus fulgens</i>	1	<i>Leopardus geoffroyi</i>	2
<i>Ailurus fulgens styani</i>	1	<i>Leopardus guigna</i>	2
<i>Arctonyx collaris</i>	1	<i>Leopardus jacobita</i>	2
<i>Enhydra lutris</i>	1	<i>Leopardus pardalis</i>	2
<i>Lutra lutra</i>	1	<i>Leopardus tigrinus</i>	2
<i>Martes americana</i>	1	<i>Leopardus wiedii</i>	2
<i>Martes foina</i>	1	<i>Leptailurus serval</i>	2
<i>Martes melampus</i>	1	<i>Lynx canadensis</i>	2
<i>Meles anakuma</i>	1	<i>Lynx pardinus</i>	2
<i>Meles leucurus</i>	1	<i>Otocolobus manul</i>	2
<i>Melogale moschata</i>	1	<i>Panthera leo</i>	2
<i>Mustela altaica</i>	1	<i>Pardofelis marmorata</i>	2
<i>Mustela frenata</i>	1	<i>Prionailurus bengalensis</i>	2
<i>Mustela kathiah</i>	1	<i>Prionailurus planiceps</i>	2
<i>Mustela nivalis</i>	1	<i>Prionailurus rubiginosus</i>	2
<i>Mustela putorius</i>	1	<i>Prionailurus viverrinus</i>	2
<i>Mustela sibirica</i>	1	<i>Profelis aurata</i>	2
<i>Neovison vison</i>	1	<i>Puma yagouaroundi</i>	2
<i>Taxidea taxus</i>	1	<i>Mephitis mephitis</i>	3
<i>Caracal caracal</i>	2	<i>Nasua nasua</i>	4
<i>Catopuma badia</i>	2	<i>Arctotherium sp.</i>	5
<i>Felis chaus</i>	2	<i>Helarctos malayanus</i>	5
<i>Felis margarita</i>	2	<i>Melursus ursinus</i>	5
<i>Felis nigripes</i>	2	<i>Tremarctos ornatus</i>	5
<i>Felis silvestris</i>	2	<i>Ursus thibetanus</i>	5
<i>Leopardus colocolo</i>	2		

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Table 4. *A. fulgens* genes and the number of four-fold degenerate sites at the third triplet position.

Species	Gene	Accession	Degenerate triplet positions
<i>A. fulgens</i>	Cytochrome-b (mitochondrion)	NC_011124.1:14171–15310	9
		AB291074.1:14173–15312	
<i>A. fulgens styani</i>	RAG1, exon 1 (nucleus)	AB188525.1	0
		AB302261.1	

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Petrified Ideas of the Williston Basin

Part I: Geologic Setting

Peter Klevberg and Michael Oard*

Abstract

The Williston Basin of central North America is famous for its “nearly complete geologic column,” and its huge fossil fuel resources. As an incratonic basin with relatively few unconformities and representatives of each of the purported geologic time periods, it has been a poster child for deep time. However, many features appear at variance with uniformitarianism and an ancient Earth. These include the thick sedimentary sequence, gravel-capped planation surfaces, petrified wood and other fossils, and fossil fuels. The geologic setting is presented, showing weaknesses and strengths in the diluvial hypothesis of the basin’s origin and history. The mental straitjacket of uniformitarianism results in petrified ideas that hinder understanding of likely geologic processes. This is particularly demonstrated by extensive planation surfaces with gravel veneers of largely exotic lithologies, which are readily explained by diluvial processes but not by uniformitarianism.

Key Words: Williston Basin, Fort Union Group, Red Wing Creek Structure, sedimentation, planation surface

Introduction

The Williston Basin is one of the “big four shale oil” plays at the heart of the U.S.A.’s revival in oil production that has virtually eliminated American dependence on foreign oil (Figure 1). But the Williston Basin is famous for other reasons. It contains a huge accumulation of sedimentary rocks that purport

to show a nearly-complete stratigraphic sequence (Fowler and Nisbet, 1985; Morton, 2001), challenging advocates of a young earth and global Flood (i.e. diluvialists).

But not so fast! Evolutionists have problems there, too. The confusion between science and natural history (Reed and Klevberg, 2017, 2018)—espe-

cially conflating a priori speculation with data—has hindered stratigraphy, but recent decades have seen a progressively more scientific (albeit uniformitarian) stratigraphic approach in the Williston Basin. As in many parts of the world, the area encompassed by the Williston Basin also exhibits planation surfaces that provide strong evidence for the Deluge. In this paper, we will discuss a few of these issues, and we will provide some geologic background for the examples of fossilization in the Fort Union Group that will be the theme of Part II, which will appear in a subsequent issue.

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Accepted for publication March 30, 2021

The Williston Basin

The basin is an oval shaped depression (Figure 2) filled with up to 5,000 meters of sedimentary rocks. Limestones and dolostones are more common in the deeper “Paleozoic” strata, and clastics are more common in shallower “Cenozoic” strata, but there is much alternation and variation, and salts (“evaporites”) also occur and act as top seals for petroleum systems. Rich petroleum plays have resulted in a wealth of borehole (subcrop) and geophysical data. Our area of study is between Watford City and Medora, western North Dakota, in the southern part of the basin (Figure 3). This covers most of the famous badlands area of the state.

Structure

The Williston Basin is widely believed to be a cratonic or intracontinental basin that gradually sank at a rate constant enough for almost continuous accumulation of sediments, representing the entire geologic column from the Cambrian to the Cenozoic (Morton, 2001). Minor Laramide folding and faulting, dated latest Cretaceous to early Tertiary in the evolution-based age scheme, is present (Hamdani et al., 1994). The center of the basin is just southeast of Watford City (Figure 4), and the depth to basement there is approximately 5,000 m (16,350 ft) from the present land surface (Anderson, 2009). Important structural features are shown on Figure 2.

Stratigraphy

While all the “periods” of the geologic column are commonly believed to be present in the Williston Basin, several unconformities are also acknowledged. Some of the most pronounced are indicated by wiggly contact lines on Figure 5. A stratigraphic column is shown on Figure 6. Some unconformities occur near the edges of the basin but transition into conformities in the center (LeFever, 1991). This supports the belief that Williston Basin unconformities represent



Figure 1. The “big four shale oil basins” of the United States:

1. Williston Basin (target formations Bakken, Three Forks)
2. Denver-Julesburg (target formation Niobrara)
3. Permian (target formations/groups Wolf Camp, Spraberry, Bone Spring)
4. West Gulf (target formations Eagle Ford Group)

sequence boundaries (and subsequence boundaries) following the current sequence stratigraphic paradigm, interpretations of which can conflict with inferred subsidence history seen through uniformitarian-colored glasses (e.g. Zhu and Hajnal, 1993; Sonnenberg, 2017).

One might think the Williston Basin would provide an unusually simple exercise in stratigraphy. But it is more complex. It is well known that efforts at radiometric dating are very much “after the fact” (i.e. chronostratigraphic) and generally forced to conform to “known” dates (Oard, 2019). This is doubly the case in a sedimentary basin such as the Williston Basin, since the sedimentary rocks are ill suited for radiometric dating (most methods are limited to igneous rocks). Most dates were assigned well prior to radiometric methods and were based on biostratigraphy, i.e. index fossil dating. It is almost impossible to read any of the early papers on the area without finding references to flora and fauna of

particular ages being used to pigeonhole various strata into the evolutionary time scheme.

Scientific progress has been made, even with the deleterious effect of evolutionary bias on the part of most geologists. Whereas early work often focused on age-classifying formations based on the assumption of evolution, modern work has focused more on unconformity-bounded units with evolution only implicit in the work. Thus, there has been a shift from age-inferred classification to physically-based criteria. We will particularly address two areas of progress: the basin as a whole, and the uppermost Fort Union strata (Figure 6) that are the focus for much of this series.

If radiometric dating is limited and evolutionary fossil succession fails to deliver its touted means of deciphering the rocks, then geologists must rely on other means—often on scientific means—to delineate rock units. Lithostratigraphy, which correlates rocks based on their

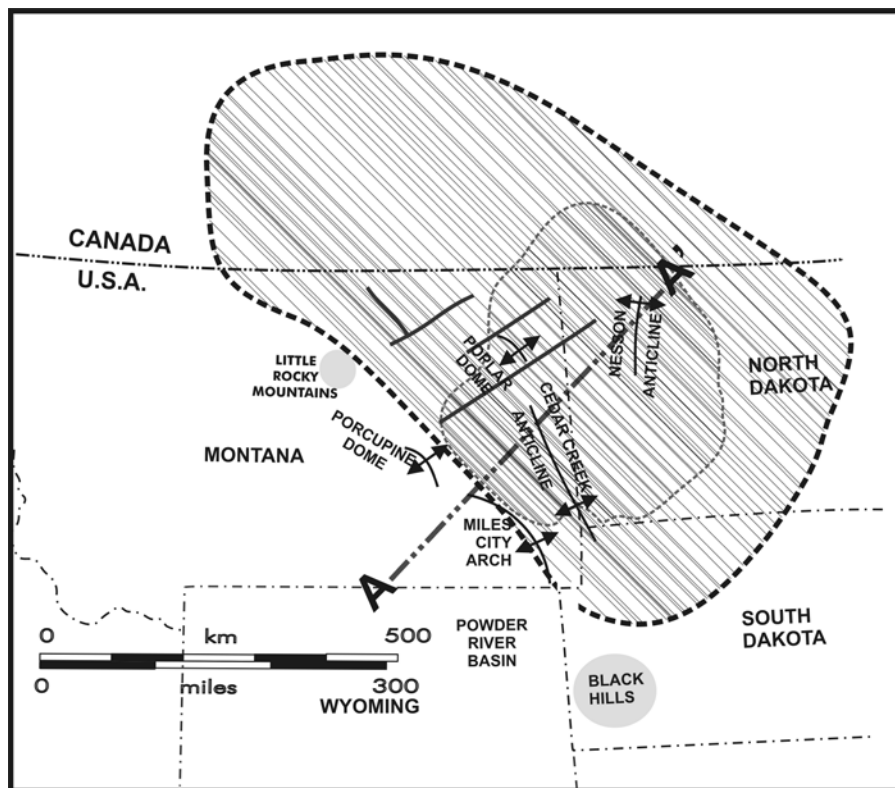


Figure 2. Relation of Williston Basin to nearby structures. Fault-controlled anticlines are found within the basin as well as to the west (Laramide effects). Area of darker hatching is central (deeper) part of basin. Cross section indicated by line A-A' is shown in Figure 5.



Figure 4. Shaded relief map of part of western North Dakota where badlands are located. Theodore Roosevelt National Park South Unit is located immediately north of Medora, and the North Unit is located 15 miles (24 km) south of Watford City. Main drainage is Little Missouri River. Valley southwest of Watford City is drained by Red Wing Creek. Base from Luther et al. (1995).

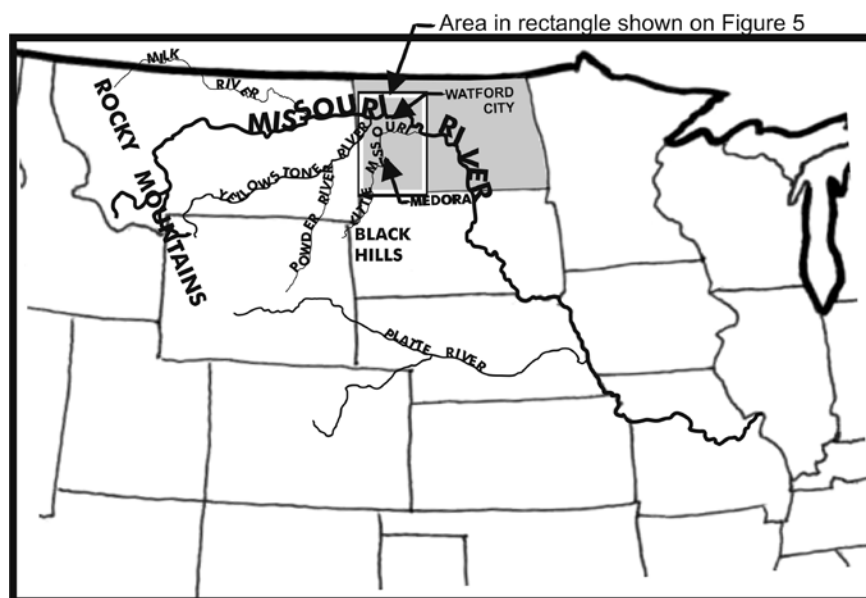


Figure 3. The study area is the vicinity of Medora and Watford City in western North Dakota, which mark the south and north extent, respectively, of Theodore Roosevelt National Park and the North Dakota badlands.

physical properties, is one method. This was complicated by “facies model” analysis, popular in the late 20th century, and recognized by the application of “Walther’s Law” to strata (see glossary). A highly successful scientific technique is seismic measurements to produce two- and three-dimensional imaging of subsurface layering and structure. This geophysical method facilitates mapping of subsurface features that previously had to be inferred between wells across the basin.

Seismic data also propagated new ideas in stratigraphy. While there were many notable participants, the man in the middle was Larry Sloss. From 1937 to 1947 he taught at the lead author’s

Figure 5 (right). Southwest-northeast cross section through Williston Basin along line indicated on Figure 2. Figure modified from Peterson (1988). Charles Formation and Spearfish Formation Fine Salt and Dunham Salt Members indicated by dashed white lines.

PRB Powder River Basin

MCA Miles City Arch

CCA Cedar Creek Anticline

NA Nesson Anticline

y Yellowstone River

m Missouri River

1 Metamorphic basement

2 Deadwood Formation

3 Winnipeg Group (Black Island, Ice Box, and Roughlock Formations)

4 Red River, Stony Mountain, and Stonewall Formations, undivided

5 Interlake Formation

6 Winnipegosis Formation

7 Prairie Formation (Prairie Salt)

8 Manitoba Group (Dawson Bay and Souris River Formations)

9 Jefferson Formation (Duperow and Birdbear Members)

10 Three Forks Formation

11 Bakken Formation

12 Madison Group (Lodgepole, Mission Canyon, and Charles Formations; Charles indicated by dashed line)

13 Big Snowy Group (Kibbey, Otter, and Heath Formations)

14 Amsden Group (Tyler, Alaska

Bench, and Devil's Pocket Formations; eastward may be referred to as Tyler, Amsden, and Minnelusa Formations)

15 Opeche and Minnekahta Formations, undivided

16 Spearfish Formation (Fine Salt and Dunham Salt Members indicated by dashed lines)

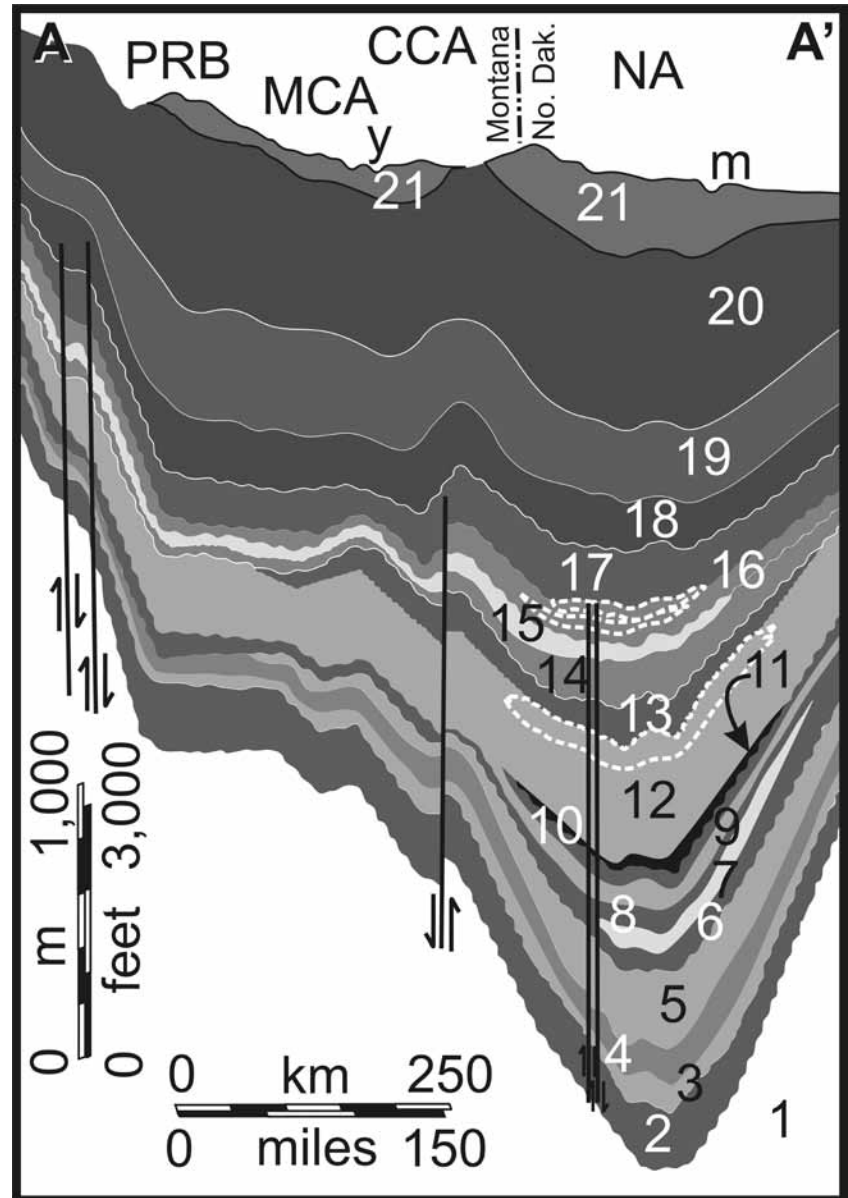
17 Ellis Group (Piper, Rierdon, and Swift Formations; strata assigned to Morrison Formation included)

18 Dakota Group (Inyan Kara, Skull Creek, Newcastle, and Mowry Formations; some refer to Inyan Kara Group with Lakota, Fusion, Fall River – Dakota; Skull Creek and above assigned to Colorado Group)

19 Colorado Group (Graneros – Mowry, Belle Fourche, Greenhorn, Carlisle, and Niobrara Formations; Skull Creek and Newcastle included by some at base)

20 Montana Group (Telegraph Creek, Eagle, Claggett, Judith River – Pierre – Bearpaw, Fox Hills, and Hell Creek Formations)

21 Fort Union Group (Ludlow, Slope, Cannonball, Bullion Creek, and Sentinel Butte Formations; in Montana, Fort Union Formation with Tullock, Ekalaka, Lebo, and Tongue River Members)



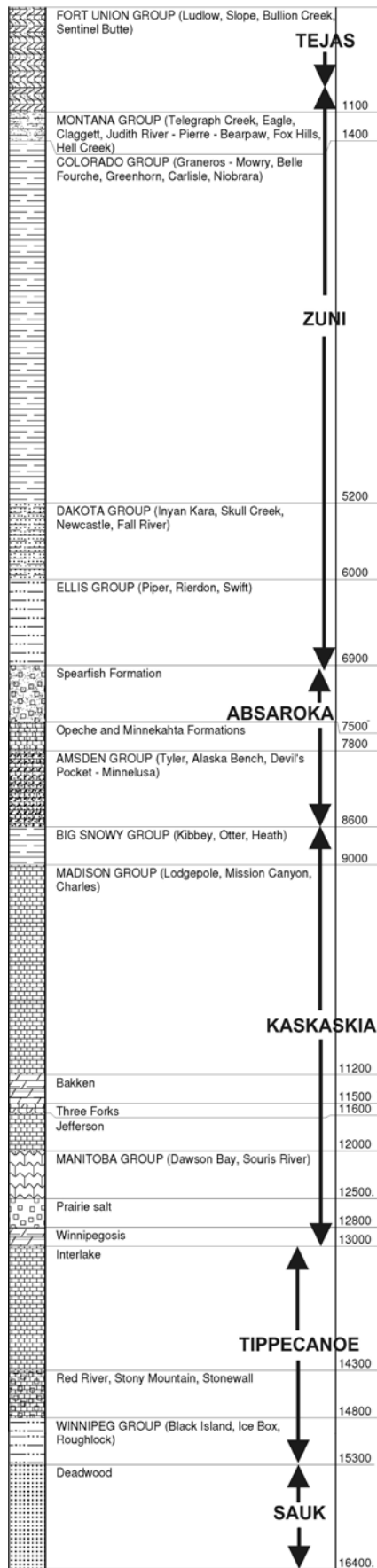


Figure 6 (left). Stratigraphic log per Figure 5. Sloss sequences (a.k.a. megasequences) indicated per U.S. Geological Survey posted sequence boundaries. Depths (right side of figure) in feet.

alma mater in Butte, Montana, and worked for the Montana Bureau of Mines and Geology doing a good deal of field work during the summers (Dott, 2014). Sloss traced "...several important unconformities in the Montana region, which did not conform to any classical, fossil-based stratigraphic divisions..." (Dott, 2014, p. 24) to North Dakota, which sparked ideas that he later developed with his colleagues at Northwestern University. Later students and successors (most famously the "Exxon Group") carried the concepts further to create sequence stratigraphy, which has become the predominant interpretive framework in sedimentary geology well beyond the oil patch.

Even as evolutionists, these pioneering stratigraphers recognized the tension between evolution and the data of science. "By the 1930s, Laurence L. Sloss noted that stratigraphy was beset with 'stupefying arguments' about abstract time versus actual rocks and how to classify such things" (Dott, 2014, p. 24). While not without uniformitarian baggage (Klevberg, 1999; 2000a; 2000b), sequence stratigraphy has been a leap in an empirical direction, a fact that garnered resistance from many establishment geologists. The Williston Basin is now almost universally mapped using sequence stratigraphic interpretations, though that entails the necessity of a fine equilibrium of gradually rising and falling sea levels (eustasy) over hundreds of millions of years. Several researchers have warned about the difficulty if not impossibility of correlating cratonic sequences (a.k.a. supersequence, sloss sequence, megasequence)

to other continents, showing the effort has met with only limited success, and asserting that eustasy is unlikely to be the sole responsible mechanism (Christie-Blick and Driscoll, 1995; Wilson, 1998; Bailey and Smith, 2010; Catuneanu et al., 2011). Some have argued from logic and experimental evidence that such correlation can only provide nonunique solutions (Milana and Tietze, 2007). Despite this lack of correspondence outside the sedimentary basin, Clarey and Werner have used sequence stratigraphic principles to attempt a global correlation and revised eustatic curve that they assert shows a diluvial signature (Clarey and Werner, 2017; 2020). The validity of the sequence stratigraphic approach to correlation is dependent on the validity of the assumption of eustasy, which is arguably easier to support on the basis of the historic Deluge than speculated fluctuations over great ages. This stratigraphic revolution began in Montana and North Dakota and the Williston Basin, and so we will examine the basin as diluvialists, particularly the Fort Union Group (Figures 5 and 6).

Fort Union Group

Fort Union strata were some of the earliest units in the Williston Basin to be studied, as they provide outcrops for study at the surface. They host the fossil wood that will be the focus of Part II and the low-rank coal (lignite) that will be addressed in Part III. Formation of badlands topography that cuts into four (possibly five) of these formations provides many outcrops for direct study. One might think the stratigraphic classification of well-exposed, undeformed strata would have been unusually simple, but not so. There has been much "evolution" of stratigraphic nomenclature over time (Figure 7), not only due to increases in data, but also from changes in interpretive frameworks.

Some of the reasons for changes in terminology are illustrated by the Lud-

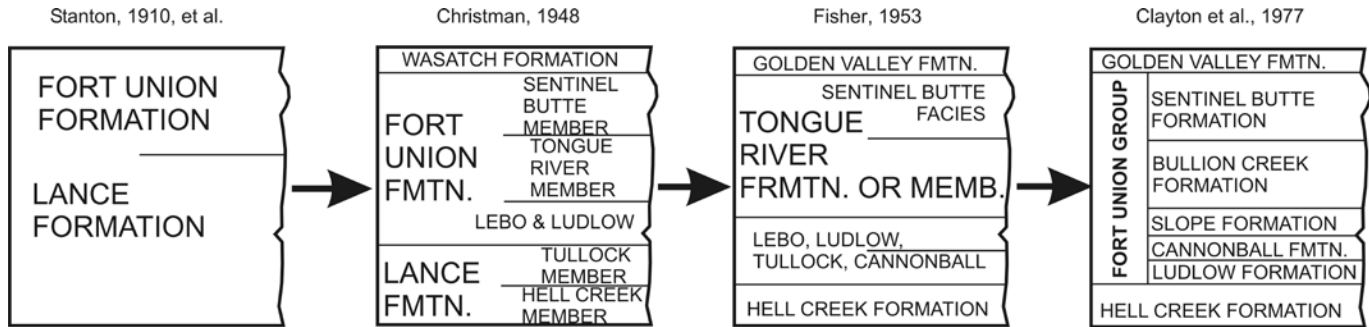


Figure 7. The entire sedimentary sequence in the Medora area was initially called Lance Formation (after the type locality at Lance Creek in Wyoming). Later, differences were acknowledged and the main units were termed the Fort Union Formation, with Wasatch Formation (named for type locality in Utah) including many of the upper strata. This became the Wasatch Group and contained the Golden Valley Formation (now Camels Butte Member of same) and an unnamed formation (now Bears Den Member of Golden Valley Formation) and the Sentinel Butte Formation, though other geologists referred to the "Sentinel Butte Facies" of the Tongue River Formation, since it takes experience or careful study to differentiate the Sentinel Butte Formation from the underlying strata. North Dakota Geological Survey staff pointed out in the 1970's that the member or formation named for the Tongue River of Wyoming and Montana was correlated with the strata underlying the Sentinel Butte Formation on the basis of inferred age, with no physical connection. They therefore renamed this the Bullion Creek Formation with the type locality approximately 17 miles south-southwest of Medora. They further distinguished the underlying Slope Formation on lithologic grounds. The U.S. Geological Survey holds to the older nomenclature.

The Hell Creek Formation is famous for its dinosaur fossils, but it also contains fossils of fish, amphibians, mammals, and a diversity of plants. Many of these same fossils appear in Fort Union strata, but by definition the highest dinosaur-fossil-bearing formation is classified as Hell Creek. The Golden Valley Formation is rich in plant fossils, particularly the floating fern *Salvinia* and a wide spectrum of temperate and tropical plants. Fewer animal fossils are found.

low Formation at the base of the Fort Union Group:

The beds now placed in the Ludlow Formation have been variously referred to as the Laramie, Lance, and Fort Union 'Formations' and thus assigned a Cretaceous, Paleocene, or Eocene age. This complexity of nomenclature and age assignment arose because of the gross similarity of the rocks above the marine Cretaceous. This thick, monotonous sequence required a long period of study over a large area by many workers before criteria were established which effectively subdivided the strata according to color and lignite content.... (Moore, 1976, p. 11).

Biostratigraphy was thereby succeeded by the more empirical lithostratigraphy. Starting with the original type section in extreme eastern Montana (Figure 8), various members were identified and mapped. The type section for the Fort Union Formation was moved from Fort Union to near Livingston, Montana, far to the southwest, which is now the section recognized by the U.S. Geological Survey. Exposures along the Tongue River in southeastern Montana and northeastern Wyoming at the north end of the Powder River Basin (Figure 2) gave the name to the Tongue River Member or Tongue River Formation. Clayton et al. (1977) decrying the fact that nothing but an interpreted age directly linked the Tongue River exposures

to the rocks observed around Medora, North Dakota, established new terminology for the Fort Union Group and a new type section for the Bullion Creek Formation in North Dakota (Clayton et al., 1977). Strata still referred to by the U.S. Geological Survey as Tongue River Member on the Montana side of the border along the Yellowstone River are Bullion Creek Formation in Klevberg's experience. We think this is an example of evolutionists who are good scientists and who allow the geologic classification to be constrained by physical evidence.

With experience, it is possible to recognize the Bullion Creek and Sentinel Butte Formations as separate formations. The two have mineralogic differences (see Table I) and visible differences in

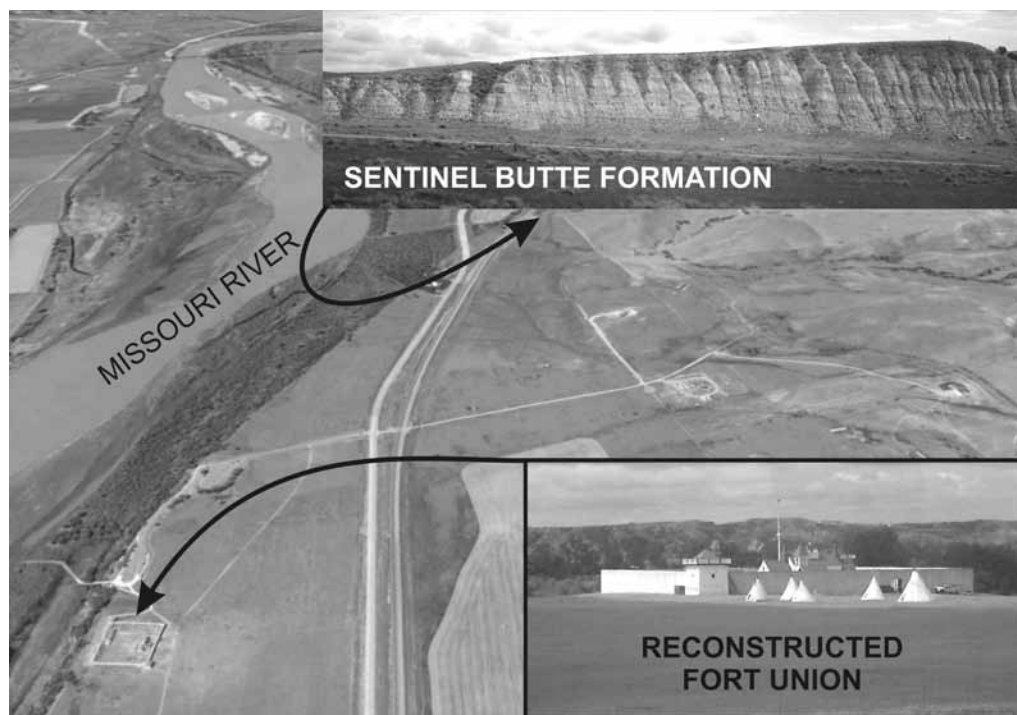


Figure 8 (*left above*). Each day, hundreds of train passengers on Amtrak's *Empire Builder* pass between the restored Fort Union and the nearby outcrop of Sentinel Butte strata (Fort Union Group), most of them staring at their screens and completely oblivious to the fine geology right outside the window. Fort Union was built two centuries ago as a trading post near the confluence of the Yellowstone River with the Missouri River. South and west of Fort Union, the relationship between the Tongue River and Bullion Creek Formations has yet to be resolved. Base oblique aerial from Google Earth, view toward the west-northwest.

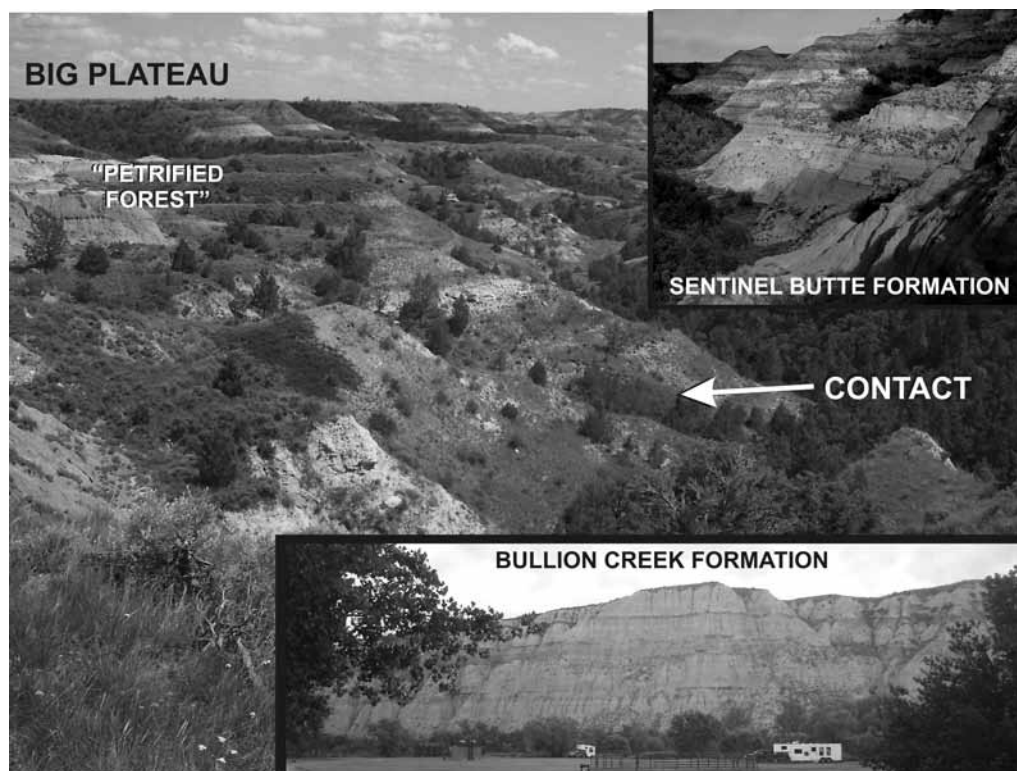


Figure 9 (*left below*). The contact between the Bullion Creek Formation and Sentinel Butte Formation is evident just south of the "Petrified Forest" in the South Unit of Theodore Roosevelt National Park. The "Petrified Forest" abuts the Big Plateau where quartzite pebbles were observed. It is stratigraphically and topographically lower than the Big Plateau.

Table I

Bullion Creek Formation	Sentinel Butte Formation
more rounded, smoother	rilling, tunnels, caves
sandstones trough-shaped, laterally restricted, friable	sandstones thick, tabular, laterally continuous, better lithified
lithic fragments most common	more igneous and metamorphic lithic fragments
zircon, tourmaline, hornblende	kyanite, epidote
mica most abundant physil	montmorillonite most abundant physil
clay fraction contains more calcite and dolomite	clay fraction contains less calcite and dolomite
silicified wood less common	silicified wood more common
weathers to yellow, buff, light gray	weathers to darker gray and brown

color and weathering patterns (Figure 9). Igneous minerals are common in these formations, including much bentonite, volcanic ash altered in sea water. However, there are also metamorphic minerals and igneous rock fragments that

indicate source areas in the Black Hills or Rocky Mountains, a great distance from North Dakota (Jacob, 1975). This is especially problematic for believers in deep time since mica and some other minerals found in the Fort Union Group



Figure 10. Outcrop of basal sandstone of Sentinel Butte Formation in North Unit of Theodore Roosevelt National Park. Note man by sign for scale.

would tend to weather rapidly and thus must have been transported quickly and deposited immediately. Fossils, both animal and plant, are typically in distinct horizons or isolated pockets only (Jacob, 1977; Biek and Gonzalez, 2001). Lignite beds are common in both formations.

While lignite beds occur throughout the Fort Union strata, petrified wood is not as widely distributed. In Klevberg's experience, while petrified wood is abundant, it appears limited to a few horizons, primarily near the base (Figure 10). This has been observed throughout the area (Biek and Gonzalez, 2001). In our experience, it occurs primarily in bentonitic strata at the base of the Sentinel Butte Formation, but it sometimes appears associated with lignite strata higher up in the formation. The specimen shown in the lower part of Figure 11 was observed part way up the lower units of the Sentinel Butte Formation approximately 68 km north-northeast of the "Petrified Forest" featured in Part II of this series. The lignite from which this specimen originated has burned at this locality to form clinker. Clinker is very apparent in the area due to the bright orange or red color commonly formed as burning lignite has been observed to bake overlying clay into "natural brick" (Biek and Gonzalez, 2001). It is possible that the larger mass of wood from which the specimen in Figure 11 formed was not petrified but only coalified and hence burned with the lignite seam. Partially petrified/coalified wood has been observed elsewhere (Williams, 1996) and appears to demand rapid chemical alteration to prevent normal decay. Biek and Gonzalez (2001) also noted silicified lignite, a combination of coalification and silicification as opposed to the either/or sample Williams (1996) wrote about (Biek and Gonzalez, 2001).

The "Petrified Forest" occupies a slightly lower elevation than the Big Plateau as indicated by the fine contours on the geologic map in Figure 12. The petrified wood horizons are extensive

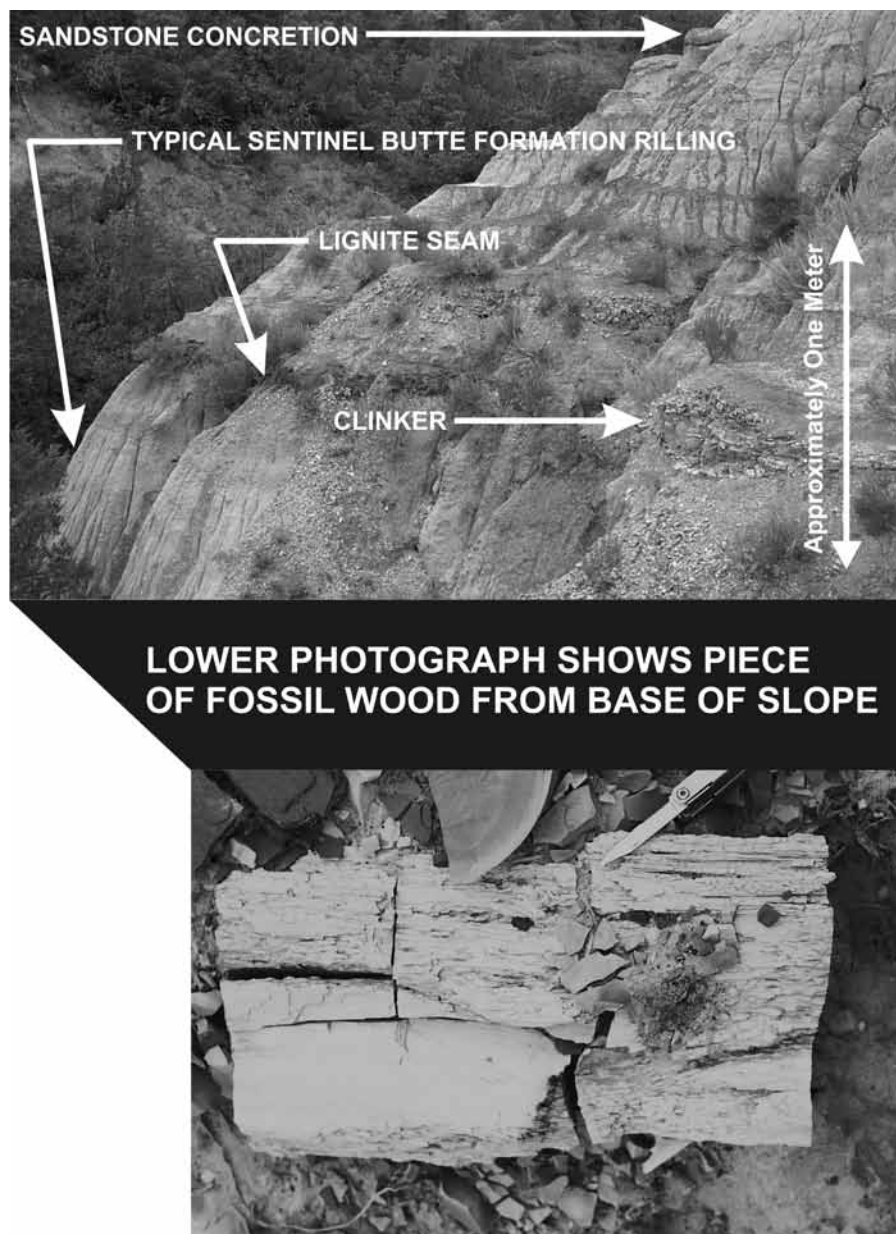


Figure 11. This piece of fossilized wood was found in conjunction with a clinker bed (burned lignite) within the Sentinel Butte Formation across the Little Missouri River from the North Unit of Theodore Roosevelt National Park. Knife blade is approximately 5 cm long.

and can be traced in the field east across the Little Missouri River and clear across the south unit of Theodore Roosevelt National Park, as well as north 70 km to the north unit of the park, where horizons proliferate higher up in the

formation (Biek and Gonzalez, 2001). Lignite horizons of various thicknesses are evident throughout, and the thickest are sometimes useful as marker beds. While some major beds can be traced for several miles or more, most are not

so laterally extensive, and a minor bed observed in one locality may not be the same as one in a similar position elsewhere.

Geomorphology

Western North Dakota is characterized by gently rolling plains, fiercely dissected by a characteristic erosional topography known as “badlands” and sprinkled with buttes formed of various formations that post-date the Fort Union Group. Vestiges of planation surfaces are not hard to find, and these are often capped by a coarse gravel veneer. Relict channels near the inferred extent of glaciation tend to be smooth, broad, and shallow, contrasting with the modern valley of the Little Missouri River.

Problems for Diluvialists

In some respects, the Williston Basin has been a poster child for traditional explanations and a daunting challenge to diluvialists. The Williston Basin is supposed to present a nearly complete example of the geologic column. While various fossils are present, fossil wood is prominent, especially in the Fort Union strata (marine microfossils are more prevalent deep in the basin). As we will develop in the next paper, fossil wood is widely presented as a “petrified forest” representing the passage of significant time.

Formation of the Williston Basin

We do not know how the Williston Basin formed. With no written record to rely on, there are only speculations and varying infusions of imagination in the stories proffered for its formation, ideally tempered with observations from the present. Was it an antediluvian feature, or did it form early in the Deluge? Oard (2013a) favors a bolide impact. Subsurface data have been interpreted as indicating an infilled impact crater beneath Red Wing Creek southwest of Watford City, North Dakota (Red Wing Creek Valley indicated by lighter colored stripe

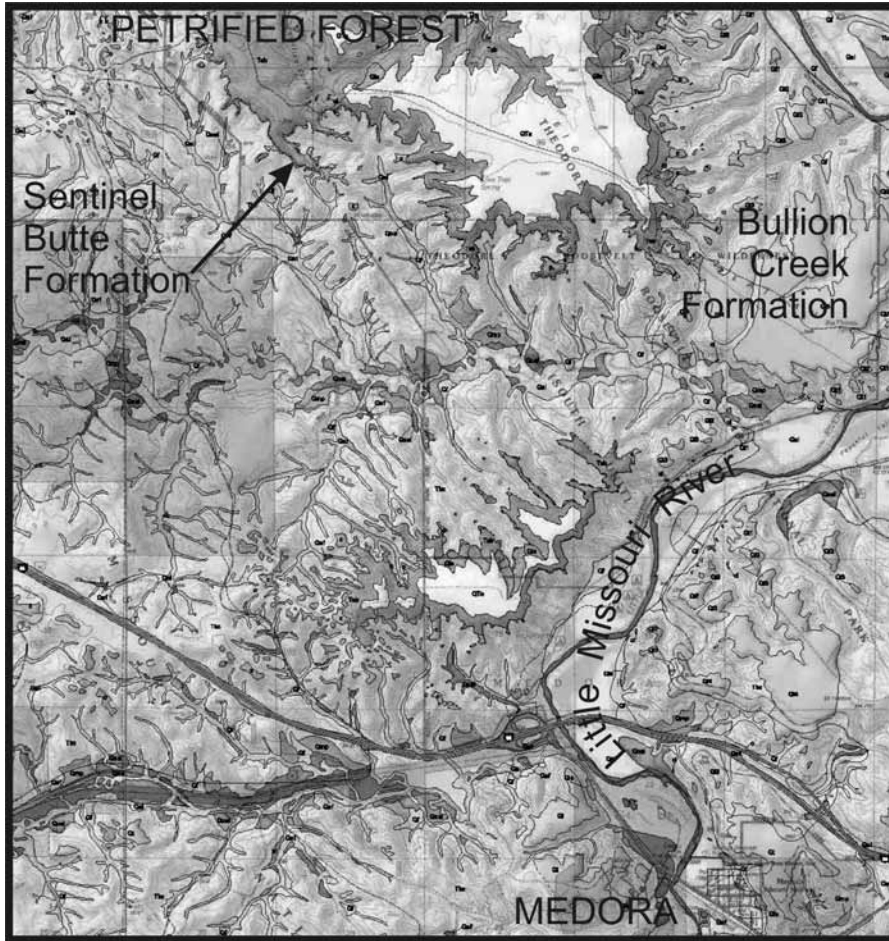


Figure 12. Snippet of geologic map of study area. Bullion Creek Formation is light gray, Sentinel Butte Formation dark gray.

on Figure 4), but that is within the basin sediments. More than 1,800 m of strata had already been deposited when this impact occurred (Biek and Gonzalez, 2001), indicating it would have happened during the Genesis Flood and affected a very limited part of the Williston Basin. Tectonic means of subsidence have been proposed, possibly linked to the fountains of the great deep and the Mid Continent Rift (Clarey, 2020). Still other possibilities include mineral phase changes and crustal cooling.

Preposterously fast sedimentation?

The Williston Basin (Figure 2) contains nearly 5,000 m (more than 16,000 ft.) of

sedimentary rocks that are believed to have accumulated in a gradually subsiding basin over much of earth history and thus provides an example of a rock column that illustrates a nearly complete geologic column (Peterson, 1988). It could be that a total of more than three times that thickness was deposited in the Williston and surrounding depositional basins (Peterson, 1988). Both the volume and inferred geologic column have been used, like the lower Mississippi Valley (Hayward, 1985), as an argument by anti-creationists (Morton, 2001).

To make matters worse for creationists, time available for deposition would have been less than a year. Deposition

probably waned and widespread erosion commenced somewhere around Day 270 of the Deluge (Oard and Reed, 2017), leaving less than a year for deposition. The rate of deposition and the volume of sediments to fill the Williston Basin dwarf anything occurring today. As long as belief in uniformitarianism or actualism discouraged research in actual sedimentation processes, the anti-creationist argument from sediment volume appeared compelling (Reed and Oard, 2017). That began to change with progress in hydrodynamics and sedimentation processes.

To fill the Williston Basin in 270 days would require a minimum of 19 m/day (62 ft/day) on average. To supply the maximum inferred basin fill thickness for the Williston and surrounding basins in that time would require approximately 60 m/day of average sediment supply (depending on how one estimates or models total thickness and compression during lithification). Is a rate between 19 m/day and 60 m/day reasonable in light of empirical knowledge of sedimentation? In applying empirical equations for sand transport and deposition to the Hawkesbury Sandstone of Australia, Allen (1996) estimated that this extensive sandstone body likely was deposited at a rate of at least 62 m/day. Barnhart (2011) studied splay deposits in New Orleans formed from a levee breach during Hurricane Katrina for which time constraints indicated deposition occurred much more rapidly than 2.3 m/hr (equal to 55 m/day) and probably closer to 43 m/hr (approximately 1,000 m/day). Applying empirical relations to the Tapeats Sandstone of the Grand Canyon of the Colorado River, Barnhart (2012a; 2012b) estimated a rate for the basal Tapeats equivalent to approximately 215–1,300 m/day and for the middle and upper Tapeats equivalent to approximately 360 m/day. While a much more detailed analysis of Williston Basin infill is certainly warranted, these findings make it clear

that filling the basin during the Flood year described in Genesis is realistic to the extent one can extrapolate from smaller scale geologic events. In fact, it is necessary for the sediments to have been deposited relatively rapidly based on these empirical relationships. Thus, for those who believe in “deep time,” nearly all of the purported millions of years of time were “dead time” in which no net deposition occurred, since the strata must be riddled with time gaps to accommodate the supposed ages of deposition, and most of these are “invisible” and not easily accommodated by recognized unconformities. While some unconformities are inferred (Figure 5), trying to explain this much “dead time” is clearly problematic for uniformitarians (Reed, 2002a,b; 2004).

Despite the fact that the sedimentation problem fits on the other foot, the idea of slow filling of a gradually subsiding basin persists and provides faulty ammunition for anti-creationists. Arguments of anti-creationist Hayward (1985) for equilibrium based on isostasy throughout central North America are readily and frequently refuted by old-earth-believing geologists themselves as attested by the various competing models for formation of the Williston Basin (Haid, 1991). Hayward’s argument for lack of accommodation space is also a straw man argument and refuted by the possibility of bolide impacts, lithospheric cooling, mineral phase changes, or other processes that create accommodation space without faulting.

Generating oil and coal

The Fort Union Group contains immense amounts of low-rank coal. Deeper Williston Basin formations contain enormous amounts of oil. We acknowledge this is an important argument of anti-creationists. Because the origin of fossil fuels deserves to be addressed at greater length than can be accommodated here, it will be the topic of Part III of this series.

Locating the D/P boundary

The geologic boundary marking the end of the Genesis Flood, the “Flood/post-Flood” or “diluvial/postdiluvial” (D/P) boundary, has been an object of intense discussion by creationists (Oard, 2014; Clarey and Werner, 2019). Clarey has argued for a higher D/P boundary than many previous researchers, some of whom were enamored with the legendary K/T (or K/Pg) boundary (Clarey, 2017). One of several important criteria for locating the D/P boundary is geomorphology (Oard, 2018), especially planation surfaces. Planation surfaces are inimical to uniformitarian processes and a clear indication of highly energetic sheet flow (Oard, 2018). While the planation surfaces are not as dramatic in highly eroded western North Dakota as some other parts of the world, erosional remnants are preserved in Fort Union and overlying strata. In addition, the Bullion Creek and Sentinel Butte Formations (Figure 6) comprise approximately 425 m (1,400 ft.) of continuous, rapid deposition completely covering the Williston Basin and surrounding areas, which is strong evidence that the D/P boundary is higher in the section. Thus, accounting for the Fort Union Group and the coal and fossil wood it contains after the Deluge is not necessary.

Problems for Uniformitarians

In our experience, what appear at first as the strongest arguments against a biblical view of earth history turn out, with further scientific research, to be some of the strongest arguments against deep time. This is true also of the Williston Basin.

Formation of the Williston Basin

Many theories have been put forth for how the Williston Basin could gradually subside over vast stretches of time. These tend to be highly speculative, dependent on many modeling assumptions, published eustatic curves, etc. (Fowler and Nisbet, 1984; Klein and Hsui, 1987;

Quinlan, 1987; Haid, 1991; Hamdani et al., 1994; Miall, 2000; Olajide and Bend, 2014). While there is some latitude for unsteadiness in the rate of subsidence for most of the formations, belief in the swamp theory of coal formation means that the late period of subsidence in which the Fort Union sediments were deposited must have remained precisely at an elevation that maintained a close correspondence between the water table and ground surface so that lateral migration of swamps was slow enough for organic material to adequately accumulate (Moore, 1976). Thick and extensive coal seams in particular require this precise and improbable balance for long periods of time.

Preposterously slow sedimentation?

While time is often viewed as the “hero of the plot” for evolutionists, it is no friend at all. For example, Peppe et al. (2011) used paleomagnetism and chronostratigraphy to assert a duration of deposition for the Bullion Creek Formation of 1.00 to 1.25 million years. For the measured section in southwestern North Dakota, this results in an average rate of deposition of 0.15 to 0.18 mm/yr. Sonnenberg (2017) estimates 20 million years were needed to deposit the Three Forks and Bakken Formations, resulting in a maximum average rate of about 0.002 mm/yr. If we take 5,000 m of central basin sediments and divide by the half a billion years (middle Cambrian age at base), the average rate of deposition for the basin would be approximately 0.03 mm/yr. For comparison, the particle size boundary between silt and sand is 0.075 mm. So the average rate of deposition would be less than half a silt grain thick per year! Since this makes no sense in light of observable sedimentation processes, especially if sands or gravels are involved, it becomes necessary to invoke innumerable small-scale paraconformities (which must be inferred ad hoc since strata appear conformable) to account

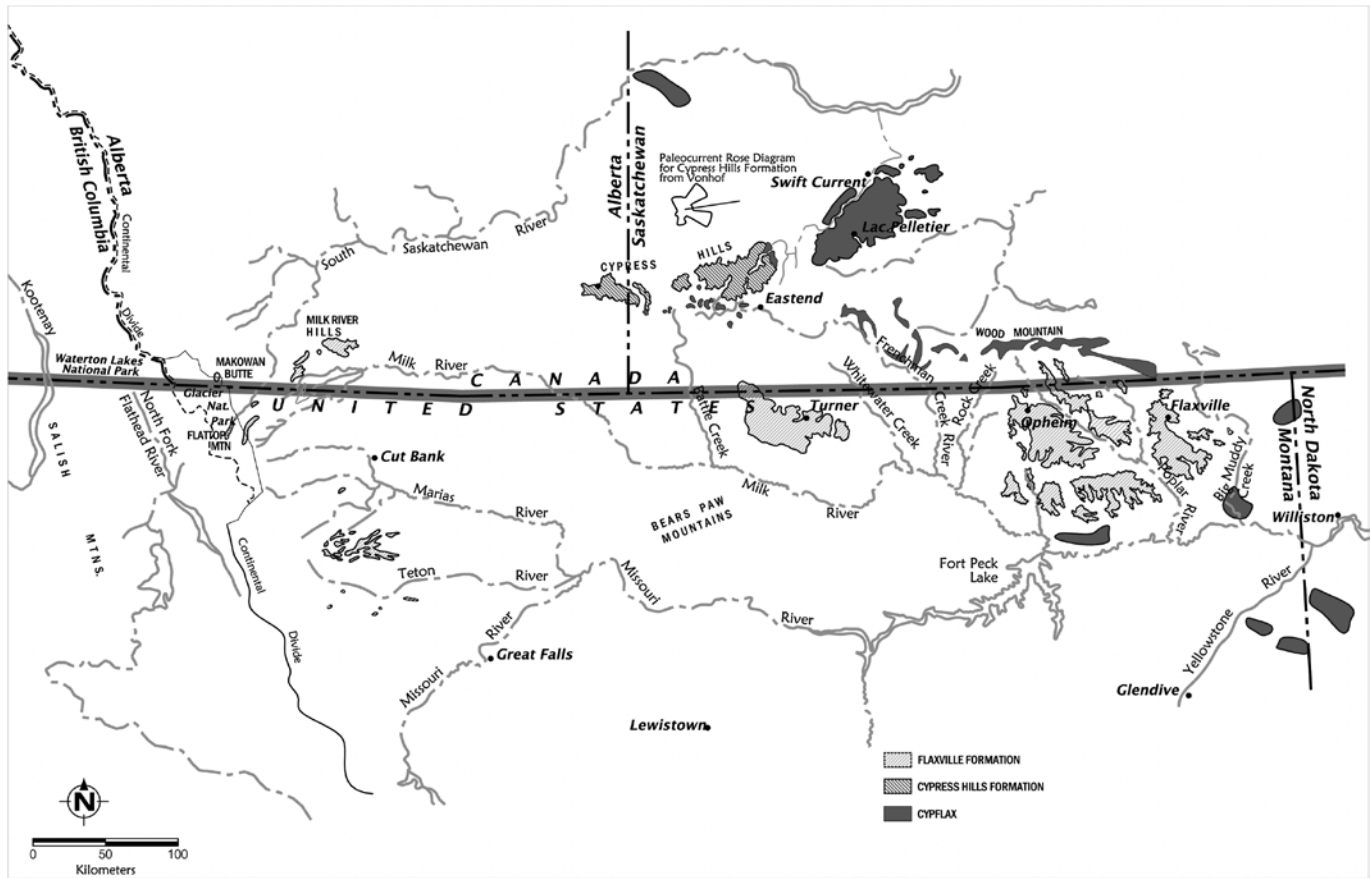


Figure 13. Map of locations of surficial quartzite gravels east of the Continental Divide.

for the nearly universal “missing” time. Miall (2014) has made a valiant attempt to save uniformitarianism in this way, but as Reed (2002a; 2002b; 2004, 2016, 2018), for one, has pointed out, most of uniformitarian time is “dead time.” How such enormous amounts of “dead time” could pass without doing violence to laterally extensive deposits—if not obliterating them entirely—is baffling at best.

The phenomenon of gravel-capped planation surfaces

In the northwest part of the Williston Basin is a gravel-capped planation surface called the Flaxville surface (Figure 13). It represents one of more than four (or five) planation surfaces in Montana,

Alberta, and Saskatchewan, east of the continental divide (Klevberg and Oard, 1998; Oard and Klevberg, 1998). The Flaxville surface crops out as a belt of plateaus within an area 300 km east-west by 80 km north-south in northeast Montana. The plateaus were likely once continuous but later dissected. The surfaces are capped with a predominantly quartzite gravel stratum that ranges in thickness from 1 m to as much as 30 m. Percussion marks are common on the gravel. Based on paleocurrent directional indicators and the closest major source, the quartzite gravel was transported up to 700 km from central Idaho. This combination of planation and gravel transport (Oard and Klevberg,

1998; Oard, 2018) is a diluvial signature, as no present process can perform this geologic work.

Gravels north of the Little Missouri River

Evidence of glaciation is largely confined to areas north of the Little Missouri River (Fisher, 1953). However, south of the Missouri River, glacial deposits are thin and spotty and sometimes appear to simply drape over previous fluvial deposits (Neven, 1946), such as at Sperati Point in the north unit of Theodore Roosevelt National Park (Biel and Gonzalez, 2001). Predictably, these are attributed to the “ancestral Little Missouri River,” which from the mapped extent of deposits,

(Murphy and Gonzalez, 2003), must have meandered over an enormous flood-plain. Klevberg has spent time investigating the largest gravel deposit in McKenzie County—the Cartwright Gravels east of the Yellowstone River, which are nearly pure quartzite with only a few crystalline rocks near the top of the deposit. The nearest potential source area for the quartzite is about 800 km west in central Idaho (Oard et al., 2005).

Gravels of southwestern North Dakota

Most surficial gravel in the study area is angular clinker that appears to have formed in place when coal seams burned. The surficial gravel deposits of interest to this study are those that show evidence of transport (Figure 14), sometimes clearly from at least as far as the western Rocky Mountains about 300 km to the west (Figure 3).

Sand and gravel unconformably cap some buttes and other scattered, isolated exposures of the Sentinel Butte Formation:

These sand and gravel deposits consist of moderately sorted, iron-stained, locally iron-cemented material of local and southwestern affinity. They contain pebbles and cobbles of well-cemented, locally-derived material (mudstone, sandstone, concretions, silicified wood, flint, silcrete, clinker, and chalcedony), and lesser quantities of quartzite and porphyry. The sand and gravel commonly have a transparent, shiny coating, probably of iron-manganese oxides (Biek and Gonzalez, 2001, p. 31).

Klevberg (unpublished information) has observed veneers of small pebbles (rocks between 4.75 mm and 75 mm—i.e. $\frac{3}{16}$ to 3 inches—intermediate axis) north of Sentinel Butte in Golden Valley County (Figure 14A) and larger pebbles north of White Butte in Slope County (Figure 14B). Exotic lithologies predominate. He also observed a most unusual pebble veneer consisting of



Figure 14. Gravel veneers are present in scattered locations in western North Dakota. A) Small quartzite pebbles north of Beach, North Dakota (42 km west of Medora) in Golden Valley County. Pencil shows scale. B) Quartzite pebbles up to 60 mm diameter capping small bench north of White Butte in Slope County. This location is ca. 51 km east-southeast of Medora. White Butte is the highest point in North Dakota. C) View north from summit of Sentinel Butte in Golden Valley County. D) The unusual gravel on the summit of Sentinel Butte is roughly 20 percent Sentinel Butte Formation sandstone and 80 percent agate.

an estimated 80 percent agate on the summit of Sentinel Butte (Figures 14C and 14D). Agate (or translucent chalcedony) is common in the gravels of the Yellowstone River in Montana (Figure 3) 70 km west-northwest of Sentinel Butte (Figure 4). Klevberg has observed diminutive, isolated patches of quartzite pebble veneers in McKenzie County in the badlands south of the Little Missouri River and Watford City (Figure 4).

Quartzite rocks found on plateaus in Theodore Roosevelt National Park

During Flood runoff while continents and mountains were rising and valleys and ocean basins sinking (Psalm 104:6–9), we would expect soft rocks to be pulverized to fine particles during

erosion, and resistant rocks would be spread long distance from their sources. We indeed see such a signature associated with mountain ranges (Oard and Klevberg, 2005; Oard, 2008, 2011, 2013b). We have examined this pattern in particular in the northwest United States and adjacent Canada.

In the northwest states, “high-grade” metaquartzite is seen as layers mostly in central and northern Idaho, extreme western Montana, and adjacent south-east British Columbia. They are part of the Belt Supergroup, which are mostly metamorphosed shale, *argillite*, with minor proportions of limestone and quartzite. There are outcrops of quartzite in the Little and Big Belt Mountains of Central Montana. There is also “low-grade” quartzite, essentially a hard, silica



Figure 15. A quartzite cobble from the Cypress Hills (“cypflax”) with abundant percussion marks. This has been broken with many blows of a sledgehammer to show a fresh surface. Quartzites with virtually no porosity form this texture that gives them the moniker “sugar agate.”

cemented sandstone, that outcrops in the eastern Rocky Mountains. None of these latter sources is large enough to provide the many billions, if not trillions, of well-rounded quartzite rocks found east of the Continental Divide.

The quartzite presumably started as a very pure, fine quartz sandstone, *quartz arenite*, a sandstone formed in only small locations today but extensive in Precambrian and Paleozoic rocks (Pettijohn et al., 1987). As burial continued, the rock became hotter, possibly over 500° C (Sanders et al., 1976), and the quartz arenite metamorphosed to quartzite. In this metamorphic process, the sandstone recrystallized and its pores filled in, forming a dense, hard rock. Breaking a quartzite open with a rock hammer reveals its vitreous or glassy texture (Figure 15).

We infer that during the Recessional Stage of the Genesis Flood (Walker, 1994), the Rocky Mountains uplifted thousands of meters, expos-

ing the quartzite to erosion. We have documented the spread of resistant, well-rounded quartzites from the outcrops of the western Rockies, as far as 700 km west to the Pacific Ocean (Oard et al., 2006), about 600 km southeast to the eastern Bighorn Basin of north-central Wyoming, and up to 1,200 km east and northeast into southwestern Saskatchewan, southwestern Manitoba, and western North Dakota (Oard et al., 2005). Nearly all of these potential sources are hundreds of kilometers away, beyond the limits of the small-scale map of Figure 13. What is significant about quartzite is that it is a very hard, tough lithology capable of enduring abrasion and impact (as indicated by percussion marks) over great distances. Few other lithologies would survive the trip. In addition, the potential source areas of the quartzite are far outside the areas where these gravels are found, indicating long-distance transport. Important erosional remnants of the Cypress Hills



Figure 16. Nathan Oard. Large quartzite boulder (estimated mass 200 kg) on top of a ridge at 2,500 m elevation near Lookout Mountain, Wallowa Mountains, Northeast Oregon (Nathan Oard provides scale). Photograph courtesy of Paul Kollas.

and Flaxville gravel sheets are shown on Figure 13.

The quartzite rocks accumulated thousands of meters deep in paleovalleys, such as east and northeast of Jackson, Wyoming, and west of Spencer, Idaho (on Interstate 15 just south of the Montana/Idaho border). They are found on the tops of the Blue Mountains of central Oregon, the tops of the Wallowa Mountains of northeast Oregon (Figure 16), on top of the deformed lava ridges of south-central Washington, on top of the Gravelly Range of southwest Montana, and on top of a flat-topped mountain in the northern Teton Range of northwest Wyoming (source of Figure 17). Such mountaintop occurrences demonstrate the spread of quartzite *before* the uplift of some ranges in the northwest United States.

We have also analyzed the well-rounded quartzite conglomerate cap on the Cypress Hills of southeast Alberta and southwest Saskatchewan (Oard and Klevberg, 1998). The Cypress Hills are a slightly dissected planation surface about 120 km east-west and



Figure 17. Well-rounded quartzite cobble from the top of Red Mountain, northern Teton Mountains, Wyoming. Note the small round pressure solution marks and fractures on the cobble, caused by rock on rock contact under high pressure of deposited quartzites in a paleovalley. Angular rock at upper left is chert.

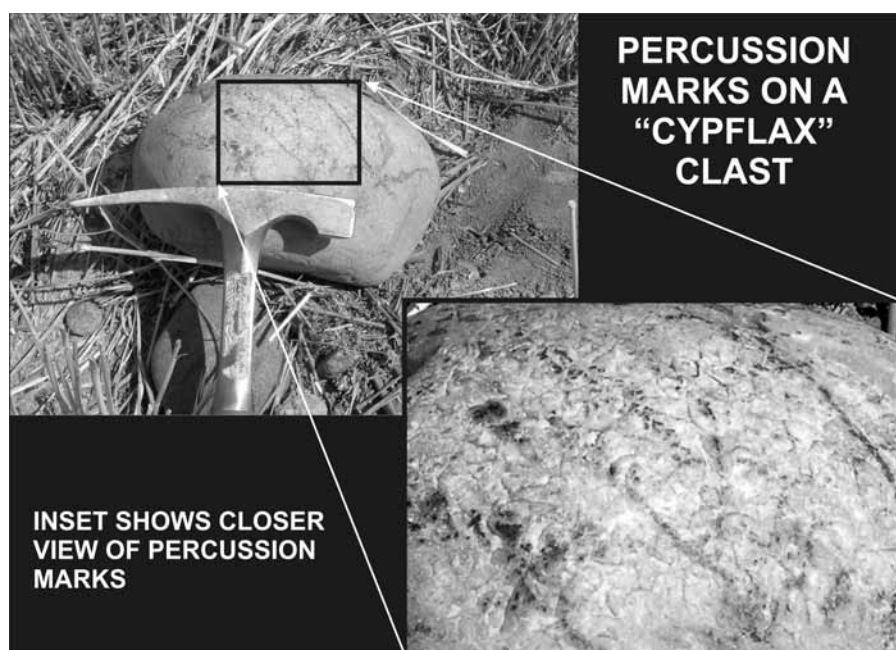


Figure 18. Percussion marks on a weathered "cypflax" cobble. Note the density of the marks, with many overlapping other percussion marks.

20 km north-south that is about 760 m above the rivers to the north and south (Figure 13). It is a high plateau which is capped with an average of 23 m of well-rounded, iron-stained quartzite rocks that range up to small boulder size. These quartzites were transported from central Idaho (Leckie and Cheel, 1989), about 400 km away, *and on the other side of the Continental Divide* (which predates these gravels), based on the nearest in situ lithologically similar high-grade quartzite body. Moreover, these quartzite rocks are covered with dozens to hundreds of percussion marks, similar to other quartzite locations, indicating powerful rock-on-rock impacts during transport (Figure 18). This would require large, fast-flowing currents. Such capping quartzite and the subsequent great erosion of the high plains that followed, leaving the Cypress Hills as a high, erosional remnant, cannot be formed by any commonplace mechanism but could by diluvial runoff (Klevberg and Oard, 1998).

So, it was not unexpected that we would find quartzite in the badlands of North Dakota. And indeed, we discovered it on a terrace just east of the "petrified forest" (Figure 19). It is interesting that we did not find any on slightly lower terraces, perhaps because these formed by less energetic, more channelized flow. The quartzites were rounded, small, and mixed in with considerable fines. The largest quartzite rock seen was about 10 cm long (Figure 20), large enough to require a significant depth of flood flow on this low slope though considerably smaller than rocks observed at higher elevations near the Continental Divide. Quartzites were also found on top of nearby Sentinel Butte, which is about 240 m above the top of the terraces in the badlands, indicating at least this much erosion in southwest North Dakota. (Other evidence indicates much more than 240 m of erosion of the area.) It is also interesting that only about 20% of the rocks on top of



Figure 19. Klevberg pointing to the Big Plateau in the distance upon which the well-rounded quartzites were found in the badlands of Theodore Roosevelt National Park (view east). Note the small, light-colored petrified trees along the slope.

Sentinel Butte are quartzites, while 80% were agates from an unknown source to the west. While the Cypress Hills and Flaxville Plain are capped by continuous sheets of coarse gravels of rather uniform, polished quartzite, the North Dakota remnants are small areas widely separated, typically pebble size rocks of more mixed lithologies and generally a bit more worn (mechanically weathered) on their surfaces. Some of the deposits appear to be reworked from Cypress/Flaxville sources.

Significance of the surficial gravels

The surficial quartzite and other gravel are evidence of powerful, regional currents and therefore powerful evidence for the runoff of the Flood-waters from the rising mountains and continents (Oard and Klevberg, 1998). This dispersion of resistant rocks occurred during the time “Cenozoic” strata were deposited

in this area, mainly the mid-to-late Cenozoic (Oard, 2018), and the distances of transport, plus other characteristics, are strong evidence against that event being related to either uniformitarianism or postdiluvial catastrophism.

The spread of resistant rocks from uplifted mountain ranges of the western Rocky Mountains is one of dozens of indications that the Flood/post-Flood (diluvial/postdiluvial or D/P) boundary is in the Late Cenozoic, defined as the Miocene, Pliocene, and Quaternary (Oard, 2014; Clarey, 2017), though evidence of simultaneity has been observed (Oard and Klevberg, 1998). While there may have been pulses or stages in this process, there is no evidence of the erosion that would occur with a significant hiatus in the flooding, only of regional or larger flows deep enough and strong enough to transport these rocks for hundreds of kilometers and plane the



Figure 20. Ten-cm long quartzite found on a terrace in South Unit of Theodore Roosevelt National Park.

landscape. Why the differences in uniformitarian ages for what is clearly the same event? The most logical explanation is that we cannot rely on their dating criteria to correlate with the timescale of Biblical Earth history (Oard, 2019). Based on numerous criteria, we might discover the D/P boundary is in the early Pleistocene at one location but in the Miocene at another location, if we assume the imprecise geological column. Each location needs to be evaluated on its own merits.

The problem of fossilization

Fossils, in particular fossil wood, pose great challenges for ancient-Earth views. We will address the problem of silicification in Part II of this series.

Acknowledgements

Oard thanks Julie von Vett for calling his attention to the “petrified forests” in the badlands of southwest North Dakota. Klevberg thanks his employer for use of the company truck in roaming western North Dakota over several seasons and coworker Jim Hiersche for assisting with work inside the North Unit of Theodore Roosevelt National Park, including

Figure 10. Reviewers provided helpful criticisms. *Deum laudamus* (Psalm 46:8).

Glossary

Carbonate – rock containing more than half calcite, CaCO_3 , dolomite, $\text{Ca,Mg}(\text{CO}_3)_2$, or other carbonate compounds. Limestone is a rock consisting of more than half calcite, and dolostone consists of more than half dolomite.

Clast – an individual rock or particle.

Diluvial – pertaining to or caused by the Deluge, the global flood described in Genesis 7–8.

Diluvialist – one who believes the Deluge was the salient event of geologic history.

Eustasy – global cycles in sea level, the fundamental assumption behind sequence stratigraphy.

Gravel – unconsolidated earth material consisting of various combinations of pebbles (4.75–75 mm b-axis), cobbles (75–256 mm), and boulders (larger than 256 mm).

Laramide orogeny – period of mountain building in Western U.S., believed by evolutionists to be about 75 to 50 million years ago, and believed by many creationists to be part of the diluvial transition from “waters prevailing” to emergence of the land and the end of the Genesis Flood (cf. Psalm 104).

Percussion mark – ring-shaped surficial crack in clast surface indicating violent collision. Seldom observed forming in modern environments.

Planation surface – erosion surface that is quite flat and typically discordant with structure, indicating catastrophic erosion (most evident where soft and hard strata are planed alike into a flat surface).

Sequence stratigraphy – approach to correlating geologic units based on eustasy and transgressive-regressive cycles (see Klevberg, 1999; 2000a; 2000b).

Subcrop – rock not exposed at the surface, accessible only to subsurface sampling methods.

Walther’s Law – the idea that sedimentary facies reflect the same lateral associations of environments as those observed in the present world. For example, mudstones and sandstones may be interpreted as an estuary and river channel, or delta splays and overbank deposits.

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Fifty-Seven Years of Creation Astronomy

Part I: A Survey

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Key Words: Astronomy, historical survey, scope of research, researcher qualifications

Abstract

Since its inception in 1964, CRSQ (along with other creation science journals) has published a significant amount of work in astronomy, with the number of articles in this field comparable to that in paleontology. In general, the fraction of articles dedicated to astronomy has fluctuated between 5 and 20%, even as total creationary output has roughly tripled since the 1960s. Contributors to creation astronomy literature include several holding Ph.D.s in astronomy or physics; many, however, do not seem to hold an earned science doctorate. This state of affairs calls, on the one hand, for continued contribution by creationists at all levels of training and, on the other, for intentional acquisition of astronomy degrees by young creationists.

Introduction

The most immediate conflict between neo-Darwinism and special creation occurs in the field of biology; likewise, the most immediate conflict between old- and young-Earth paradigms occurs in the field of geology. Astronomy is not separate from these disciplines, and it also brings its own share of perceived conflicts with a straightforward reading of Scripture.

It has been noted (e.g., Faulkner and DeYoung, 1991, p. 87) that there is less creationary work in astronomy than in these other fields, and there is as yet no astronomical young-Earth “consensus paradigm” analogous to Flood geology. However, it is desirable to quantify the actual amount of creationary astronomy work, which is possible only by sifting through the literature and comparing the work in various fields. To that end,

this article (Part I of a planned two-part series) seeks to answer the following questions: first, how does the quantity of creation research in astronomy compare to that in other natural sciences? Second, has the focus of creationary astronomy been characterized by breadth or by narrowness? Third, what qualifications are typical of contributors to creation astronomy?

Articles and Frequency

This work surveys four YEC (young-Earth creationist) journals (see below). These journals publish on a wide variety of topics, including Biblical exegesis, physics, chronology, and education. However, to determine the frequency

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Accepted for publication August 18, 2021

of astronomy articles relative to other natural sciences, we here select the fields of biology, geology, and paleontology as standards of comparison. Of these three, biology is the most relevant to the critique of neo-Darwinism, which attempts to explain the origin, unity, and diversity of life on a purely naturalistic basis. Because of this relevance, a diverse array of anti-Darwinian scientists (young-Earth, old-Earth, intelligent design, etc.) often converge in their critiques of neo-Darwinian biology (see, e.g., the essays in the first section of Moreland et al., 2017)—whereas these scientists would sharply disagree in their interpretation of geology and paleontology.

These latter two fields are relevant specifically to YECs, who conclude that a straightforward reading of Scripture requires an Earth on the order of ten thousand years old, as opposed to the 4.5 billion years claimed by mainstream science. Mainstream geology arrives at this age by assuming, in general, that one can extrapolate the types and rates of today's geological processes into the distant past; in particular they thus extrapolate the observed rates of radioactive decay. Thus the YEC community has given significant attention to the field of geology, usually reinterpreting the geologic record in terms of the Noachian Deluge, which involved processes well beyond those occurring today. Likewise, mainstream paleontology interprets the fossil record as a more or less sequential history of terrestrial life, whereas the YEC community typically interprets it as largely the result of the Flood, along with ecological zonation, hydraulic sorting, etc.

Because of their relevance to origins, these three fields have seen significant YEC activity. Quantification of the number of articles published in each field requires somewhat arbitrary decisions regarding the boundaries of each. For this article, we define biology to include biochemistry (relevant to the origin of life) and biogeography (rel-

evant to speciation and dispersion) as well as baraminology (relevant to the stasis or fluidity of created kinds) and cryptozoology. We define geology, in turn, to include topics such as radiometric dating (the basis for the mainstream understanding of geological rates) and ice-age simulations (relevant to the Flood model, i.e., the post-Flood 'Ice and Storm Event'); we also include the pre-Flood canopy theory, due to its relevance to the Flood mechanism. Finally, we define paleontology to include both prehistoric archaeology and the study of mammoth remains (both relevant to early postdiluvian prehistory) as well as of Neandertal mitochondrial DNA (a biological matter, but approachable primarily through study of preserved remains). One could make good arguments for the inclusion of some excluded topics or for the reverse; however, these are the field boundaries employed in this article.¹

We now consider the frequency of articles in each of these three fields, plus astronomy, in four journals.

Creation Research Society Quarterly

CRSQ is arguably the flagship journal of creation science, with essentially uninterrupted publication since 1964. Article tallies must handle the fact that the journal format has changed over the decades. For instance, at various times the journal has featured compendia of brief thoughts on current scientific issues; e.g., Armstrong's (1974) "Comments on Scientific News and Views" includes short speculations on topics such as stellar composition, astronomi-

cal distance determination, redshifts, and in-transit creation of light—as well as topics from other fields of science. Such comments are not included as articles, due to the (designedly) superficial treatment of the topics and the lack of focus on any particular field. It was difficult to handle "Panorama of Science" notes consistently: usually they are brief reports of recent developments, but in some cases (e.g., Froede, 1995) they are lengthy enough to almost force recognition as an article. Such instances were handled on a case-by-case basis.

After excluding abbreviated treatments such as these, we can tally the number of articles per year in the fields of biology, geology, paleontology, and astronomy, as well as the total number of CRSQ articles each year. The resulting tallies display significant stochasticity (see thin curves, left panel of Fig. 1), which we smooth with a Gaussian kernel ($\sigma = 1.5$ yr.) to obtain the thick curves in the same figure. Figure 1 also displays the data as a fraction of the total articles per year.

The figure shows that while biology and geology occupy a substantial fraction of CRSQ output, the field of astronomy has not been neglected; indeed, except during the 1960s, the astronomy output has been comparable to that in paleontology. Note that the large decrease of total articles from the late 70s to early 90s seems partially due to an increase in the length of the articles themselves. For instance, in 1977 a total of 43 articles occupied about 180 journal pages, for an average of slightly more than 4 pages per article. In 1995, however, a total of 19 articles occupied about 160 journal pages, averaging over 8 pages per article. Considering the fraction of total articles (rather than their absolute number) helps normalize such changes in overall article length.

To further investigate whether statistically significant shifts have occurred over the history of CRSQ, we group the articles by decade and calculate, for

¹ Note that, under these definitions, biology and geology are much broader fields than paleontology; furthermore, paleontology depends largely for its interpretation on geology and biology. For these reasons we expect *a priori* a greater number of articles devoted to the first two fields.

each field, the mean number of articles per year, both in absolute terms and as a fraction of total articles per year (right-hand panel of Fig. 1). The most consistent shift appears in the field of geology, which accounted for 13% of total articles in the 1960s but 34% in the 2010s—an increase of 4.7σ . Astronomy has also increased (by 3.1σ), and biology decreased (by 3.0σ) during the same period; however, both of these results are heavily influenced by the final data point and thus do not seem to represent the general trend apparent in geology. Another method of analysis confirms these conclusions: fitting a line to the geology fractions (assuming Poisson error) yields a slope differing by 5.0σ from zero. The same procedure for biology and astronomy yields slopes that differ from zero by only 1.7σ and 2.0σ , respectively.

We conclude that there have been some realignments in the frequency of articles in various fields; the fraction of articles devoted to geology seems in particular to have increased. However, the frequency of articles in the other three fields seems to follow no consistent trend over the half-century history of CRSQ.

Other creation science journals

One can now perform a similar analysis for three other creation research journals. The first, originally entitled *Ex Nihilo Technical Journal* and now *Journal of Creation* (JoC), is published by Creation Ministries International. It first appeared biennially (beginning 1984), then semiannually (starting in 1991), and now three times a year (starting in 1996). This journal publishes several types of submissions; for this work we include “Countering the Critic” and “Overview” publications as articles, but not “Perspective,” “Viewpoint,” or “Essay” contributions, since the latter three seem to be of a less-technical nature. We also count each “Forum” entry as a separate article.

We next consider the *Proceedings of the International Conference on*

Creationism (ICC). The first of these conferences occurred in 1986 and recurred quadrennially until 1998, then quinquennially (starting 2003). All submissions to the *Proceedings* are included as articles.

The final publication, and the most recent, is the online *Answers Research Journal* (ARJ), published by Answers in Genesis beginning in 2008. We include all ARJ contributions as articles in our count.

The resulting tallies appear in Figure 2. Inspection of this figure reveals, first, that in two of these venues astronomy continues to be roughly comparable to paleontology in the fraction of total articles. The exception is ARJ during most of the last decade, in which astronomy articles have significantly exceeded those in paleontology, sometimes even exceeding those in geology. This surge is largely due to the efforts of Danny Faulkner, who authored 23 of the 38 ARJ astronomy articles from 2013–2019.

We also note that, during the first few years of what is now JoC, the normal pattern was reversed, with the output in astronomy and paleontology dwarfing that in biology and geology. In astronomy, this fact reflects the large number of articles dealing with the light-speed decay hypothesis: of the 21 astronomy articles published from 1984–1992, 19 dealt primarily with light-speed decay, and the remaining two assumed it as a foundation. Likewise, for paleontology, the early years of JoC carried a large number of articles dealing with the Guadeloupe skeleton (13 out of the 19 paleontology articles from 1984–1990). These two topics are almost single-handedly responsible for the large astronomy and paleontology tallies in the early issues of that journal.

Combined Journal Totals

The preceding analysis does not address whether the availability of additional publication venues increased the total

number of articles or merely distributed them over more journals. For instance, one might wonder whether the increasing popularity of, say, JoC reduced the number of articles in CRSQ. To investigate this question, we combine (in Fig. 3) the tallies from CRSQ, JoC, and ARJ.²

Considering first the total number of articles, it seems that the number of CRSQ articles was already declining before 1990, when JoC began yearly publication (although, as noted before, this might be due to longer—albeit fewer—articles). More significantly, after 1990 the increase in JoC articles is not matched by a commensurate decrease in CRSQ articles; in any case, by 2000 the total yearly combined number of articles significantly exceeded the quantity published by CRSQ prior to the start of what is now JoC. Likewise, even if the addition of ARJ is responsible for the decline in JoC articles after 2005, the result seems still to have been a net increase in published creation research. Indeed, the average total output has more than tripled since the 1960s. Thus, although it is certainly likely that the availability of other journals caused some authors to submit articles to JoC or ARJ rather than CRSQ, the addition of available journals seems to have resulted in a net increase of articles.

Turning to the field of astronomy (the thick curves on the lower part of the figure) we see that the addition of JoC (and, later, of ARJ) accompanied a net increase in the total number of astronomy articles published. And while the number of CRSQ astronomy articles seems to have been low in the 1990s and 2000s, it increased again after 2010, even while ARJ was publishing

² We omit ICC from Fig. 3 since it is not straightforward to combine, in a consistent manner, the four- or five-year ICC publication cadence with the much more frequent publication of the other journals.

more astronomy articles than ever before. It is always difficult to disentangle causation and correlation, but it seems likely that the literature expansion has in part been driven by the addition of new journals and that the inception of alternative outlets for peer-reviewed creation research has been net-beneficial, both for creation science in general and for astronomy in particular.

Note the large spike in astronomy articles during 2014, which reflects 14 *ARJ* articles and 3 in each of *CRSQ* and *JoC*. Of the *ARJ* articles, 6 were by Danny Faulkner (on a wide variety of issues), 3 were by Andrew Snelling (on radiometric dating of meteorites), and 3 were by John Hartnett (again on a variety of issues). A lesser spike is apparent in 1990, during which *CRSQ* and *JoC* published 8 and 4 astronomy articles, respectively; not included in the total are 3 *ICC* articles that same year. Of these 15 total articles, 11 dealt with the light-speed decay hypothesis, with *CRSQ* holding a minisymposium on variable constants that year.

In summary, by considering the number of astronomy articles in creation research journals since 1964, we can conclude that significant effort has been devoted to understanding astronomy from a young-Earth perspective. If we use the number of articles as our metric, the effort in astronomy has not been as great as that in biology or geology, but it is certainly comparable to the effort in paleontology, a field which, though relatively narrow, is directly relevant to the young-Earth apologetic. Furthermore, the fraction of articles addressing astronomy has not shown any long-term trends over the last five decades, typically fluctuating between 5 and 20%.

Subfields

The second question here addressed is whether creationary astronomy has been marked by a narrow focus or by breadth. For instance, one of the first issues that

arises when comparing astronomical discoveries to the Genesis record is the light travel-time issue: if a given astronomical body is more than about 10,000 light years distant, how has its light already arrived at Earth? In this section we seek to determine whether or not YEC astronomy has focused narrowly on one or two such issues, or whether it has been distributed throughout the major subfields of astronomy.

To this end, we classify each astronomy article into one of five categories: light travel-time, planetary/solar system, stellar/Milky Way, extragalactic/cosmological, and miscellaneous. (The latter category includes topics such as extra-terrestrial life, the star of Bethlehem, “Gospel in the Stars,” etc., as well as astronomy-wide reviews.) Not all articles fall neatly into one category; for instance, many (but not all) of the articles exploring light travel-time overlap with cosmology, and thus there is an element of arbitrariness in the categorization. However, the statistics presented here should suffice to elucidate the range of creation astronomy.

Figure 4 displays the results, showing both the total number of articles per year as well as the fraction of total astronomy output in each subfield. In this figure we again apply Gaussian smoothing ($\sigma = 2.0$ yr.) to all curves to reduce stochasticity; for reference we also show (as thin lines) the unsmoothed data for total astronomy and for selected subfields. (For years with no astronomy articles—and thus undefined subfield fractions—the smoothing routine assumes interpolation between years for which the fraction is defined.)

The left-hand panel focuses strictly on *CRSQ* with its longer publication history. Perhaps the most salient feature in the upper part of the plot (displaying total number of articles) is the predominance of light travel-time articles around 1990, largely the result of two minisymposia (1988 and 1990) dealing with the issue. However, con-

tributions to all five subfields are visible in the figure.

Two subfields which frequently have the highest (smoothed) curves are planetary science and cosmology. Neither of these results is surprising. Regarding planetary science, many solar system bodies display prominent craters, which the present-day cratering rate is insufficient to explain on a young-Earth timescale. Regarding cosmology, it was 1964—the first year of *CRSQ*’s publication—which saw the discovery of the cosmic microwave background (reported in Penzias and Wilson, 1965); this discovery boosted the big bang hypothesis over the competing steady-state model, resulting in its current domination of cosmology. The steady-state model (featuring an eternal universe and continuous creation) was even less Biblical than the big bang, but creation science has of course had to grapple with the observations that led to the dominance of the latter.

The bottom left section of the plot (displaying the fraction of total *CRSQ* astronomy articles) shows a prominent spike in planetary science³ articles during the mid-1980s. This spike reflects the combination (due to smoothing) of the fractions for 1984 and 1987. In 1984, one of the four astronomy articles dealt with diluvial asteroid impacts (Unfred, 1984), and another (Humphreys, 1984) considered the creation of planetary magnetic fields. In 1987, all three articles dealt with solar system issues: the existence of short-period comets (Steidl, 1987), speculation that Martian flybys are responsible for terrestrial mountains (Patten, 1987), and the possibility of solar contraction (Benton, 1987).

The right-hand panel displays the same counts and fractions for all four journals combined (marking the *ICC*

3 Strictly speaking, solar system science.

years with magenta bars).⁴ Here we see more clearly the large percentage of speed-of-light articles around 1990. We also see the near-dominance of cosmology articles after the turn of the century, 19 of them published in *JoC* (11 of them by John Hartnett) during the first decade, and 13 in *ARJ* (7 of them by Danny Faulkner) during the second.

Finally, however, we note that after 1990 none of the smoothed curves ever dip down to zero. We conclude that all of the major branches of astronomy (from planetary science to cosmology) are represented, and consistently so, in the past half-century of creation research, and especially during the three most recent decades. However, this breadth has not prevented a significant focus on the issues most relevant to a young-Earth scientific synthesis, in particular the issues of light travel-time, cosmology, and the timing of crater formation throughout the solar system.

Author Qualifications

The final issue we here consider concerns the qualifications of contributors to creation astronomy. Two problems hinder investigation of this issue. The first is the absence of a completely satisfactory metric. Ideally a metric for qualification would reflect general familiarity with astronomy and particular familiarity with the subfield under discussion; experience in formulating—and testing—scientific hypotheses; and an intangible, intuitive “feel” for the plausibility of various statements and speculations.⁵ Unfortunately, any attempt to measure such factors would require intimate familiarity with the

authors and their work—and even then would involve unavoidable subjectivity.

Only one objective proxy seems readily available, namely, educational degrees in astronomy, physics, or some other natural-science field. Of course, degrees do not guarantee qualification, nor does their absence guarantee its lack; nevertheless, the two are surely correlated. Furthermore, while undergraduate and master’s degrees provide general familiarity with a particular discipline, a terminal degree is intended to provide particular familiarity with (a portion of) one subdiscipline; it also provides an introduction to the actual practice of science and (one hopes) begins to build the aforementioned intuitive “feel.” In addition, the closer the degree field to astronomy itself, the better the proxy. In the author’s experience, a terminal mathematics degree provides experience with scholarship in general, but regarding qualification to write on astronomy, it compares poorly with the knowledge and experience provided by a corresponding astronomy degree.

Thus, the proxy we here adopt for author qualification is an earned doctorate in one of the following fields (in order of preference): astronomy, physics, or another science (including mathematics).

Two caveats are essential at this stage. First, adoption of this metric does not imply that those without terminal degrees in a science field are unqualified to write about astronomy. Indeed, it is a writer with (to the author’s knowledge) no earned doctorate and no astronomy degree who has made some of the most significant contributions to understanding solar system cratering in a YEC framework. Nor is the inverse statement true: a terminal degree in astronomy does not automatically certify someone as an expert, especially when they address a different subdiscipline than that of their dissertation. Unfortunately, no better proxy for qualification seems to present itself.

Another caveat: use of this metric should not discourage potential authors *without* terminal degrees from contributing articles to creationary literature; indeed, interaction with the community—which includes writing and responding to articles—is one of the ways to *build* expertise, intuition, etc.—and, thus, qualification.

However, another problem now presents itself, namely, that of incomplete data: the creationary literature does not always publish authors’ degrees—or will publish the degree without the degree field. While it is possible to fill some of these gaps by cross-referencing (and also through internet searches), the data remains incomplete. One should keep this fact in mind throughout the remainder of this section.

Figure 5 displays the (known) qualifications—in terms of terminal degrees—for authors of astronomy articles. As in previous figures, the left-hand panel considers *CRSQ* only, whereas the right-hand panel considers all four journals. Again, we smooth the raw data with a Gaussian kernel ($\sigma = 2.0$ yr.), showing the smoothed data as thick curves and selected unsmoothed data as thin lines.

One conclusion we can draw from Figure 5 is that there seems to be no “typical” profile for a contributor to creation astronomy. Contributors range from those with doctorates in astronomy (and respectable publication records in the mainstream astronomical journals) to those with no terminal degree in any natural science field. Again, at least one member of the latter group has made significant contributions to a young-Earth understanding of astronomy.

However, we also note that holders of terminal astronomy degrees almost never predominate (at least when considering the smoothed curves). This fact reflects the small pool of individuals involved; the great bulk of the contributions in this category, during the last two decades, has come from three authors, namely, Danny Faulkner, Jason

4 Before 1984, of course, these plots are identical to those of the left-hand panel.

5 Another ingredient is a commitment to the straightforward reading of Scripture; however, the journal publishers’ doctrinal statements help safeguard this area.

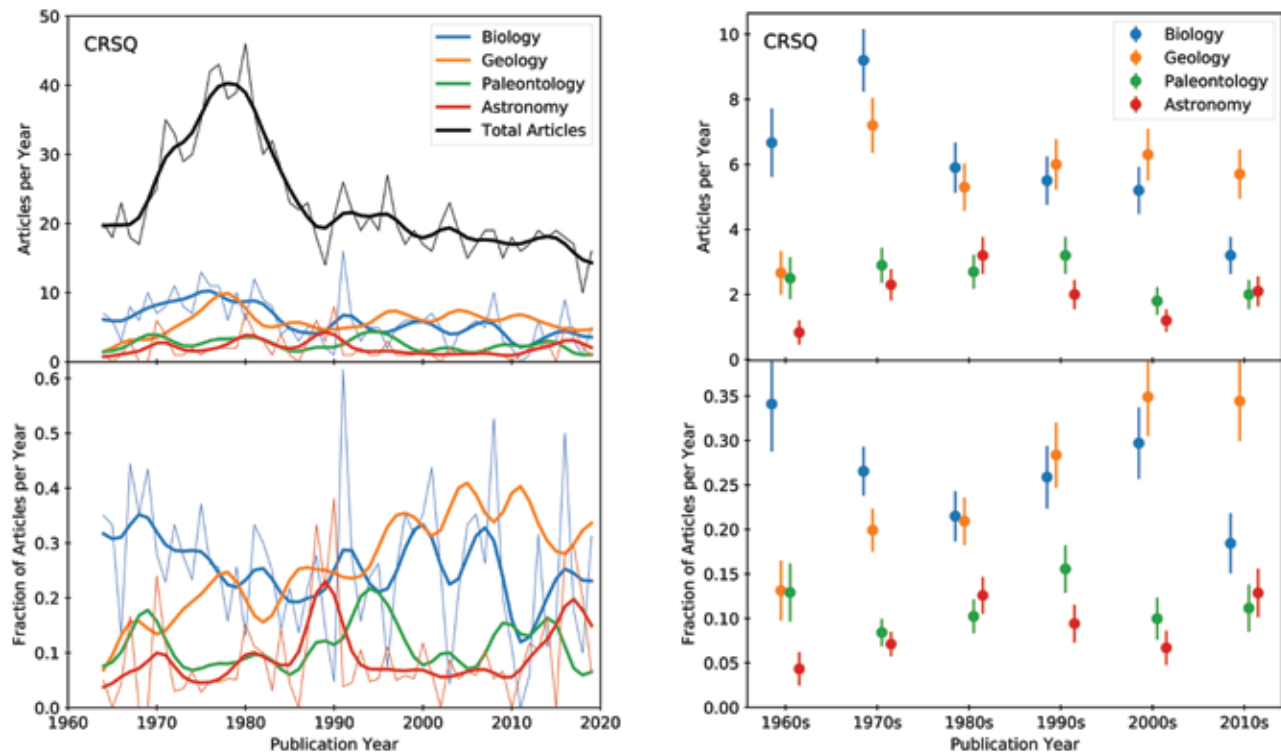


Figure 1. Left-hand panel: number of CRSQ articles per year dealing with biology, geology, paleontology, and astronomy, both in absolute terms (top) and as a fraction of all articles (bottom). Thick curves reflect smoothing with a Gaussian kernel ($\sigma = 1.5$ yr.); for comparison, thin lines show unsmoothed data for selected fields. Right-hand panel: the same data grouped by decade, with Poisson error bars.

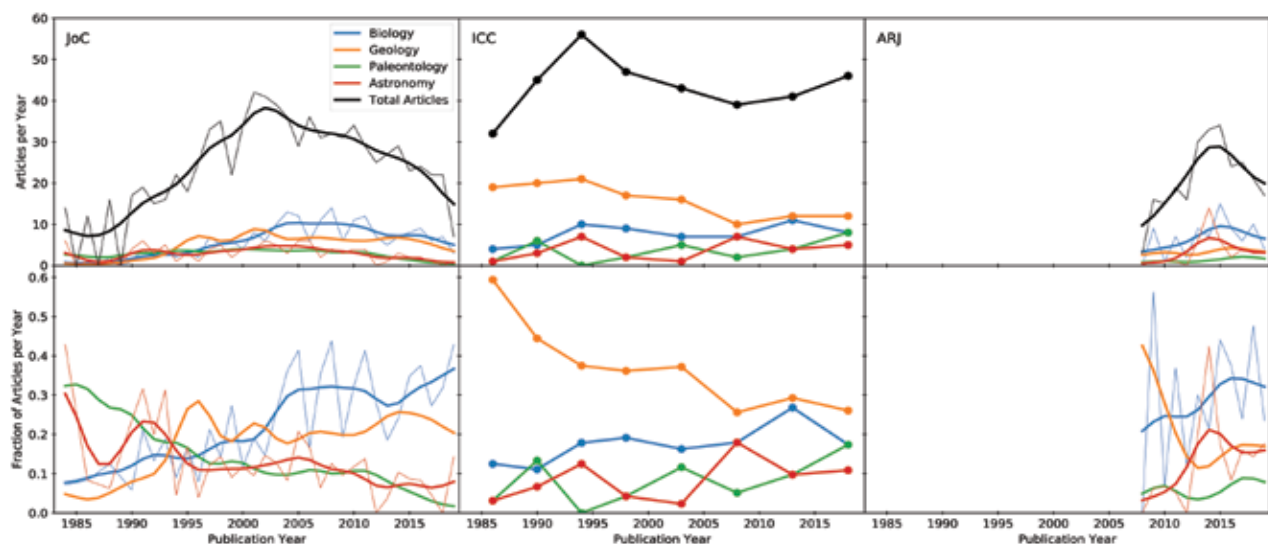


Figure 2. Articles per year devoted to biology, geology, paleontology, and astronomy, in *Journal of Creation* and predecessors (left column), in *Proceedings of the International Conference on Creationism* (middle column), and in *Answers Research Journal* (right column). The top panels display the absolute number of articles per year (or, for ICC, per conference); the bottom panels express the number as a fraction of all articles in the journal. For *JoC* and *ARJ*, thick curves have been smoothed with a Gaussian kernel ($\sigma = 1.5$ yr.); for comparison, thin lines show unsmoothed data for biology, astronomy, and total articles.

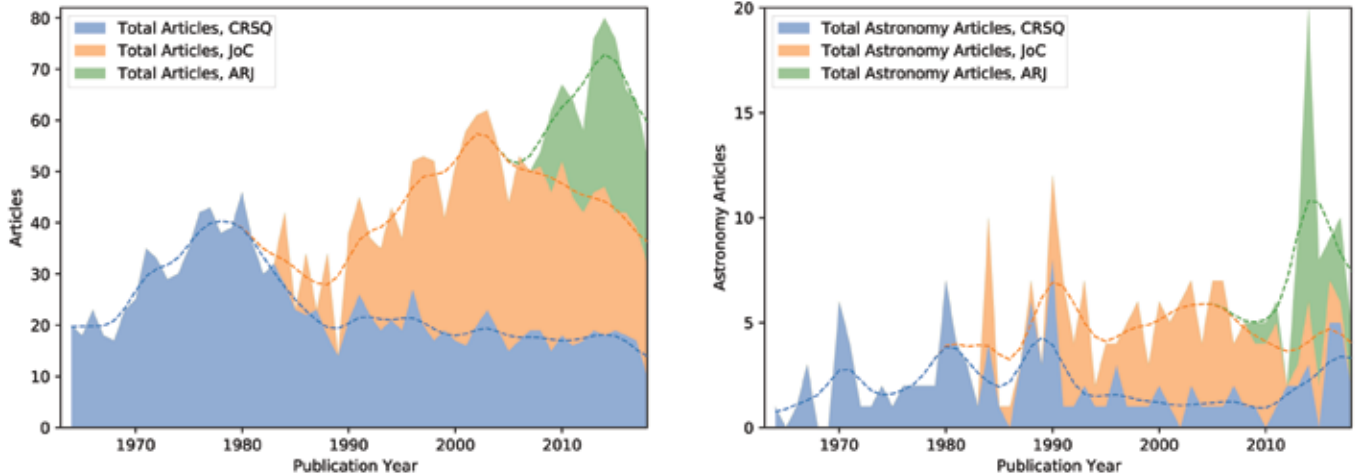


Figure 3. Left-hand panel: total number of articles per year published in *CRSQ*, *JoC* and predecessors, and *ARJ*, from 1964 to 2018. The heights of the shaded regions indicate the total number of articles per year in each journal. Note that the shaded regions stack rather than overlapping, so that the total height of all shaded regions together represents the total number of articles published in a given year, in all three journals together. The dashed curves (matched in color to the shaded regions) show the result of smoothing the number of articles with a Gaussian kernel ($\sigma = 1.5$ yr.). Right-hand panel: the same, for astronomy articles only.

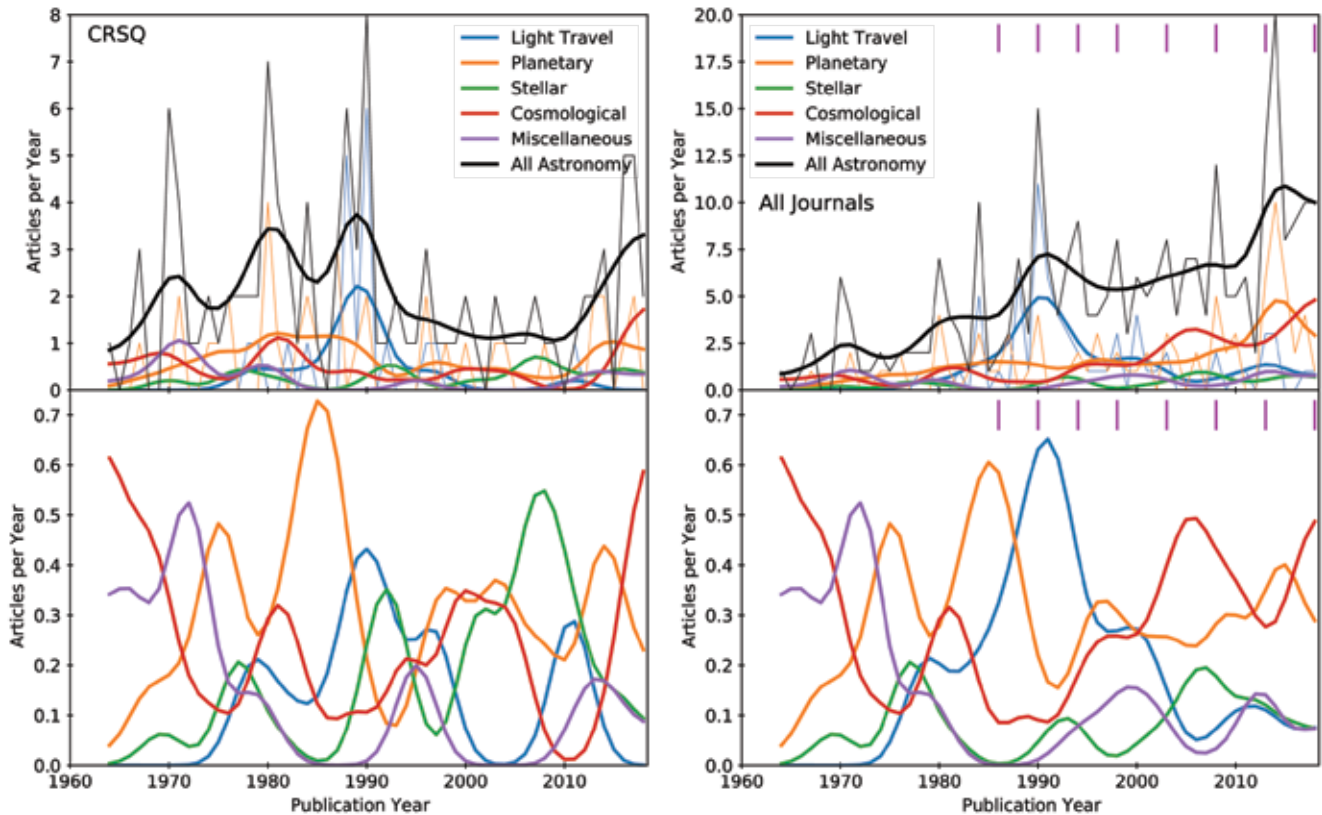


Figure 4. Left-hand panel: top – number of *CRSQ* astronomy articles per year for each subfield identified in the text. Thick curves reflect smoothing with a Gaussian kernel ($\sigma = 2.0$ yr.); for comparison, thin lines show unsmoothed data for total astronomy and for selected subfields. Bottom – the same data as a fraction of total *CRSQ* astronomy articles. Right-hand panel: the same totals and percentages for all four journals combined. Magenta bars denote ICC years.

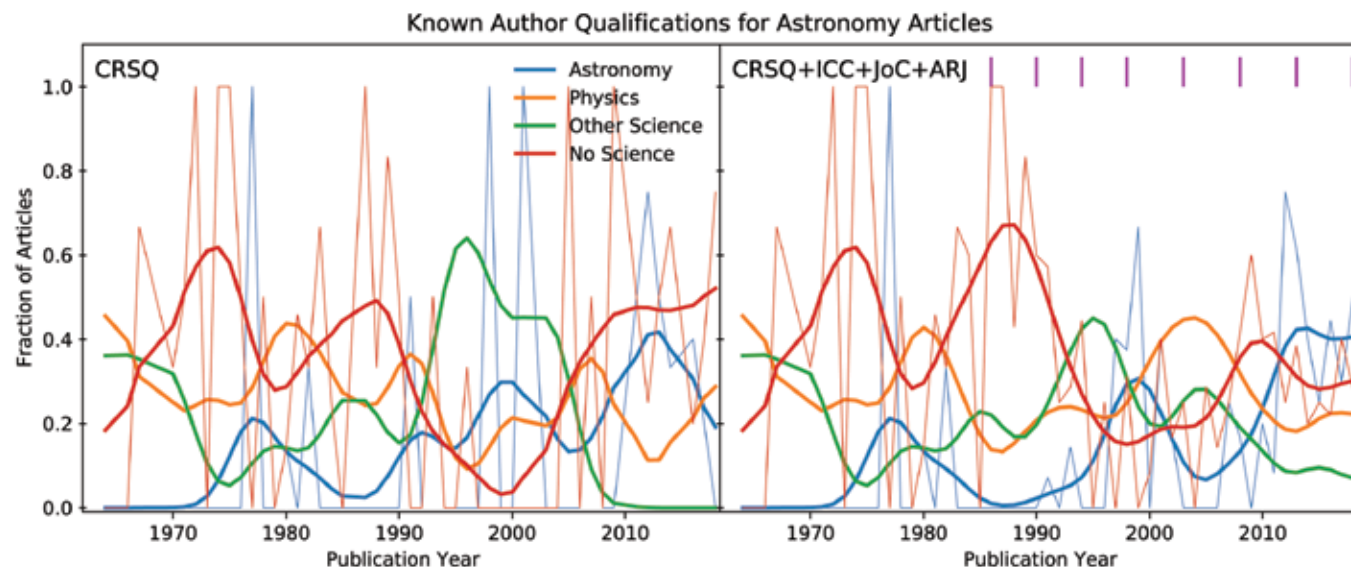


Figure 5. Areas of expertise (defined as a terminal degree in the field) for authors of astronomy articles, in CRSQ (left-hand panel) and in all four journals (right-hand panel). In the right-hand panel, magenta bars denote ICC years. Thick curves reflect smoothing with a Gaussian kernel ($\sigma = 2.0$ yr.); for comparison, thin curves show unsmoothed results for astronomy and “no science.” The figure is based on available—but incomplete—information.

Lisle, and Ron Samec. (Likewise, two individuals have contributed the bulk of recent articles from physics Ph.D.s, namely, Russell Humphreys and John Hartnett.) It would be highly desirable to increase this pool, and the most obvious means of doing so is for more YEC believers (especially the young) to earn astronomy doctorates. Obviously this course of action is not feasible for everyone, and the process involves significant commitment. Nevertheless, the payoff (in the author’s experience) is immense.

However, the impact on the field by authors without a doctoral science degree has been both significant and beneficial. The breadth of input into creationary astronomy is a strength, not a weakness, and is to be encouraged. It is hoped that creationary astronomy will continue to attract a broad range of contributors, even as the pool of astronomy Ph.D.s continues to grow.

Conclusions

This article (Part I of a planned two-part series) has sought to address three questions regarding creation astronomy over the past half-century. The first question involves how much effort (reflected in published articles, and compared to other natural sciences) has been devoted to development of a creationary understanding of astronomy. We find that the quantity of creation research in astronomy is significantly lower than that in biology and geology—as one might expect, given the focus of Scripture on terrestrial events; nevertheless, the astronomy output is comparable to that of paleontology—and has remained so even as the total number of creationary articles has more than tripled. In addition, the availability of more outlets for creationary research seems to have multiplied rather than divided creation astronomy output. We conclude that the field of astronomy

has not been neglected by creation researchers.

We next considered the distribution of this effort among the subfields of astronomy in order to characterize its breadth. We find that creation research has addressed, in some manner, each major subfield of astronomy, from planetary science to cosmology. Naturally, much of the work has focused on a few significant issues relevant to a young-Earth framework, such as light travel-time and the place of meteoric bombardment in the Creation/Flood paradigm. We intend Part II of this series to include a more detailed analysis of the topics, foci, agreements, and disagreements of this research effort.

We finally considered the typical qualifications of creation astronomy contributors. Based on admittedly incomplete information, there seems to be no common profile of a “typical” contributor to the field. Contributors

range from those holding doctorates in astronomy to those with no terminal science degree—and members of the latter group have made significant contributions to YEC astronomy.

However, contributors holding astronomy doctorates constitute a small pool of individuals, which it would be desirable to increase.

We conclude that creationary efforts in astronomy have been both vigorous and diverse.

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eKINDS Project Paper

Strategies for More Clearly Delineating, Characterizing, and Inferring the Natural History of Baramins III:

Evaluating Relationships and Proposing Post-Flood Dispersal, with Application to the Order Galliformes (Class: Aves)

Jon Ahlquist[†] and Jean K. Lightner [‡]

Abstract

In part I of this series, we laid out and applied a simple heuristic to the study of landfowl (traditional order Galliformes). We established that all families in this order share continuity consistent with them being identified as a created kind (baramin). In part II we took a closer look at the diversity and specializations that appear in various species of landfowl. Here, we continue our examination of the data, traditional characters as well as genome sequences, to understand relationships within the group, and propose likely routes of dispersal after the original ancestors of this baramin left the Ark.

All of the currently accepted genera and more than 85% of the world's landfowl have had their genomes examined in part or in whole, making this taxa ripe for baraminological study. Our analysis has upheld much of the traditional classification but has given insight especially into the large family Phasianidae, including both the pheasants and the Old World quail and partridges. Of the 12 identified landfowl groups, eight are within the family Phasianidae. All of the genera of this family can be assigned to a group either unequivocally, or with a high degree of probability. We explore the novel suggestion of the African Rock Partridge (*Ptilopachus*) as a possible link to the New World quail, and uphold this conclusion. Further findings are discussed under each of the constituent groups.

Finally, we show that dispersal of landfowl from the mountains of Ararat fits well with available data, with several lineages invading the New World, probably by more than one route.

Key Words: Landfowl, Galliformes, post-Flood dispersal, baramin, baraminology, natural history, Megapodiidae, megapodes, Cracidae, cracids, quail, Numididae, guineafowl, Phasianidae, pheasants, grouse, turkey, partridges, junglefowl

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Accepted for publication August 9, 2021

Introduction

Landfowl are familiar to everyone. The domestic chicken (*Gallus gallus*) is the most abundant bird on Earth and is the most intensively studied. The landfowl which have commercial value—such as quail, grouse, and guineafowl—and those of avicultural interest—such as the brightly colored pheasants—are also well-known. The number of molecular studies devoted to landfowl is extensive and has been challenging to synthesize. Unfortunately, there are some species that are almost unknown to scientists because they occupy limited ranges in parts of the world where study is difficult. Many of the partridges are not spectacular in their plumage and have received limited attention. Nevertheless, there is abundant information, making this order attractive for detailed baraminological investigation.

The landmark baraminological study on landfowl is that of McConnachie (2007) and McConnachie and Brophy (2007, 2008). It is the most thorough prior study of any bird group, and synthesized data from morphology, the Biblical record, and hybridization. Their morphological analysis utilized data from Dyke et al. (2003). These data had been “pre-selected” for use in parsimony analyses and hence emphasized characters that were apomorphic within the landfowl. As a result, many characters used by Holman (1961, 1964) were omitted because they were considered to be plesiomorphic. In the end, the Dyke et al. cladistic analysis yielded a single character (the tomial notch) uniting the New World quail and only two (the breeding habits and large feet) attesting to the monophyly of the megapodes.

Given the bias of the Dyke dataset, it is not surprising that the study by McConnachie (2007) yielded four groups based on morphological characters. Hybrid data unites three of these four groups, leaving the megapodes as the only one of the five landfowl families where continuity could not be demonstrated with the core group. Thus, McConnachie and Brophy (2008) conservatively suggested the order Galliformes is comprised of two baramins, with the megapodes being separate from the rest.

However, that the landfowl represent a single monophyletic assemblage has never been seriously contested. The history of the classification of landfowl has been given in detail by Sibley and Ahlquist (1972, 1990). In part I of this series (Ahlquist and Lightner, 2019) we built on the pioneering work of McConnachie and Brophy (2007, 2008), though we assert that all Galliformes comprise a single baramin. We add a more thoroughly documented hybrid between cracids and a chicken, as well as append a list of numerous morphological characters that unite all landfowl. In part II (Ahlquist and Lightner, 2020) we examined diversity within landfowl; numerous families contain members with some impressive adaptations, while clearly retaining their identity as landfowl.

Establishing baraminic status and evaluating diversity within a group provide a basis for understanding relation-

ships within a baramin. Through the synthesis of available data, including morphological, physiological, behavioral, and genetic data, it is evident the landfowl have diversified into 12 identifiable groups (Figure 1). Four of these groups correspond to families: Megapodiidae (megapodes), Cracidae, Numididae (guineafowl), and Odontophoridae (New World quail). The remaining 8 groups are within the large, diverse family Phasianidae (pheasants and allies).

Megapodiidae (Megapodes)

Despite the unique breeding system, no one has denied the affinities of megapodes to landfowl. Although hybridization occurs among some megapode genera (McCarthy 2006, pp. 39–40), no hybrids are known between them and other landfowl. This is not surprising given the genetic distance between them and other families of landfowl, as well as the limited opportunities for potential hybridization to occur. All studies, whether morphological or molecular attest to a sister-group relationship of megapodes to other landfowl.

A study of relationships within Megapodiidae has produced conflicting opinions.

For the megapodes we consider five principal studies: Clark (1964), traditional characters; Dekker and Brom (1992), traditional characters; Mey (1999), parasites hosted by the birds; Birks and Edwards (2002), mitochondrial and nuclear DNA sequences; Harris et al. (2014), emphasis on biogeography and nesting habits.

In a broad sense these studies show similar relationships. A brush-turkey group consisting of the genera *Alectura*, *Leipoa*, *Aepyodius*, and *Talegalla* is sister to a second containing *Megapodius* and *Eulipoa*. The Maleo (*Macrocephalon*) clusters with each group twice.

The principal of using bird parasites as indices to relationships (Mey, 1999) is not new but requires explanation to the non-specialist. The underlying idea is simple: birds harboring similar parasites are likely to be closely related. In a secular sense one thinks of the parasites co-evolving with their hosts. The problems are twofold. One needs to determine accurately the relationships of the parasites; not always an easy task. The problem of secondary infestation (or accidental transfer) cannot always be accounted for. Nonetheless, some interesting systematic proposals have come out from this work.

One of the pioneering studies on feather lice is that of Rothschild and Clay (1952), which is a delightful read in spite of its age. Dame Miriam Rothschild was part of the Rothschild banking family and possessed the intelligence, motivation, and financial resources to devote her long and productive life to a study of bird parasites. She was the niece of the famous (and infamous) Lord Walter Rothschild who used his family fortune to amass a huge collection of birds at Tring, England.

This private collection, eventually dispersed to both the British Museum (Natural History Museum in London) and American Museum of Natural History, was one of the most important in the world.

Perhaps the best solution is to recognize *two* clades of megapodes, thus agreeing with Dekker and Brom (1992) and Harris et al. (2014), and differing from the parasite evidence of Mey (1999) and the molecular data of Birks and Edwards (2002), only in the placement of *Macrocephalon*. This produces a clear split between the two groups on the basis of incubation strategy and facilitates the interpretation of other features on an ancestral-descendant framework.

The first group (A) consists of *Alectura*, *Aepyodius*, *Leipoa*, and *Talegalla*. The second group (B) contains *Macrocephalon*, *Eulipoa*, and *Megapodius*. *Eulipoa* and *Megapodius* are clearly related to each other. Some authorities lump them into *Megapodius*. Those who do not (e.g., Jones et al., 1995) emphasize

three or four distinctive features of *Eulipoa*. (1) The strongly barred pattern of the upper parts, consisting of maroon and pale blue-grey bands, and seen also in the chicks. (2) The tarsus, toes, and claws are relatively, and absolutely, longer than in *Megapodius*. (3) The tail is relatively longer than in *Megapodius* with the central shafts of the feathers elongated, a feature unique among megapodes. (4) The birds fly at night to the islands at which they construct their burrows nocturnally.

In its simplest expression, wing loading is defined as the mass of the bird divided by the area of the wings. The lighter wing loading of members of Group B *Megapodius-Eulipoa* is obvious. The unknown is *Macrocephalon*.

A scan of the weights and wing lengths among *Macrocephalon* and the similar sized *Talegalla* and *Aepyodius* as given by Jones et al. (1995) shows no obvious differences, but this may not be a valid comparison. We may conjecture that since the Maleo had colonized Sulawesi, presumably from New Guinea, it may be a better flyer or at least possess the propensity to displace over water compared to the obligate mound builders.

Dekker and Brom (1992, p. 30) argue,

The maleo of Sulawesi, on the other hand, does use Sulawesi's beaches to incubate the eggs. In contrast to the megapodes of New Guinea, the forest-dwelling maleo is not a mound-builder but a burrow-nester which lays its eggs in volcanically heated soils. This may suggest that burrow-nesting at beaches can only be applied by species which are (or formerly were) burrow-nesters at volcanic soils. Burrow-nesting at beaches therefore seems to be derived from burrow-nesting at volcanic soils and not directly from mound-building.

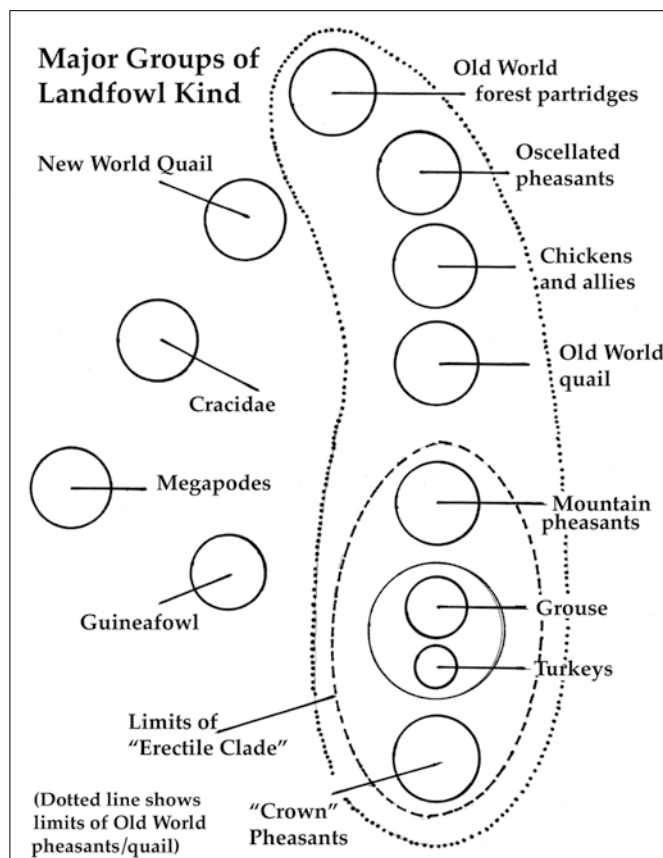


Figure 1. A simplified diagram depicting relationships within landfowl (Galliformes). Four families form smaller groups: New World quail (Odontophoridae); Cracidae; Megapodes, (Megapodiidae); and guineafowl (Numididae). The Old World pheasants and quail (Phasianidae) comprise a very large group, with numerous groups within it. Drawn by JA.

Cracidae (Chachalacas, Curassows, Guans)

Readers familiar with the Sibley-Ahlquist-Monroe (1988) classification of birds based largely on DNA evidence will note that the writers placed the Cracidae and Megapodiidae together in a separate suborder, the Craciformes. Here, we reach conclusions different from that of Sibley-Ahlquist-Monroe (1988) and in accord with those of Lightner (2013). Since Ahlquist was co-author of the 1988 classification, some comment is in order.

In Sibley and Ahlquist (1990) we entertained a relationship between cracids and megapodes despite the lack of unambiguous evidence. It was our conviction and intention, if not explicitly stated, to maintain some nodes in the hopes of stimulating further research. If we collapsed the node, it was an admission that we knew nothing or that we had no opinion regarding our own data or the data from other aspects of avian biology. Such was disingenuous.

The temporal framework of the Sibley and Ahlquist (1990) work was the secular geological time scale, including the ideas of continental drift and vicariance biogeography. As such, a putative relationship between cracids and megapodes was ten-

able via an ancient Gondwanaland (i.e., Australian-Antarctic-South American) connection. In a Genesis Flood scenario this is precluded.

More recent molecular evidence in favor of a cracid-megapode relationship has not been forthcoming (Crowe et al., 2006a, b; Cox et al., 2007; Kriegs et al., 2007; Wang et al., 2013; Kimball and Braun, 2014; Meiklejohn et al., 2014; Shen et al., 2014; Hosner et al., 2016; *inter alia*).

Given 25 years' hindsight, the number of comparisons ($n = 11$) reported for a cracid-megapode by Sibley and Ahlquist (1990) is too small to withstand statistical scrutiny. Inexplicably, they did not include melting curve data from a labeled megapode, although those values were used in their calculations. Thus, the elimination of Supraorder Craciformes is justified. A more plausible dispersal and invasion hypothesis is presented below under the heading Biogeography.

The fascinating and complex story of natural hybrids between cracids and other landfowl is told in Part I of this series. To summarize briefly, there existed a few reports in the literature which were not trustworthy. Anecdotal evidence of such hybrids abounded, though the genetic distance between cracids and the main landfowl families is relatively large. Many ornithologists were informed by villagers that chicken X cracid hybrids were frequent, yet specimens were not forthcoming. It was not until we discovered the work of Jose Ricardo Gunski (2001) who had produced and published work on such hybrids and backcrosses that the vexing question of cracid X phasianid hybrids had a definitive answer.

The question of relationships among the genera and species has received much discussion. Following are the genera of Cracidae recognized by Gill and Donsker (2016) with the number of species in parentheses; presumably their list implies a phylogenetic sequence: *Ortalis* (16), *Penelope* (15), *Pipile* (4), *Aburria* (1), *Chamaepetes* (2), *Penelopina* (1), *Oreophasis* (1), *Nothocrax* (1), *Mitu* (4), *Pauxi* (3), *Crax* (7). We use these names to unify our discussion.

The traditional groups are (a) the chachalacas (*Ortalis*), (b) the guans (*Penelope*, *Pipile*, *Aburria*, *Chamaepetes*, and *Penelopina*), and (c) the curassows (*Mitu*, *Pauxi*, and *Crax*). The basis for them are relative size, coloration, crest development, and bill shape. The relationships of the Horned Guan (*Oreophasis derbianus*) and the Nocturnal Curassow (*Nothocrax urumutum*) are debated. Principal papers are summarized below.

Vuilleumier (1965), Vaurie (1964, 1965a,b,c, 1966a,b, 1967a,b,c,d, 1968), and Delacour and Amadon (1973) have provided detailed accounts of relationships among the Cracidae based mainly on traditional characters. Their conclusions, however, are not easily entered into cladograms without doing the authors injustice. The papers are "must read" for the student of cracid relationships, so we cite them for their historical value.

There is general acceptance that the Cracidae consist of two groups: the smaller chachalacas and guans (*Ortalis*, *Penelope*, *Pipile*, *Aburria*, *Chamaepetes*, and *Penelopina*) and the larger curassows (*Nothocrax*, *Mitu*, *Pauxi*, and *Crax*). The problem species has been, and continues to be the Horned Guan (*Oreophasis derbianus*).

Of the two molecular data sets, one study (Pereira et al., 2002) places *Oreophasis* with a combined chachalaca-curassow group and the other (Frank-Hoeflich et al., 2007) places *Oreophasis* with the curassows and recognizes a second clade with the chachalacas and guans. Another paper (Pereira and Baker, 2004) has examined the relationships among the curassows using mitochondrial DNA (mtDNA). A discussion of this last paper is outside the scope of this review; however, the scenario of speciation within the 14 large curassows would be a fertile study for the baraminologist armed with different analytical techniques and the perspective of a single 'ice age' following the worldwide Flood.

The study by Frank-Hoeflich et al. (2007) is notable in that it utilized three sets of data, osteological, integumentary, plus behavioral, and molecular. These data are presented separately as well as in combined form. A suite of 74 morphological and behavioral characters placed *Oreophasis* at the base of a clade of chachalacas and guans. The mtDNA tree (661 base pairs from cytochrome *b* gene) recovers a clade consisting of *Ortalis* (chachalacas) plus the large curassows with *Oreophasis* as its sister. A combined tree of 661 molecular characters, 151 osteological characters, and 74 behavioral and morphological characters moves *Ortalis* to the clade with the guans and has *Oreophasis* as the basal lineage of the curassows.

Hosner et al. (2016) provided a more complete and better resolved picture of cracid relationships. They sampled 36 species of Cracidae plus nine from previous studies, giving a total of 47 of 55 currently recognized species or 85% coverage. Their data set included mtDNA, nuclear introns, and ultra-conserved sequences (UCEs) and strongly supported four groups: the curassows (*Crax*, *Mitu*, and *Pauxi*), the chachalacas (*Ortalis*), Horned Guan (*Oreophasis*), and the remaining guans (*Aburria*, *Chamaepetes*, *Penelope*, *Penelopina*, and *Pipile*).

Of these four groups two major clades are inferred. One (at left) includes the curassows, chachalacas, and Horned Guan; the second (at right) includes the remaining genera of guans, as follows:

<i>Oreophasis</i>	<i>Penelopina</i>
<i>Ortalis</i>	<i>Chamaepetes</i>
<i>Nothocrax</i>	<i>Penelope</i> , <i>Pipile</i> + <i>Aburria</i>
<i>Crax</i> , <i>Mitu</i> + <i>Pauxi</i>	

In our notation *Mitu*+*Pauxi* indicates that the species of each genus were interposed among one another. The difficulty of resolving the species of *Mitu* and *Pauxi*, in our opinion, is likely not a "failure" of the molecular data but most likely

represents the artificial constructs of each genus. Other studies, morphological as well as molecular, report conflicts in this area. Taxon sampling was not a problem as all four species of *Mitu* were represented and two of three species of *Pauxi*. The third species of *Pauxi*, the Sira Curassow (*P. koepckeae*), was described as a subspecies of *Pauxi unicornis* by Weske and Terborgh (1971) and is known from only a few specimens from a limited range in central Peru. A re-evaluation of the characters of the genera and their constituent species in light of the molecular data is needed.

The same is true of *Pipile*+*Aburria*. In this case the nuclear intron and UCE data separated *Aburria* from *Pipile*, whereas the mtDNA data did not. The authors commented that relationships among species of *Ortalis* and *Penelope* were only moderately resolved indicting the rapid and recent radiation of the two genera.

Overall, the authors favored a hypothesis of a North and Central American origin and radiation of Cracidae followed by a diversification in South America after the closure of the Panamanian water gap.

Numididae (Guineafowl)

The major study of the morphology of guineafowl is that of Crowe (1978) in which he clarified the multiple subspecies of the Helmeted Guineafowl (*Numida meleagris*) and provided a cladistic analysis of all the species. Crowe favored an Asian origin of this African endemic family.

Above the family level the relationships of the guineafowl are unambiguous. All molecular studies recover them as a sister-group to the Phasianidae plus Odontophoridae:

Megapodiidae

Cracidae

Numididae

Phasianidae, Odontophoridae

Asampling of the range of papers substantiating this include Crowe et al. (2006a); Crowe et al. (2006b); Kriegs et al. (2007); Kimball et al. (2011); Wang et al. (2013); Meiklejohn et al. (2014); and Hosner et al. (2016).

Of significance is the existence of reputable hybrids between *Numida* and *Gallus* (mainly), *Pavo*, and *Phasianus*; McCarthy (2006, pp. 51–53) devotes considerable space to the topic. Sibley and Ahlquist (1990) estimated at least a 10% difference across the genome between *Numida* and phasianids, making such a cross the most distant among birds. The guineafowl are more distant from phasianids than are the New World quail for which no reliable hybrids with phasianids exist.

It would be enlightening if a living *Numida* X phasianid hybrid could be genomically sampled. Given existing technology, and the existence of the complete genome of *Gallus*, such a hybrid could yield potentially valuable information

on the genetic architecture that led to such an improbable occurrence.

It is highly probable that guineafowl colonized Africa from Asia and diverged there. It is likely that the guineafowl were adapted to an open-country ecology; if so, then the presence of the two species of *Agelastes* in the rain forests of central and west Africa are a secondary specialization. This would explain the smaller size (crypsis) and loss of the spotting characteristic of *Numida*, *Guttera*, and *Acryllium* as being of little value in the low light of dense forests.

Phasianidae (Pheasants and Allies)

Grouse and turkeys

One can paraphrase a century of discourse on the relationships of these groups in a sentence. They are both unquestionably members of a large “phasianoid complex” but most discussion centers on whether they should be treated as families or subfamilies within this group. Taxonomic rank tells little about relationships. Hard data have not been forthcoming until recently.

Grouse are considered to be pheasants specialized for a boreal existence (Potapov and Sale, 2013). A number of pheasant genera live in mountainous regions of China, so it is easy to suggest an Old World origin for grouse. We may mention the eared-pheasants (*Crossoptilon*), monals (*Lophophorus*), and Koklass Pheasant (*Pucrasia*) that regularly breed at elevations of 3000–4000 meters or higher in eastern China. The snowcocks (*Tetraoagallus*) are also high-altitude landfowl, living above the timber-line, but they are rightly viewed as offshoots of partridges (compare plumages to *Alectoris* and *Ammoperdix*), and their ecology is that of a partridge (open-country, seed-eaters).

Grouse, however, have a greater radiation in the New World. Only three genera (*Tetrastes*, *Tetrao*, and *Lyrurus*, each with two species) are exclusively Palearctic. Depending on one's classification, *Falci pennis* has an Old and New World representative, and the ptarmigan (*Lagopus*) are Holarctic in distribution with one species, the White-tailed Ptarmigan (*Lagopus leucura*) being endemic to the New World. This leaves *Bonasa*, *Centrocerus*, *Dendragapus*, and *Tympanuchus* in the New World with eight species.

Grouse breed farther north than any birds, up to 83°30'N latitude in Greenland. Grouse in both hemispheres hardly penetrate below latitude 28° N, with the prairie chickens (*Tympanuchus*) ranging south to Texas, and the Ruffed Grouse (*Bonasa umbellus*) extending to the south Appalachians. In the Old World, the Chinese Grouse (*Tetrastes sewerzowi*) occurs where it can find favorable conditions in mixed boreal forests above 4,000 meters near the Sino-Tibetan border. Potapov and Sale (2013) rightly conclude that the ecological adaptations of

grouse restrict them to habitats that include significant periods of winter temperatures below freezing.

The large size and accompanying morphological peculiarities of turkeys have not yielded many clues to their relationships. Sibley and Ahlquist (1990; see Fig. 357, p. 842) provided an answer in placing both grouse and turkeys in the same clade but, inexplicably, never discussed their finding nor attempted any follow-up to it. That did not preclude other investigators from observing this finding and adding data in support of it.

Virtually every study has concurred in a sister-group relationship of grouse and turkeys. Supporting studies include the following papers, but are not limited solely to them: Kaiser et al. (2007) noted a sister-group relationship between grouse and turkeys on the basis of insertion pattern of CR1 retrotransposons, a conclusion which was supported by a similar study by Kriegs et al. (2007). Complete mitochondrial genomes (Shen et al., 2010) support the relationship, as do over 15,000 sites, primarily from nuclear introns but also including three mitochondrial regions (Pereira and Baker, 2004; Kimball and Braun, 2008; 2014; Kimball et al., 2011).

Moreover, these investigators have found that the turkey-grouse group is nested among other groups in the larger pheasant-partridge assemblage, and this has had implications in rending asunder the traditional Phasianinae and Perdicinae, as we shall see below.

The first molecular study to examine relationships among grouse was that of Ellsworth et al. (1995) who compared restriction fragment polymorphisms of mtDNA. They concluded that the prairie chickens (*Tympanuchus*) were the first to differentiate with *Bonasa* and *Dendragapus* being most derived. This agreed with a study by Short (1967) in placing the prairie chickens first and suggesting that the earliest grouse were grassland dwellers. Short's analysis was based on characters of egg color, natal plumages, number of tail feathers, feather color patterns, and others. Allowing for his merged genera, Short's "tree" reduces to:

Tympanuchus
 Bonasa
 Centrocercus
 Dendragapus
 Lagopus, Tetrao

Subsequent studies based on DNA sequences are in contradiction. Although details differ among them, a consistent pattern emerges in placing *Bonasa* and *Tetrastes* sister to the remaining grouse and *Tympanuchus* as most derived. Gutierrez et al. (2000); Crowe et al. (2006ab); Wang et al. (2013); Hosner et al. (2016); *inter alia* have variations on this perspective. Parsons et al. (2016) provided well-resolved relationships among all 19 species of grouse using mtDNA, nuclear intron, and nuclear UCE sequences.

We agree with Parsons et al. (2016, p. 130) that the "ancestor of the turkeys and grouse dispersed to the New World prior to diversification." If they have assessed the relationships correctly, then there would be a recolonization to the Old World with the hazel grouse (*Tetrastes bonasia* and *T. swerzowi*), two species of ptarmigan (*Lagopus lagopus* and *L. muta*), and the capercaillies (*Tetrao*) and black grouse (*Lyrurus*), with one recolonization from Old to New World in *Falci pennis canadensis*. Since their data do not indicate strict monophyly of *Falci pennis*, it may be necessary to reconsider the generic allocation of *F. canadensis*, which formerly was placed in a monotypic genus *Canachites*.

Finally, it is worthwhile pointing out that the display postures of grouse and turkeys are quite similar. The lekking behavior, fanned tail, drawn-in neck, and drooped wings all are suggestive, but given the variety of postures in typical pheasants can hardly be considered conclusive.

"Typical" pheasants (Phasianinae)

When we turn to the remainder of the phasianoid complex, we are met with a group of diverse taxa and a number of taxonomic studies, most of them molecular in nature. It is indeed gratifying that so many of them have been produced in the three decades since the Sibley and Ahlquist (1990) work concluded. Especially satisfying are the efforts to examine a wide range of species and to include in the authorship one or more ornithologists who have lent their expertise in the areas of morphology, ecology, and biogeography in analyzing and interpreting the significance of the data. We have reached a point where an integration of the molecular data with that of "natural history" is to be lauded.

These studies differ among one another in the nature of the sequence data collected, the number of species examined, and the methods of data analysis. To simplify discussion we concentrate on the most important general studies of landfowl (Pereira and Baker, 2004; Crowe et al., 2006 a,b; Kaiser et al., 2007; Krieg et al., 2007; Kimball and Braun, 2008, 2014; Kan et al., 2010; Shen et al., 2010, 2014; Wang et al., 2013; Meiklejohn et al., 2014; Hosner et al., 2016). This eliminates repetition of the citations of individual studies and provides a broad picture, namely, the eight Phasianidae groups that emerge from a synthesis of all the data. We have cited smaller studies and portions of the longer papers where they have special bearing on the major groups.

To our knowledge all genera of landfowl have been studied; thus, the constituents of these groups are more or less consistent. As expected, there are outliers, genera or species that seem not to fit well given our state of knowledge. This is not to be disparaged and is understandable for several reasons, as noted below.

1. Some genera branched off early in rapid sequence. These deep branches are often difficult to disentangle. Every

molecular study has commented on a rapid diversification of landfowl. This phenomenon is readily understood in a Genesis Flood scenario where the lineages branched from one another in a matter of a few hundred years. There are correspondingly few gaps to separate groups.

2. As already pointed out, different studies use different sources of sequence data. Some, such as those derived from mtDNA, are most effective in resolving taxa that have recently differentiated and give little “signal” at deeper levels. Other sequences, particularly those from slowly changing nuclear DNA genes or UCEs, are effective at resolving deeper-branch lengths.
3. Different labs have employed different numbers of species. It is obvious that, within limits, a sparse coverage of taxa will yield different patterns of relationships than a study that employs a wider coverage. Even examining 100% of landfowl will not guarantee a fully resolved tree, due to the limitations posed in item (2).
4. Not all taxa can be represented by fresh material. It is astonishing, and laudable, that usable DNA samples can be obtained from dried material (especially toe pads) of old museum specimens. That these sources yield somewhat degraded DNA is, of course, known to the investigators, and they are careful not to overestimate the conclusions to those derived from such specimens. Given the factors of time, funding (or lack thereof), and political conditions, it is not possible to obtain fresh samples of all desired taxa. We are fortunate, therefore, to have some, albeit imperfect data rather than none.
5. For a variety of reasons different laboratories utilize different methods of data analysis, and each research group has its reasons for doing so. To attempt to take a position on the validity of these methods is beyond the scope of this paper and would engage the authors in endless debate. Suffice it to say that analytical methods can lead to different conclusions. Constructively, they can help an investigator evaluate the validity of his data.
6. Further, we have the taxonomic equivalent of the theologians’ *hapax legomena*, those species represented (so far) by a single sample in a single study. We have no context in which to evaluate what the data from that sample tells us. In some cases, its morphological characters are unambiguous; in others they are difficult to evaluate, especially when the molecular and traditional evidence are not congruent.
7. Finally, we have used our own knowledge and taxonomic judgment in accepting, rejecting, or modifying the conclusions of others. In each instance we have stated that this represents our opinion, and we attempt to give reasons for our conclusions.

Using these data from the studies mentioned above, we are able to postulate groups within the Phasianinae (typical pheasants) plus *Perdicinae* (Old World quail) (Figure 1). These groups are approximate and not all papers agree with the placement of some genera. The grouse and turkeys, which comprise two related groups, have already been discussed because their constituents are unambiguous; a grouse is a grouse and a turkey is a turkey; there are no “problem” genera. We defer a discussion of the Rock Partridge (*Ptilopachus*) and the New World quail (*Odontophoridae*) until the end because they represent a special case.

If our discussion seems to be biased toward the work of Crowe’s group, it is not because we believe their data to be superior in all cases;] of DNA bases, and utilized more thorough analyses. Their studies have been carried out over 30 years. Their taxonomy (although cladistic) is holistic, embracing an array of attributes including morphology, behavior, advertising vocalizations, ecology, and biogeography.

The groups are listed below, not in a taxonomic sequence, with discussion from individual studies as necessary along with our comments. Several of the scientific names may be confusing to the non-specialist. However, Madge and McGowan (2002) provide a succinct identification guide to all the pheasants with full-color illustrations of each.

Mountain Pheasants

The mountain pheasant group, includes *Tragopan*, *Lophophorus*, *Tetraophasis*, and possibly *Lerwa* and *Ithaginis*. This group was not recognized as distinct by Crowe et al. (2006a) who included it in their subfamily Phasianinae, which comprise the crown pheasants.

Grouse and Turkeys

These two groups were discussed in detail above. There is consistent relationship of turkeys (*Meleagris*, subfamily *Meleagridinae*) and grouse (subfamily *Tetraoninae*, grouse and capercaillie (*Falcapennis*, *Dendragapus*, *Tetrao*, *Lyrurus*, *Bonasa*, *Tetrastes*, *Centrocercus*), ptarmigans (*Lagopus*), prairie-chickens (*Tympanuchus*). All studies recover them as sister to each other, although nested within the Phasianidae.

The location of the Koklass Pheasant (*Pucrasia*) at the base of a grouse-turkey group is intriguing. MtDNA alone does not recover this branch, suggesting that the Koklass is an outlier to typical pheasants (Bush and Strobeck, 2003; Huang and Ke, 2015). With the addition of nuclear genes and wider taxon sampling, the relationship becomes clearer (Wang et al., 2013; Kimball and Braun, 2014; Hosner et al., 2016). We accept this classification as tentative, pending an investigation of morphological characters for congruence. *Pucrasia* is somewhat of an aberrant pheasant with no obvious close relatives. It is found over a discontinuous range in montane

forests from 2000–4000 meters from the Himalayas through western China to Manchuria.

Note that the Grey Partridge (*Perdix*) in some molecular studies branches at the base of this group (Crowe et al., 2016a, b). This intriguing suggestion deserves further study.

Crown pheasants

The “crown” pheasants, also called gallopheasants, include *Catreus*, *Lophura*, *Crossoptilon*, *Phasianus*, *Chrysolophus*, *Syrmatiscus*, and possibly the grey partridges *Perdix*. With the exception of *Perdix* this group includes the typical pheasants, characterized by elongated tail feathers with characteristic barring.

Turkeys, grouse, mountain pheasants and crown pheasants comprise a larger group called the “erectile clade” (Kimball and Braun, 2008). Various members of the landfowl possess bare regions on their heads; however, the ability to *erect rapidly* such combs or wattles is restricted to members of this assemblage, which has been definitively established by Hosner et al. (2016). In their study *Perdix* is recovered as a sister-group to the gallopheasants (crown pheasants); the Koklass Pheasant *Pucrasia* is basal to the turkeys and grouse; and the Snow Partridge *Lerwa* forms the first dichotomy to this erectile clade.

Forest partridges

This corresponds roughly to the subfamily Arborophilinae of Crowe et al. (2006a) and contains Old World partridges, also appropriately termed forest partridges, that are sister (meaning ancestral) to the rest of the Phasianidae: *Rollulus*, Black Partridge (*Melanoperdix*), Ferruginous Partridge (*Caloperdix*), hill partridges (*Arborophila*), and *Xenoperdix*. All members of this group are found in southeast Asia and western Indonesia with the exception of the recently discovered *Xenoperdix* which is African (Dinesen et al., 1994; Bowie and Fjeldsa, 2005).

The skeptical systematist would have predicted that the former *Perdicinae* (Old World quail and partridges) was potentially ripe for surprises. Of 108 species the genera *Francolinus* comprising 41 species and *Arborophila* with 21 form the largest groups (57% of total species). The characters used in determining relationships have included the number and presence of tarsal spurs, the number of tail feathers, and relative lengths of the tail and wings. Otherwise, with the exception of a few genera, the plumage is designed for crypsis of ground dwelling birds and not for taxonomic insight. The advent of molecular data has provided such surprises, and the task is to determine how the molecular and morphological data dovetail with each other.

Old World quail and partridges

This assemblage consists of Old World quail/partridges including snowcocks (*Tetraogallus*), sand partridge (*Ammoperdix*), *Alectoris* partridges, quails (*Coturnix* and *Excalfactoria*),

Madagascan Partridge (*Margaroperdix*), bush quails (*Perdicula*), spur-fowls (*Pternistis*, formerly *Francolinus*), and the Snow Mountain Partridge (*Anurophasis*). Three or four smaller “sub-groups” are seen among these genera.

Junglefowl and allies

The “chicken” group or subfamily Gallinae of Crowe et al. (2006a) includes the bamboo-partridges (*Bambusicola*), junglefowls (*Gallus*), francolins of the genera *Scleroptila* (formerly *Francolinus*), *Peliperdix* (formerly *Francolinus*), *Dendroperdix* (formerly *Francolinus*), and *Francolinus*.

Considering that the chicken (*Gallus gallus*) is arguably the best known bird on Earth—whether from its economic importance as food for man, its use as the “standard bird” in anatomical, embryological, physiological, and immunological studies, or a host of other criteria—it is surprising that conclusive evidence of its near relatives was not established until relatively recently. Fumihito et al. (1995) discovered a clear link between *Gallus* and bamboo partridges (*Bambusicola*) using a relatively small set of sequences of mtDNA. Subsequent studies have confirmed this. For a discussion of francolins please see subheading ‘Rock Partridge’ below.

Thus, the chicken and the junglefowl (*Gallus*) consistently fall outside of the main pheasant assemblage. Of their characters Madge and McGowan (2002, p. 292) write:

Junglefowl form a very familiar and distinctive genus, indeed they are sufficiently distinct that it is difficult to consider them ‘pheasants’ at all. They have no close relatives and almost form their own subgroup. Cocks have a prominent flashy coronal comb, throat wattles and ear lappets, and extensive bare facial skin. Tails are laterally compressed of 14–16 feathers, those of cocks with elongated, rather soft-sifted, decurving central feathers which fall either side of the supporting shorter feathers of the ridged tail. Neck, back, and rump feathers are elongated and usually pointed, forming hackles in cocks (these are shed following breeding in some species). Legs are relatively long. those of cocks bearing a single spur, hens usually unspurred.

Ocellated pheasants

This is the subfamily Pavoninae of Crowe et al. (2006a) and is referred to as the ocellated clade by Hosner et al. (2016). Members include *Pavo*, *Afropavo*, *Argusianus*, *Rheinardia*, and *Polyplectron*. (*Galloperdix* and *Haematortyx* apparently cluster here as well; see below.)

Kimball et al. (1997) provided the first clear evidence from mtDNA for the affinities of the Congo Peafowl (*Afropavo*) to the typical peafowl (*Pavo*), thus confirming the earlier immunological data of Mainardi (1963). Further, Kimball et al. (2001) examined complete mitochondrial cytochrome b (CYB) and control region sequences, as well as sequences from intron G

of the nuclear ovomucoid gene (OVOG) to derive relationships among the peacock-pheasants (*Polyplectron*). Their data established the reality of this group, the members of which are characterized by the presence of ornamental eye-spots (ocelli) variously on the tail, tail coverts, flight feathers, wing coverts and the mantle. The included genera are *Polyplectron*, two peafowl (*Pavo*), the Congo Peafowl (*Afropavo*), and the two argus pheasants (*Argusianus* and *Rheinardia*).

In a broader sense one might argue that lack of ocelli is ancestral in landfowl, that it is gained as a derived character in the peafowl group, and subsequently lost in one or more taxa. In the initial paper (Kimball et al., 2001) a loss is clear in the Bronze-winged Peacock-Pheasant (*Polyplectron chalcureum*) and the Congo Peafowl (*Afropavo*). The writers claim that ocelli are lost also in the Crested Argus (*Rheinardia*), but this depends on how one defines ocelli. In their narrow definition, requiring an iridescent patch as a component of the ocellus, they are correct. On the other hand a look at the plumage of the Crested Argus reveals a multitude of spots lacking only the iridescence. It might be preferable to code the character in three states: 0 = ocelli absent; 1 = ocelli present; 2 = ocelli modified. In this case there are only two losses of ocelli, and the character in *Rheinardia* becomes apomorphic.

In subsequent papers, Sun et al. (2014) and Hosner et al. (2016) added two species of spurfowl (*Galloperdix*) and the Crimson-headed partridge (*Haematortyx*) to the dataset, and they clustered with *Polyplectron*, between that genus and the peafowl. This surprising finding suggests five losses of ocelli. However, it might be premature to accept the placement of the two quail-like genera within these pheasants without further corroboration. The natural inclination is to “expect” *Haematortyx* and *Galloperdix* to cluster among the other quail (forest partridges) sister to the remaining Phasianidae. The genetic differences are too great to permit this. We would, therefore, prefer to amend the members of this group to include possibly the Crimson-headed Partridge (*Haematortyx*) and spurfowl (*Galloperdix*) with a precise placement awaiting further evidence.

The Rock Partridge (and New World quail)

We reserve a separate section for this interesting bird. No taxonomic inquiry would be complete without one enigmatic member to challenge the *status quo*. Most writers have commented on the distinctiveness of *Ptilopachus petrosus*. Mackworth-Praed and Grant (1970, p. 195) wrote, “A very distinct and aberrant monotypic genus with peculiar characteristics.” Johnsgard (1988, p. 242–243) noted that its most likely relatives are the Asian genera *Bambusicola* and *Galloperdix*.

It is one matter to note the distinctiveness of a taxon but quite different to provide actual evidence of relationships. Over three decades Timothy Crowe and colleagues have attempted

to accomplish that. Their work on African landfowl extends back 40 years (Crowe, 1978). He and his colleagues have built up an array of evidence from various sources in assessing relationships among the landfowl, especially the African francolins. Crowe’s data range from traditional morphology (external and skeletal characters), behavioral features, ecology, and vocalizations, as well as molecular data from mitochondrial and nuclear genes. Their synthesis, involving all data, exemplify the methods that we outlined previously, namely a holistic approach of successive approximations.

The name *Francolinus* derives directly from the French *francolin* and that from the Italian *francolino*, meaning a grouse. Lewis and Short (1879) do not give any Latin word resembling “francolinus.” In its traditional application the genus *Francolinus* comprises 41 species, the most speciose of the landfowl. The hill partridges (*Arborophila*) make up another 21 species. Together they comprise nearly 15% of landfowl species. Hall (1963) made a thorough study of the francolins based mainly on plumage and other characteristics. She supported monophyly of *Francolinus* and separated them into eight groups, with the exception of four species (*F. lathami*, *F. pondicerianus*, *F. nahani*, and *F. gularis*) that did not fit well. In Hall’s view the francolins were distinguished from the other *Perdicinae* (quail) on the basis of a long, hooked bill, a short tail of 14 feathers, an upright stance, and, in a majority of species, tarsal spurs in the males.

Milstein and Wolff (1987) reached different conclusions, separating two major groups, an Asian (containing the genera *Francolinus* and *Ortygornis*) and an African (*Pternistis*, *Scleroptila*, *Dendroperdix* and *Peliperdix*). They were using the “oversplit” genera of Wolters (1975). They did not, however, challenge the monophyly of the group.

Crowe et al. (1992), following up on the previous study of Crowe and Crowe (1985), established the paraphyly, if not polyphyly, of the francolins using a combination of mtDNA sequences and 25 morphobehavioral characters. Bloomer and Crowe (1998, p. 236) provided additional evidence for 20 francolin species:

quail-francolins (including *Scleroptila*, *Dendroperdix*, *Peliperdix*, and *Ortygornis* species) are small, ground-roosting birds with chestnut and white striped or barred dorsal plumage and high-pitched tonal calls. Partridge-francolins (*Francolinus* and *Pternistis* species) are larger, tree-roosting birds with dark dorsal plumage vermiculated with white or buff and emit lower pitched raucous calls.

The sister group to the partridge francolins is an assemblage of Old World partridges including *Alectoris*, *Coturnix*, and *Margaroperdix* (monotypic of Madagascar).

Dyke et al. (2003) carried out a study of the Galliformes using cladistic analyses of 102 characters, 89 of which were osteological and the remaining 13 involved plumage. The

study is valuable in that the characters and character states are described, and illustrations of the less obvious ones are provided. The results overall confirmed the traditional groups of the landfowl, but grouped both New and Old World quail together and were unable to resolve relationships among the pheasants. The placement of the quails together is not unexpected due to “convergent” similarities in morphology and the fact that many of the characters listed by Holman (1961) as being distinctive of the Odontophoridae were considered to be symplesiomorphic (“shared primitive”) and hence not amenable to cladistic analysis.

In the “final” analysis (Crowe et al., 2006a) the large genus *Pternistis* of francolins is in our Old World quail and partridge group (above), equivalent to Crowe’s subfamily Coturnicinae. The remaining francolins (*Francolinus*, *Dendroperdix*, *Peliperdix*, *Scleroptila*) are in Crowe’s subfamily Gallinae (our junglefowl and allies) which includes the bamboo-partridges (*Bambusicola*), and junglefowls (*Gallus*), and is in turn sister to the peafowl and peacock-pheasants. This study concluded that the francolins originated in Africa and subsequently spread into Asia.

As these studies were unfolding, the question of the Rock Partridge (*Ptilopachus petrosus*) was coming into focus. The prevailing opinion shared by Hall (1963), Johnsgard (1988), *inter alia*, was that *Ptilopachus* has its nearest relatives in southeast Asia with species such as the forest partridges (*Gallopardix*, and *Bambusicola*).

Such an alliance is possible. The Congo Peafowl has its closest relatives with the peafowl (*Pavo*) and peacock pheasants of southeast Asia (Kimball et al., 1997), and the recently discovered African forest partridges *Xenoperdix udzungwensis* and *X. obscuratus* are most closely allied to the Asian forest partridges (*Rollulus*, *Caloperdix*, and *Arborophila*) (Dinesen et al., 1994; Bowie and Fjeldsa, 2005). In these latter cases, the authors presented evidence that Asia and Africa were formerly linked via continuous rain forest, and that present desert conditions through the Middle East and Arabian Peninsula are recent phenomena.

With *Ptilopachus* a different scene was created when the molecular data showed that it, as well as Nahan’s Francolin (*Francolinus nahani*), are actually sister to the New World quail (Odontophoridae). As is the case with other molecular “epiphanies,” this remarkable finding led to the investigation of other evidence.

In her 1963 study, Hall was unable to place the small, dark, forest-dwelling *Francolinus nahani* into any of her eight groups. Bowie et al. (2013) observed that both *Ptilopachus* and *F. nahani* share small size, bare red skin around the eye, lack tarsal spurs, and are not sexually dimorphic. Both taxa regularly cock their tails in the manner of a bantam hen. This was confirmed for *F. nahani* by Cohen et al. (2012) with photographs of wild birds. The calls of both taxa consist of a series of whistles which

suggest the calls of New World quail rather than typical francolins or spurfowl. Sande et al. (2009) provide additional field observations on the elusive and endangered Nahan’s Francolin.

Cohen et al. (2012) also provided sonograms of the calls of *Ptilopachus* and *F. nahani*. The syringeal structure and vocalizations of francolins were studied by Mandiwana-Neudani et al. (2011, 2014). The results of the first study showed differences between the two groups of francolins. The second was more ingenious in that the authors demonstrated that the sonograms of francolin advertising calls could be broken down into individual units (called strophes) and then analyzed cladistically. Although the number of resulting characters was small (n=9), the results separated the two francolin groups but were ambiguous in determining statistically significant groups of species.

The results are contrary to the generally perceived notion that bird vocalizations are dependent upon ecology (Morton, 1975), or are species-specific, and hence are unlikely indicators of relationship. There is, on the other hand, a great deal of information in a sonogram, and these data suggest that some of this information may be relevant for taxonomy.

Bowie et al. (2013) concluded that the Rock Partridge and Nahan’s Francolin are similar enough to warrant their placement into a single genus, *Ptilopachus*, and as a subfamily Ptilopachinae within the Odontophoridae. Furthermore, the dispersion of the ancestor to the New World quail likely was via a North Atlantic land bridge, as has been shown for various plants (Tiffney, 1985; Milne, 2006). This biogeographic scenario was challenged by Hosner et al. (2016) who favored a Bering Land Bridge route. The differences in the conclusions rest on the allocation of the fossils and the secular dates utilized. Given the vagaries presented by both, we favor the North Atlantic connection simply because it is shorter.

We emphasize that the conclusions regarding *Ptilopachus* derive not solely on the DNA evidence, but on the congruence of several lines of data including external morphology, behavior, and vocalizations.

Crowe et al. (2006a, p. 521) made two important conclusions regarding the use of molecular data:

It is phylogenetically more sensible to analyze all character data partitions in combination rather than use a divisive “process”—partition approach as the different partitions in combination complement one another. Discarding [morphological behavioral] and non-coding molecular characters results in massive losses of phylogenetic resolution and nodal support, particularly at deeper nodes within Galliformes.

Unresolved Relationships

As of this writing, the DNAs of *all* landfowl genera listed by Gill and Donsker (2016) or recognized since 1990 have been sequenced to a greater or lesser extent. The results have been

gratifying, as reasonable, robust hypotheses of relationships have been proposed. Also satisfying is that these relationships are not in conflict with a reconsideration of traditional characters of anatomy, behavior, vocalizations, or ecology. In no small measure such congruence has been due to the efforts of the investigators who have been aware of the biology of the landfowl as well as the analyses of the molecular data themselves.

Despite the amount of data that have accumulated regarding landfowl, relationships of several “problem” genera remain. Of typical pheasants, the Koklass (*Pucrasia macrolopha*) and Blood Pheasant (*Ithaginis cruentus*) have been difficult to place consistently. Traditionally both have been thought to fall within the *Tragopan-Lophophorus* cluster of pheasants.

On the basis of molecular data *Pucrasia* most often appears basal to the grouse-turkey assemblage, or basal to the main pheasant group. *Ithaginis* appears to be an outlier to pheasants with no close relatives. While neither of these findings is unacceptable—the *Pucrasia*-grouse-turkey group is, in fact, appealing—we feel that more data are needed to have a high degree of confidence in existing results.

Biogeography

In a Genesis Flood scenario biogeographical dispersal is aided by having a *locus a quo*, a place of origin, namely disembarking from the Ark on or near Mount Ararat.

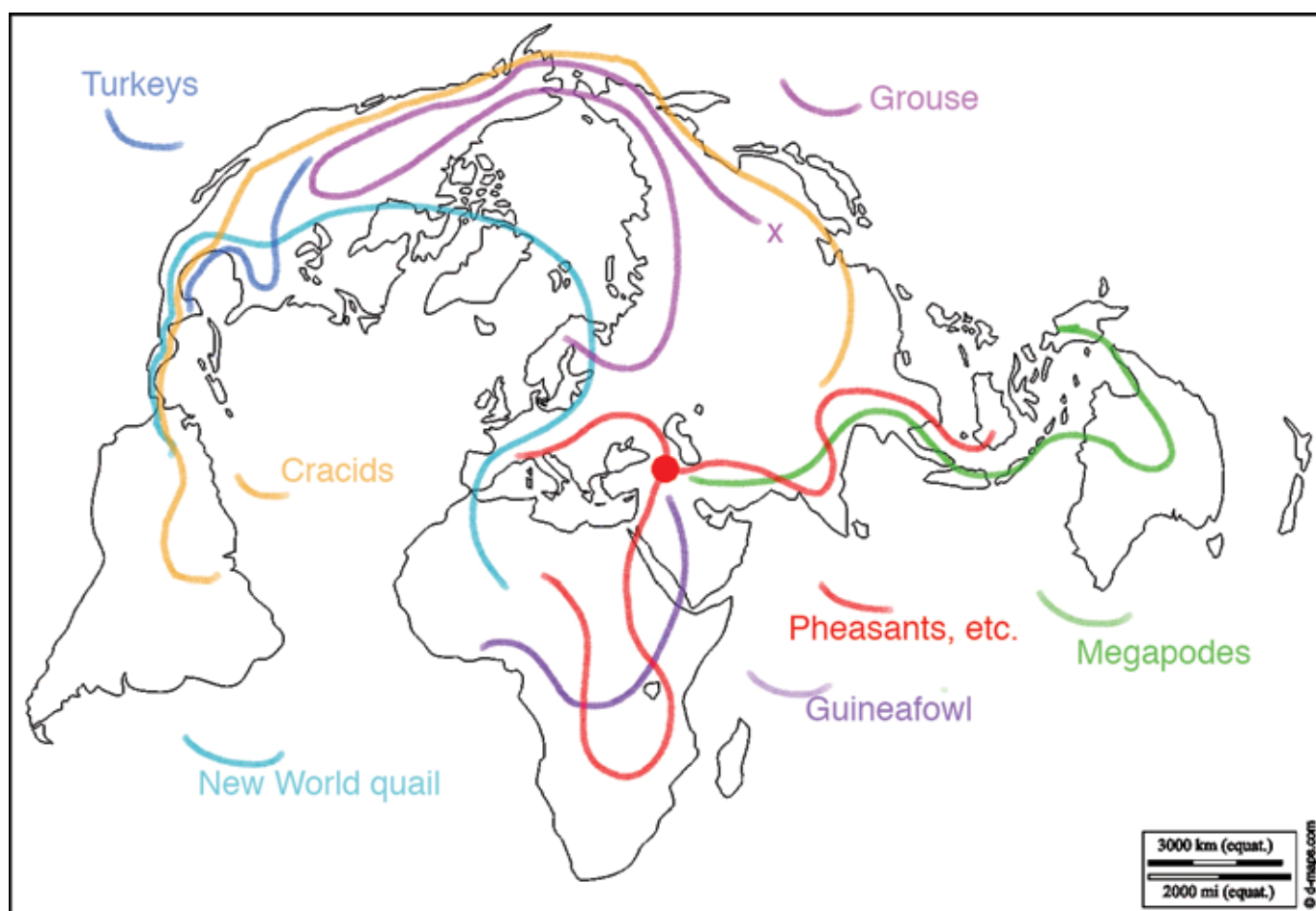


Figure 2. A diagram depicting major landfowl dispersal after leaving the Ark. The megapodes (green) dispersed toward Australasia; the cracids (brown) colonized the New World, probably from Asia. A radiation of guineafowl (deep blue) took place in Africa. It appears New World quail (light blue) colonized the New World from an ancestor in Africa, likely entering via a different route than used by the cracids. The pheasants (red) radiated throughout the old world (Europe, Africa, and Asia); not shown is the grouse invasion of the New World, from which the turkeys may have developed. Map used courtesy d-maps with data added by JA.

On all grounds an Old World origin and primary radiation of the landfowl kind is justified. Following that approach, the principal dispersals are given below in probable chronological sequence (Figure 2).

1. The megapodes represent the first dispersal to the Australo-Papuan region, probably via land bridges from Asia and thence to outlying islands. Although megapodes are seemingly sedentary, they have proven to be good colonizers of islands, and even partly-grown young birds have been observed flying at sea many miles from land.
2. The Cracidae next colonized the New World from Asia, presumably via a Bering Land Bridge, and became centered in Central and tropical South America. Since living cracids are sensitive to cold temperatures an alternative, but less probable, hypothesis involves colonization directly across the Pacific by rafting.
3. A small but distinct radiation of the Numididae (guinea fowl) took place in Africa. There are no geographical problems for these birds colonizing Africa from Asia.
4. The Odontophorinae form a second invasion of the New World. If a relationship to the African Rock Partridge (*Ptilopachus*) is maintained, then the most parsimonious route of colonization would be from the Old World via a North Atlantic land bridge. Such has not been invoked for birds, but is well known for plants (Tiffney, 1985; Milne, 2006) in the early Tertiary (post-Flood).
5. The grouse are clearly a boreal component of the pheasants and an offshoot therefrom. Based on present-day distributions, their dispersion to the North America is easily accounted for via the Bering Land Bridge. Given the probable close relationship of grouse and turkeys, a diversification of the latter in the New World is likely. Ancillary evidence for this scenario is that of the 20 species of grouse (recognized by Potapov and Sale, 2013), two are Holarctic in distribution, seven are Palearctic, and eleven are found in the New World.

Lucchini et al., (2001, p. 157) examined the probable geographical origin of grouse using mtDNA sequence data with a parsimony analysis of possible colonizing events:

Use of DIVA with the phylogeny showing *Lagopus* linked to the *Tympanuchus*–*Centrocerus*–*Dendragapus* clade ... the distribution of each species classified as present/absent in four different areas, and the assumption that ancestral stocks were limited to, at maximum, two areas, showed that the most optimal reconstruction required 18 dispersals ... The ancestral area of the grouse was inferred to be the western part of the Nearctic ... According to the most optimal scenario, the grouse have dispersed out of the Nearctic on at least three occasions: in the ancestors to the Palearctic *Bonasa*, in the ancestors to the circumpolar *Lagopus mutus*/*L. lagopus*, and in the clade leading to *Tetrao*/*Falci pennis*. However, it

is equally parsimonious to assume that ancestors of *Tetrao* have dispersed independently into the Palearctic and that speciation in *Falci pennis* is the result of a vicariance event when the rise of the Bering Sea split a previously continuous ancestral *Falci pennis* stock into two reproductively isolated populations.

This hypothesis is reasonable. Of typical phasianids the widespread Ring-necked Pheasant (*Phasianus colchicus*) extends farthest north, being found north of Korea. It is, however, more of an open-country bird and shuns high mountainous forests. Of the truly montane pheasants the Koklass (*Pucrasia macrolopha*) and Brown Eared-pheasant (*Crossoptilon mantchuricum*) have the most northerly distributions, breeding in northeastern China. This does not preclude a former distribution (pre-Ice Age) into regions such as Beringia, but we lack conclusive data.

6. Given that the relationships among the large assemblage of pheasants, partridges, and Old World quail are imperfectly known, it is premature to attempt a fine geographical analysis of their radiation. We have noted above some aspects, namely the division of the francolins and affinities of the Congo Peacock.

Conclusions and Perspectives

The landfowl are defended as an unambiguous example of a Biblical kind (baramin). The congruence of morphological, biological, and genetic evidence permits the recognition of the main lineages within landfowl—megapodes, cracids, guinea fowl, New World quail, grouse plus turkeys, and a large assemblage of pheasants, partridges, and Old World quail—and probable pathways of their post-Flood colonization and diversification. Studies along several lines suggest sub-groups within the pheasant–Old World quail assemblage. It is premature to make definitive conclusions, but we have suggested several interim cognatum groups that are loosely upheld by biochemical as well as traditional data.

It may be at first perplexing that so many species of landfowl differing vastly in size, breeding habits, general ecology, and especially plumage diversity can be derived from a single pair of birds on the Ark. However, astounding diversity has been observed to arise within domesticated species, as well. Creationists recognize the importance of created diversity (Jeanson and Lisle, 2016) as well as designed mechanisms affecting genetic change (homologous recombination, gene conversion, transposable elements, etc.; briefly summarized and referenced in Lightner, 2016). While more random processes and natural selection may have played some role in shaping diversity, too, there is no question God created his creatures with the ability to reproduce and adapt, filling the world with an astounding array of diversity even within a created kind.

It would be informative to have contributions from a baraminological perspective on four aspects of using molecular sequences:

1. A discussion of the relative value of various types of molecular data: mtDNA, various nuclear DNA sequences, UCEs, retroposons, etc.
2. A primer on the methods of data analysis giving the rationale, practice, and meaning of each for systematics. Such a study would explain to the nonspecialist how such manipulations are *not* a matter of tossing sequences into a mythical black box and having “truth” emerge.
3. Given that nearly all secular methods of DNA sequence analysis involve some evolutionary assumptions, the enterprising baraminologist could adapt existing protocols or write his own programs without evolutionary anlagen. This would require not much more than mathematical talent, the ability to write code, and a computer. Data in the form of DNA sequences abound and are accessible. The participant need not learn cloning, reading a sequencing gel, nor engage in forming his own biochemical laboratory.
4. Perhaps the most exciting prospect is that of proteomes. Here, all protein-coding genes are utilized and the data may be analyzed using statistical methods of baraminology, thus eliminating evolutionary assumptions and biases. Lightner and Cserhati (2019, p. 137) have compared the proteomes of humans plus Neanderthals and Denisovans and found them to be distinct from all other primate groups:

This supports the humanity of Neanderthals and Denisovans, as much as it contradicts evolutionary narratives about common descent between humans and apes. In conjunction with other lines of evidence of human morphological, cognitive, and genetic (including non-protein coding regions) distinctiveness, it clearly demonstrates that the evolutionary ideas on the origin of man have no plausible scientific foundation.

Cserhati and Ahlquist (2019) compared the proteomes of a number of the nightjars (avian order Caprimulgiformes) and found evidence for paraphyly if not polyphyly. Among several possible baramins suggested by the authors, the most intriguing supports a baramin consisting of swifts, hummingbirds, and the New Guinea family of owl-nightjars (Caprimulgiformes: Aegothelidae). Once one compares the skulls of Aegothelidae with a typical swift, the similarities become apparent.

Acknowledgments

This work was funded by the Creation Research Society's eKINDS research initiative.

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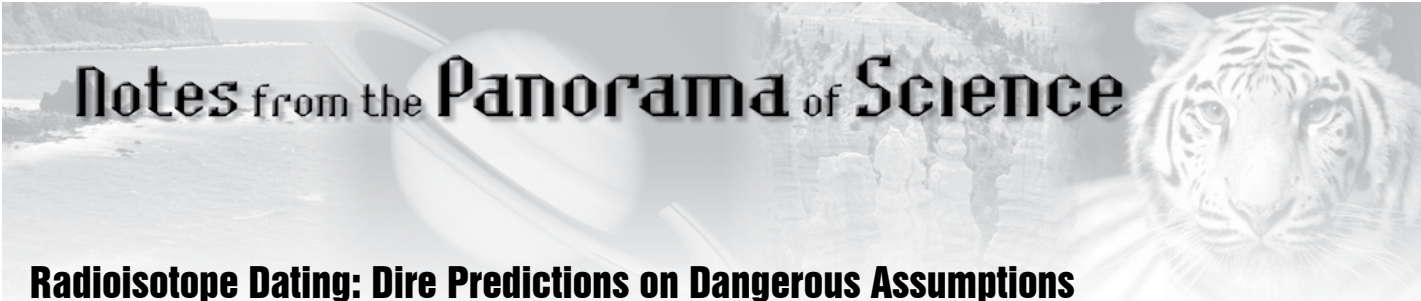
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Notes from the Panorama of Science

Radioisotope Dating: Dire Predictions on Dangerous Assumptions

Earth's surface was drastically altered by a global cataclysm in the recent past—one that was recorded in the sixth to ninth chapters of Genesis. Artifacts from the Genesis Flood are readily seen across Earth's surface, testifying to the ramifications of such a widespread disturbance in geologic history. Though an understanding of the Genesis Flood comprised the basis for early geologic thought, eighteenth-century geologists abandoned Genesis in favor of the assumption that geologic processes occurred gradually without any supernatural intervention (naturalism). Based merely on a predisposed dismissal of Biblical history, this paradigm shift led to a radically distinct geology. What was first viewed as evidence of past catastrophism was re-envisioned as the product of gradual geologic processes over untold eons.

Since the eighteenth century, naturalistic geologists have attempted to quantify this vast chasm of 'deep time,' but no numerical method was found adequate until radioisotope dating schemes were introduced in the mid-twentieth century. Over the succeeding decades, radioisotope dating has bolstered the deep-time geologic paradigm and evolutionary naturalism. Notwithstanding the use of radioisotope dating, a return to the

understanding of the Genesis Flood and its implications for interpreting geologic history has led to a growing awareness of the flaws plaguing radiometric dating. The assumptions undergirding radioisotope dating methods have repeatedly produced faulty results in the present, casting doubt on the extrapolation of radiometric schemes into the unobserved past. Diluvial geologists and others have often revealed these flawed presuppositions, but world-renowned naturalistic geologists have recently admitted to the assumptions inherent in radioisotope dating.

Admission of Assumptions

Dr. Gunter Faure has been the premier educator on radioisotope geochronometry for several decades through his volume *Principles of Isotope Geology*. In a more recent coauthored graduate textbook *Isotopes: Principles and Applications*, Faure and Mensing (2009, p. 57) state that:

"The interpretation of this date [received through radioisotope methods] depends on certain assumptions about the geologic history of the rock or mineral being dated... The assumptions are as follows:

1. The rock or mineral sample being dated has not gained or lost parent or daughter atoms except by decay of the parent to the stable daughter.
2. The decay constant of the parent nuclide is independent of time and is not affected by the physical conditions to which the nuclide may have been subjected and its value is known accurately.

3. An appropriate value of [the quantity of daughter atoms before radioisotopic decay] is used in the calculation based on either knowledge of the chemical properties of the daughter element or its isotope composition in the terrestrial reservoir from which the rock or mineral originated.
4. The measured values of D and N are accurate and representative of the rock or minerals being dated." (Brackets mine).

Because of these assumptions, geologists rarely date sedimentary rocks. Clastic sediments, such as sandstone or conglomerate, can be highly weathered and likely leached before being deposited, and any dating of the rock would determine only the age of the clast rather than the deposit as a whole. Instead, igneous and metamorphic rocks are most commonly dated due to the assumption that the original concentration of radiogenic elements can be known based on the geologic conditions, such as that heat and hydrothermal fluids released or dissolved the daughter elements from the host rock to leave only parent material present to create daughter atoms (for a review of the specific assumptions associated with each methodology, see Dicken, 2005; Faure and Mensing, 2009; and references therein).

The Assumptions Exposed

As in all pursuits for knowledge, science must necessarily rest upon certain assumptions, such as the fixation of physical laws except when superseded by supernatural intervention. In order to gain credence, these assumptions

Key Words: Radiometric Dating, Potassium-Argon, Mount St. Helens, Grand Canyon, Helium Diffusion, Polonium Radiohalos, Accelerated Radioactive Decay.

must be internally consistent and not have been falsified, but what if these assumptions are at best naïve and at worst patently false?

The foundational presupposition ungirding radiometric dating is that any daughter atoms present in a sample were produced solely by steady radioisotopic decay of the parent element, but research of historically cooled lavas reveals a different story. The potassium-argon method is based on the supposition that argon, being inert and incapable of bonding to the crystal lattice, is expelled from the cooling lava, but Dalrymple and Moore (1968) and Dalrymple (1969) documented a number of historical lava flows that retained “excess Argon” rather than releasing the argon with the volatiles, resulting in erroneous old age calculations for the flow.

This example of the radiometric clock not being set to zero has been demonstrated to plague a variety of methods, but the initial presence of non-radiogenic daughter elements is not the only problem. Whether buried or exposed at the surface, rocks are susceptible to water seepage slowly transferring elements both out of and into the specimen. Some elements used in radiometric dating are particularly susceptible to leaching (Snelling, 2009, p. 830), which can either make the specimen appear older or younger based on the relative increase or decrease in parent and daughter atoms.

Some decay rates have also been observed to change based on the environment. For example, the decay rates of silicon-32, radium-226, and others have been found to oscillate as much as 0.3% throughout the seasons, possibly due to Earth’s varying distance from the sun (Castelvecchi, 2008). Such a minor fluctuation pales in comparison to certain extreme conditions that have experimentally accelerated the decay rate a *billion*-fold above the assumed half-life (see Cupps, 2014, and references therein). To overcome these

variables, a complete understanding of a rock’s geologic history must be known, which would furthermore require assumptions on the age and the geologic environment. Without constancy, age determination of rocks cannot be made with certainty.

Errors and Contradictions: The Last Straw

If radiometric dating methods were based on correct assumptions, one must suppose that the true age of rocks could be determined no matter which method was used, yet studies have indicated that this is not the case (Austin and Snelling, 1998; Froede, 2010). A classic example of “isotopic discordance,” as it is called, compares the age of the titled Cardenas Basalt (Grand Canyon Supergroup) incised by Grand Canyon[?] to lavas at the Grand Canyon rim (Austin, 1994; Snelling, 2004). Not only did different methods yield different ages, but one method even suggested that the Cardenas Basalt is younger than the lavas on the rim of the Grand Canyon despite the Cardenas Basalt being logically older than Grand Canyon and thus the lavas on the canyon’s rim. Similarly, geologist Steve Austin found that the dacite lava dome at Mount St. Helens dated between 0.35 ± 0.05 to 2.8 ± 0.6 Ma (Austin, 1996), all at a time when the specimen itself was no more than a decade old!

Other contradictions arise from studying how radionuclides alter their environment, such as radiohalos. These structures form as the repeated release of radiogenic alpha particles damages the surrounding crystal lattice (Snelling, 2005). Such deformation leaves structural ‘fingerprints’ such as the thickness of concentric rings characteristic of the responsible radioisotope (such as uranium-238) and estimate elapsed time. For instance, a mature uranium-238 radiohalo requires 500 million decays, thus suggesting 100 million years elapsed (Gentry, 1988, p.

19). However, uranium-238 radiohalos are often accompanied by nearby radiohalos formed by short lived polonium isotopes that lack an apparent source. This indicates that enough polonium had to be transported from the uranium-238 centers within a matter of days in order to produce polonium radiohalos independent of the uranium-238 radiohalos, which requires heightened uranium-238 decay to generate the polonium isotopes within a short time span (Snelling, 2005, 2008).

Another anomalous by-product of uranium-238 decay is the alpha particles themselves. Comprised of two protons and two neutrons, alpha particles become chemically inert helium nuclei that easily diffuse through the surrounding crystal lattice at a predictable rate. Geothermal gradient profiles of the Precambrian granite of Fenton Hill, New Mexico, show the helium generated from the alleged 1.5 Ga of uranium-238 decay would diffuse from the host zircon crystals within 100 Ma, yet Humphreys (2005) found helium levels nearly 60% of the total helium levels generated from 1.5 Ga of uranium-238 decay. As corroborated through later studies (Humphreys, 2010, 2011), billions of years’ worth of radioisotope decay appears to have occurred within thousands of years. While some have challenged whether this is supportive of accelerated radioisotope decay (Froede and Akridge, 2012), the fact remains that two independent chronometers provide wildly different ages, challenging the very notion of radiometric dating.

Based upon faulty assumptions, radiometric dating has routinely led to faulty geochronologic and chronostratigraphic models, as has been noted in Southwest Washington (Isaacs, 2020b). Mount St. Helens overlies a truncated fold system of volcanogenic strata transected by a myriad of primarily Miocene to Holocene intrusions, which have been used by secular geologists to date the folding of Tertiary bedrock from

20 to 15 Ma. Evarts et al. (1987) suggested that folding had largely ceased by 15 Ma because some intrusions, such as two dikes southeast of Mount St. Helens dated at 12 and 8 Ma, retain an undeformed posture, indicating the dikes postdate regional folding. However, later study by Evarts and Ashley (1993) determined that these two dikes were instead up to 12 Ma *older* than regional folding, yet the researchers did not explain why these dikes were undeformed despite predating regional foreshortening. Similarly, the folding of the Tertiary bedrock in Washington and Oregon during the Cascade Orogeny has been dated as either 20 to 15 Ma or 4 Ma based on chronostratigraphy and radiometric dating (Isaacs, 2020b). Rather than providing a better glimpse into geologic history, radiometric dating muddles geologic interpretation (for an example, see Isaacs, 2020a).

Conclusions

Ever since their *a priori* dismissal of Biblical geologic history, secular geologists have been grasping at ways to quantify deep time, with each attempt being greeted in triumph only to be later overturned. Though touted as a definitive means to define geologic history, radioisotope dating is yet another example of an errant geochronometry device allegedly disproving the Biblical account. Leading radioisotope geologist Dr. Gunter Faure explored the assumptions underlying radiometric dating in his coauthored volume *Isotopes: Principles and Applications* (Faure and Mensing, 2009) but ignored the overwhelming challenges to those assumptions. Not only does the radiometric clock fail to be set to zero or remain uncontaminated, but the decay “constant” may not be constant at all! Its basis on flawed assumptions results in radioisotope dating muddling geologic interpretation rather than enhancing it, resulting in numerous examples of enigmatic or even contradictory chronostratigraphy. Rather

than challenging Biblical geologic history, radioisotope dating is yet another failed attempt to exclude Biblical revelation from geoscience.

Edward A. Isaacs

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Letters to the Editor

The policy of the editorial staff of CRSQ is to allow letters to the editor to express a variety of views. As such, the content of all letters is solely the opinion of the author, and does not necessarily reflect the opinion of the CRSQ editorial staff or the Creation Research Society.

Discrediting Evolution

I just received the latest issue of the CRSQ (Spring 2021). Along with other criticisms of Dr. Jerry Bergman in this issue (letters to the editor), I could hardly believe what Robert Hill and the HEAD of Bob Jones University biology had to say, concerning Bergman's responses to Hill's original article titled, The CRS Mission is Model Building (Hill, *Creation Matters* 22(1):5).

The Lord Himself, as far as I know, never hesitated to confront heresy with TRUTH.

It is necessary, and proper, for creation scientists/engineers to have

a great focus, even a central focus, on DISCREDITING the FALSE scientific claims of evolutionists until vertical evolution over billions of years is no longer taught in the public schools as a scientific fact or viable theory.

This would especially include the periodic copying and republishing of great scientific articles of the past that thoroughly discredit vertical evolution over billions of years, for example, the late Dr. Duane Gish's excellent article in ICR's *Impact* publication, January 2007: "A Few Reasons an Evolutionary Origin of Life Is Impossible."

Lastly, the periodic republishing of the many excellent Morris/Gish debates with evolutionists would be very helpful.

Dr. Bergman should not compromise with his critics. He is RIGHT and, sadly, some or many of his critics may know that.

Sincerely in our Lord Jesus Christ,
 David A. Danello
 VA Tech community
 Blacksburg, VA

Comment: Exegesis and Geological Notes on Genesis, Chapter 7 by Johnson and Clarey

I am happy to see the article in the Spring 2021 issue of the *CRSQ* by Johnson and Clarey (2021) on the exegesis and geological notes on Genesis, Chapter 7. As Flood geologists we need to know what Genesis 6 to 9 says in the Hebrew and the geological implications. Exegeting Genesis 7 is difficult, and I appreciate that Johnson and Clarey consider the article *preliminary*.

With that reminder, I have several comments to make. It is interesting that the heavy rain started immediately at the beginning of the Flood, likely as a result of the action of two Biblical mechanisms: the bursting of all the fountains of the great deep and the opening of the windows of heaven. So, whatever the bursting of fountains of the great deep and the opening windows of heaven were exactly, the result of their activity was an immediate and lasting heavy rain. My question is: Are the proposed physical mechanisms able to do this?

I noticed that Johnson and Clarey (2021, p. 252) theorize that the “fountains of the great deep” were worldwide volcanic eruptions: “This cataclysmic change, which soon convulsed Earth globally, began with catastrophic volcanism.” They propose this volcanism would produce water vapor, possible from the dehydration of wadsleyite and ringwoodite from the mantle transition zone, and also produce cloud condensation nuclei needed for rain. Although the amount of water vapor produced by volcanism is uncertain, it makes sense that there would be a fair amount from worldwide volcanism. There certainly is much evidence of volcanism during the Flood. Volcanic eruptions as the fountains of the great deep may be a problem for the Hydroplate and the Catastrophic Plate Tectonics models that rely upon the jetting upward of water from mid-ocean ridges.

Johnson and Clarey (2021, p. 253) go on to suggest that the breaking open of the fountains of the great deep likely caused great rifting of the continental crust:

There is a lot of geological evidence for the simultaneous development of multiple rift zones across the globe, including several along the edges of North America and possibly[?] the Midcontinental Rift in the continental interior (Reed, 2000; Clarey, 2020, pp. 182–186).

It follows that the tremendously catastrophic mechanism of the early Flood would have caused rifting, volcanism, tectonics, erosion and sedimentation, and eventually developed very strong currents accompanied by powerful turbulence. If all the rifting were pre-Flood, a catastrophe this powerful would likely wipe out all the living creatures on the Earth.

I also noticed that Johnson and Clarey (2021) did not give a precise meaning of the “*opening* of the windows of heaven” and the possible meanings of the phrase, but they assume that these verses refer to heavy rain. However, Genesis 7:11 (ESV and NASB) mentions the two mechanisms followed by a *period*. Verse 12a then says “And rain fell upon the earth forty days and forty nights...” It would appear from this Hebrew rendering, rain was the *result* of the two mechanisms, so that the second mechanism, the “opening of the windows of heaven,” does not necessarily mean the rain. That leaves open other possibilities, such as asteroid impacts, which I noticed in the long quote from Cooper (2009) where he thought asteroid bombardment was a possibility.

Johnson and Clarey (2021) also believe that the mantle could have been up to 300 °C hotter, which was one of the initial conditions used in

Baumgardner’s (1986) early analysis of runaway subduction. This would, of course, make the upper mantle and crust unstable, and I have always thought that this initial condition, which would greatly aid runaway subduction, was incorrect because God would have created a ticking timebomb. It appears to me to be an ad hoc initial condition. I am happy to discover that Baumgardner (2021) has given up on this mantle warmth as an initial condition and so should Johnson and Clarey (2021). The initially hot upper mantle in Baumgardner (1986) shows how crucial initial conditions can be in producing desired results.

Johnson and Clarey (2021) plot relative sea-level curves during the Flood in Figures 1 and 2, which they propose are what would be expected during the six megasequences. However, the relative level of the Floodwater is unknown and the megasequences could just as well be caused *more directly* by waxing and waning current velocity.

In Figure 2, Johnson and Clarey (2021, p. 260) correlate the Paleozoic and Mesozoic with the first 150 days of the Flood. I do not think the correlations between the geological column, the six megasequences, and the days in Genesis 6–9 are correct. First, the beginning of the Flood is put in the upper Precambrian, probably at the base of the Sixtymile Formation in Grand Canyon, just below the Tapeats Sandstone, which was suggested by Austin and Wise (1994). This is related to the issue of the location of the pre-Flood/Flood boundary, which is still being debated among Flood geologists. Johnson and Clarey (2021) did suggest earlier that the boundary could be in the Mesoproterozoic because of all the rifting. I suggest that the boundary is at least below the Mesoproterozoic because of the quantity of continental crustal rifting and from my study of the Meso-

proterozoic Belt Supergroup in western Montana, northern and central Idaho, northeast Washington, and adjacent Canada. The contact between the Belt Supergroup and the Cambrian Flathead Sandstone, correlative with the Tapeats Sandstone, the bottom horizontal layer in the Grand Canyon, is mostly conformable. There is around one billion years of uniformitarian time missing at the contact. One would expect that if the Belt Supergroup were pre-Flood, and the Flathead Sandstone deposited in a few days during the beginning of the Flood, all contacts would be highly unconformable.

Second, Figure 2 in Johnson and Clarey (2021, p. 260) has the Cambrian sediments deposited a few days after the beginning of the Flood with most of the Paleozoic within the first 40 days. I do not believe this is correct for the following reasons. First, time is needed early in the Flood to create the widespread Great Unconformity, a planation surface that is sometimes rolling with a few monadnocks, on all the continents from the early Flood catastrophism. The very early Flood mechanism(s) would be too catastrophic for deposition that soon, especially when the spectacular view of the Paleozoic sediments in Grand Canyon and Mesozoic sediments in the Grand Staircase to the north show very little deformation from faulting during deposition. Great faulting would be expected very early in the Flood, while the deposition of the 1,300 m of horizontal Grand Canyon sediments and 3,000 m of the Grand Staircase sediments, projected over the top of the Grand Canyon area, must have been laid down in lower-energy water. Faulting and erosion of course did occur after deposition during the Recessional Stage of the Flood. In Oard and Reed (2017), we placed

sedimentation during the first 40 days mostly in the deep rifts and basins, where currents would be slower, forming the Precambrian sedimentary rocks. Then the more than 4,000 m of deposition in the Grand Canyon area with little deformation we placed between Days 40 and 150 when the water “prevailed” and called it the *Great Deposition*.

Third, in Figure 2 of Johnson and Clarey (2021, p. 260), Day 150 is placed in the Late Cretaceous. However, there are dinosaur tracks, eggs, and scavenged bonebeds in the very Late Cretaceous (Oard, 2011), which often were covered by hundreds of meters of sediment that was later eroded during the Recessional Stage. Thus, the peak of the Flood must be after the Late Cretaceous. I have previously shown that the Paleogene and Neogene are diachronous within the Flood, depending upon the particular region of the Earth (Oard, 2001, pp. 89–90). Because of massive erosion of valley fill sediments in the basins of the Rocky Mountains, best placed in the Recessional Stage of the Flood, the remaining Paleogene, and even Neogene sediments, from the Rocky Mountain valleys and high plains would be before Day 150. This deduction is reinforced by rather rare mammal and bird tracks of live animals in the Paleogene and Neogene, which would better be placed in the early Flood.

Michael J. Oard

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Reply to Mike Oard

We would like to thank Mike Oard for reading and responding to our recent article in *CRSQ* (Johnson and Clarey, 2021). However, we would like to address a few topics Oard brought up, and to clarify a few misconceptions in the process. Overall, I think we agree more than we disagree. That said, one of the things we disagree on is the mechanism God used for the Flood. We accept Catastrophic Plate Tectonics as the best mechanism because it is supported by the most geologic data. Oard does not. This is reflected in his letter. We will address some of his specific topics in the same order as his letter.

First, at the end of his sixth paragraph, Oard mistakenly injects something we never said in our article. We never claimed the rifts that opened up across the globe on Day 1 of the Flood were pre-Flood. These were definitely part of the Flood and are tied directly to Genesis 7:11. These rifts originated prior to the Sauk megasequence and the flooding of the continental margins that came a bit later. There is clear evidence of this in the rocks and their relative ages are clearly discernable also. For example, the Midcontinent Rift in the Great Lakes region exhibits tremendous volumes of lava flows and localized sedimentary deposition in and near the rift. Lying directly on top of these earliest Flood volcanic and sedimentary units is the basal Sauk sandstone of the Munising Formation in the Upper Peninsula of Michigan. This demonstrates that the Sauk megasequence strata were deposited on top of the rift system that had originated earlier in the Flood. The Sauk deposition merely occurred later, possibly after a week or more of the rift opening. But they are both part of the Flood.

Secondly, a few paragraphs later Oard claims that we theorized the mantle was up to 300 °F (he actually wrote 300 °C by mistake) hotter at the onset of the Flood. And he went on to say John Baumgardner has since lowered the temperature of his initial conditions in his runaway subduction models. Oard then suggested we drop this higher temperature condition also. However, the 300 °F hotter mantle we claim for the onset of the Flood is based on real rock data, not speculation. In 2013, cores from the Atlantic Ocean crust were studied, finding a systematic change in chemistry from the continental margins to the deeper ocean. The chemistry differences were best explained by temperature. The authors of the study suggested that the mantle source for the ocean crust was up to 300 °F hotter initially, and cooled with time. This was in our article (Johnson and Clarey, 2021, p. 253).

In the next paragraph, Oard expressed concern about our Figures 1 and 2 (Johnson and Clarey, 2021, pp. 252 and 260). These figures show our suggested diagrammatic sea-level curve during the Flood. Oard said, “However, the relative level of the Floodwater is unknown and the megasequences could just as well be caused *more directly* by waxing and waning current velocity [*italics in original*].” I wholeheartedly disagree with this statement. In fact, we can infer the relative extent of the Floodwaters from the sedimentary rocks that are still there today (Clarey and Werner, 2017; Clarey, 2019, 2020). The maps we have created for each of the megasequences across multiple continents and the thicknesses in our Table 1 (Johnson and Clarey, 2021, p. 255) clearly show a progressive Flood. This is what we drew as a diagrammatic sea-level curve. It is

directly tied to the actual rock data in place. Admittedly, it is diagrammatic and is not supposed to be exact. It is merely to show the progressive trend. But that trend is data-based.

In the final two paragraphs, Oard again disagrees with our interpretation that most of the Early Paleozoic (the earliest three megasequences) was deposited in the first 40 Days of the Flood. Surprisingly, Oard argues that there isn’t enough *time* to deposit all of the first three megasequences in a mere 40 days or so. This is normally the uniformitarian argument used against creationists. We totally disagree. Forty days is plenty of time to deposit the first three megasequences, especially considering the unique, catastrophic conditions of the Flood. And the fact that the first three megasequences are the thinnest and exhibit the least extent of all the megasequences (Clarey and Werner, 2017; Johnson and Clarey, 2021, Table 1). Furthermore, the first three megasequences contain almost exclusively marine fossils. As we pointed out in our article, the Ark did not begin to float until after Day 40 (Johnson and Clarey, 2021, p. 256). Therefore, by Day 40 of the Flood, land would have had to have begun to be inundated and this is reflected in the fossil record. It is not until the Absaroka megasequence (megasequence number 4), beginning in the Upper Carboniferous, that we see massive volumes of coal from plants and trees that were ripped off the coastal regions and buried in Flood rocks (Clarey, 2015). And prolific numbers of land animal fossils also first show up at the onset of the Absaroka megasequence. We do not believe these observations are mere coincidence, but evidence of a rising, progressive Flood. These are some of

the reasons we interpret the first 40 Days of the Flood as the interval when the Early Paleozoic sediments (through the Lower Carboniferous) were deposited. It is data-based.

Towards the end of his letter, Oard discusses some of his previous hypotheses on Grand Canyon and Grand Staircase sedimentation. Unfortunately, he does what most secular and most creation geologists have done in the past, and that is to project the same thicknesses of rock strata great distances from place to place. He argues the entire 1300 m-Paleozoic section in Grand Canyon can be projected north beneath the rocks of Grand Staircase. Similarly, he projects the entire 3000 m of mostly-Mesozoic section in Grand Staircase south, claiming it once completely covered Grand Canyon, giving over 4000 m of total strata at Grand Canyon prior to much of its removal during the receding phase. However, this is in error.

The projection of 1300 m of Paleozoic Grand Canyon strata underneath Grand Staircase is disproven by examination of the rocks themselves. Oil wells and stratigraphic columns north and northeast of Grand Canyon show dramatic thinning of the Paleozoic section (Clarey, 2020, pp. 248–250). The 1300 m becomes just a few hundred meters in many places and is non-existent in others. Likewise, even though there are few Mesozoic rocks to observe south of Grand Canyon today, there are some local Triassic outcrops (Absaroka megasequence) between the South Rim and Flagstaff. These represent the entire extent of Grand Staircase rocks in existence today south of the canyon. It seems highly doubtful that the entire 3000 m of Grand Staircase strata were ever deposited on top of Grand Canyon rocks. Instead, it is likely only 1000 m or less of Mesozoic strata was deposited, or less than a third of what Oard and others have suggested. Admittedly, there is

little evidence to support this thickness estimate for the Mesozoic section as it is nearly all missing today, except for a few Triassic outcrops as noted above. Nonetheless, since the strata do show a dramatic thinning of the Paleozoic rocks of Grand Canyon to the north (based on oil wells and measured stratigraphic columns), it seems likely the Mesozoic section similarly thinned dramatically to the south. Stratigraphic thicknesses cannot be just arbitrarily projected for hundreds and hundreds of miles.

We would also like to point out that the earlier interpretation by Oard and Reed (2017), claiming the first 40 days of Flood sedimentation was all pre-Paleozoic (Precambrian) strata, conflicts with both the actual rock data and the fossil record (Clarey, 2020). Recall that the Bible says in Genesis 7:17 that the Ark began to float after Day 40. This tells us the dry land was being inundated at this point in the Flood. Therefore, if Oard and Reed (2017) were correct, that only Precambrian sediments were deposited in the first 40 days, there should be prolific coal beds and massive numbers of land-animal fossils within the overlying Early Paleozoic strata, indicating the flooding of the land. Yet, we find virtually no land-animal fossils and few extensive coal seams until reaching the Upper Carboniferous (Upper Paleozoic). Again, nearly all land-animal fossils and most coal beds first appear in Upper Paleozoic rocks and continue throughout the overlying strata as more land was progressively flooded between days 40 and 150 (Johnson and Clarey, 2021). The fossils tell the tale and match the Biblical account perfectly.

Finally, in the last paragraph of his letter, we do see the rationale for Oard's criticism. In our defense, these sea-level curves are highly 'diagrammatic' and the Flood days were superimposed on the curve after the fact. In the future we plan to revisit this diagram. It is possible

Day 150 should be a bit higher and the peak water level also. A better location may be near the base of the Tejas megasequence, in the Lower Paleogene section.

We appreciate this opportunity to reply to Mike Oard and to clarify our position. The geologic interpretations in our original article were based on the actual rock data compiled across three continents. We pray we are laying the framework for a new, data-based creation model to build on in the future.

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Thoughts on the Creation Model Controversy

It was with great interest and some degree of alarm that I read Jerry Bergman's timely well-reasoned letter "Thoughts on the Creation Model Controversy" (CRSQ 57(2):153), warning about the direction in which creationist dialog is moving, especially within the CRS.

I was first introduced to the Creation/Evolution debate over 40 years ago when I discovered the pioneering works of Whitcomb and Morris (*The Genesis Flood*), and Duane Gish (*Evolution: The Fossils Say No!*). I was so elated with the discovery of these books, for this was at a time when I was greatly distressed by the observation that the men in "black suits" (the clergy) were not teaching the same narrative as the men in "white smocks" (the scientists). The notion that the former dealt only with "matters of the heart" while the latter dealt with "matters of the head" made no sense to me, but I instinctively knew that in the real world, the latter was always assumed to trump the former.

I was first introduced to Bergman's prolific works when I read *The Criterion*, back in the 1980s. Now Bergman is making some astute observations that have seemingly become lost in the fray. I would like to elaborate on several of them:

Firstly, it must be recognized that at an elementary level, there are only two basic philosophical approaches to origin-of-life models—naturalistic, or super naturalistic. Therefore, if it can be shown that one of the two primary models is defunct, the other wins by default. I think this helps to explain why the Creation Movement grew by leaps and bounds during the years that "Creationist Bulldog" Duane Gish slugged it out with Darwinists in over 300 debates, often leaving them demoralized to such an extent that advisories were published against debating with creationists. Gish and other early creationists recognized the folly of the "Mr. Nice Guy" ap-

proach, an approach that will never be reciprocated by the Darwinists.

Secondly, why would anyone adhere to an "outdated" religious worldview, when it is just one among many other new and improved "scientific" options on the smorgasbord of ideas? Glitzy secular models which are presented as purely scientific, with no appeal to miracles, will always seem more attractive to the rational mind. With all the government funding, and the prestige of the entire educational establishment promoting Darwinism, how could the creation model ever hope to compete? This me-too approach can never work, for the Darwinists will always "out-glitz" anything the creationists present to the public eye.

These well-founded concerns have resulted in three letters of response to Bergman: Larry Rinehart (CRSQ 57(4):292), Robert Hill (CRSQ 57(4):293), and David W. Boyd, Jr. (CRSQ 57(4):295). Rinehart supports Bergman's thesis that an over-reliance on creation model-building fosters a slide into naturalism. It is axiomatic that any effort to present an attractive creation model in the marketplace of ideas must inevitably cause a drift into secularism. Any attempt to gain respect will lead to watering down the miraculous nature of 'the Creation Model,' but the end result is they will simply feed you to the crocodiles last. We must eventually learn to say with Rodney Dangerfield, "I can't get no respect," and move on.

The other two letters seem intent on obfuscating the issue. Hill's letter advances a straw man argument, best represented by his closing line: "I am uncertain why Dr. Bergman remains so insistent that model building is not a major part of the CRS mission or why it is not a necessary part of promoting creation." Bergman's letter never advocated for a single-pronged "evolution bashing" approach to the controversy. His position

is best summed up in his closing paragraph, "Both the Flood and the Ark are important topics that should be covered, but so should the rest of creation, **as well as the major problems with Darwinism in explaining creation,**" (emphasis added). Bergman advocates for a two-pronged approach, which is apparently being discouraged, and even censored in some venues. Bergman again: "...as the 2018 International Conference on Creationism illustrated, outright censorship against refutation of the claims of evolutionists exists in some quarters of the modern Creation Movement (Bergman, 2018)." This was the primary focus of Bergman's letter.

For Hill to claim that early creationists such as Duane Gish advocated for a single-pronged, model-building approach, is revisionism at its finest. The very title of the book, *Evolution: The Fossils STILL Say No!* (ICR, 1995) illustrates Gish's finely-honed skill in deconstructing evolutionary theories. Neither was he averse to poking fun at the Darwinists. On the flyleaf at the end of his book, we find this quote, "Now Evolution Is the Substance of Fossils Hoped For, The Evidence of Links Not Seen." So much for Gish's single-minded model building.

Boyd's letter also attacks the same single-prong straw man approach, with a laser beam (and mistaken) focus regarding Bergman's concerns: "...**instead of focusing solely on demoting evolution.**" (emphasis added). It boggles the mind that Bergman's letter could be misread to such a degree.

An unhealthy over-emphasis on model building can only end in disaster for the Creationist Movement. We must heed Bergman's warning and return to the two-prong approach of the early "Creationist Fathers." Off with the gloves!

Ivan Martin
Penn Yan, NY



July 23–24, 2021 • Glendale, AZ

On July 23–24, 2021, the Creation Research Society held its tenth conference on the campus of Arizona Christian University, Glendale, Arizona. There were nearly 150 registered, plus CRS staff. Great fellowship was enjoyed by all attendees, especially during the opening reception on the evening of July 22 at the new Van Andel Creation Research center on the ACU campus. Dr. D. Russell Humphreys delivered the Henry M. Morris Memorial Lecture the evening of July 23. His talk was entitled *Henry Morris and The Genesis Flood*. In addition, there was an optional field trip with 48 participants on July 25 to the South Rim of Grand Canyon led by Timothy Clarey.

The primary purpose of the meeting is to provide a venue where people can present preliminary research and gain valuable input from their peers. We hope that some of the research presented at these meetings will eventually be published in the *Creation Research Society Quarterly* as full papers. Since these are works in progress no attempt was made to record them. However, below are the abstracts from the 2021 meeting as submitted.

Cratering the Sevier Orogeny and the Grand Canyon: 40 days that changed geological processes forever

W. R. Barnhart

Farside moon craters and Mare Orientale form a model of energy envelope used to recognize crater patterns in gravity maps. The Sevier Orogeny within Plate Tectonics is credited with providing the shear thrust that shaped much of the western edge of North America. Yet, the energy envelope pattern suggests alternate sources of thrust in astral-impact cratering to form the continental margin. The cratering

model is expanded to show how the lithology, topography and tomography of the Mackenzie Mountains in Northwest Territory, Canada is better explained by a series of cratering events. The 40 days that the “windows of heaven” were open and “bursting forth the fountains of the deep” changed all geology forever. Seven of the days will be highlighted for which the geological record in the Grand Canyon is clear. 1. Tatanka crater laid-down the Unkar Group. 2. Alvord crater laid-down the Chuar Group. 3. Maka Luta crater laid-down the Tapeats Sandstone. 4. Grand crater laid down the Coconino Sandstone. 5. Blowout Mountain provided the thrust for the Kaibab Uplift. 6. Flagstaff crater initiated the

opening of the Canyon. 7. Small erosional craters eroded the Canyon as seen today. Cratering is responsible for the Grand Canyon's structure from the bottom to the top. Understanding Flood judgement (Psalm 82 and 29) and the cratering source for earth geomorphology gives Creation Geologists a new framework to understand post-Flood geology (crateringearth.com).

When the Flood Hit: Comparing Genesis 7 to Global Geological Data

Timothy L. Clarey and James J.S. Johnson

The Flood's catastrophic cataclysm was forewarned (and prepared) in Genesis Chapter 6. The Flood's continuance (from highwater climax at Day 150, followed by drainage) and aftermath are reported as narrative history (i.e., not "Hebrew poetry") in Chapters 8 and 9 of Genesis. This multidisciplinary research paper examines Genesis Chapter 7, which reports a critical timeframe during the global Flood. Many earlier attempts at matching the Biblical account to geological studies relied largely upon secular data sets and/or were limited in scope and geographic range. This study presents verse-by-verse expository commentary, with insights from the original Hebrew text (including observations regarding chronology and how the animal pairs boarded the Ark), with geological insights, gleaned from 1500+ newly compiled stratigraphic columns (relatively unrestricted by secular biases) across three continents. The stratigraphic column-based data give insight into water levels and flooding of the continents at key moments during the Flood, including Flood Days 1, 40, and 150. The overall analysis informs a geological data-based picture of the Genesis Flood, connecting sedimentary rock record to historical highlights in Genesis Chapter 7, with special attention to Flood Days 1, 40, and 150. The Flood initiated on Day 1 with the bursting of the fountains of the great deep. The Flood-water continued to rise thereafter until it reached the Ark on Day 40, causing it to float freely. Between days 40 and 150, the water progressively rose until it reached its zenith, covering the highest hills by 15 cubits, where Chapter 7 ends.

Analysis of Seafloor Features Revealed Earth Accreted Astronomical Mass

Kenneth Click

Our creation model will never be compelling until adequate cause, capable of producing catastrophic flood events resulting in earth geology, is identified. My research correlated:

non-parallel intersecting "stretch" marks in the Pacific, Hawaii's "Hot Spot" trail, magnetic reversals in the Atlantic, Necker Ridge, arc features surrounding the Pacific, movements of India, the Australian complex, Lesser Antilles and Sandwich Islands, Isostatic seafloor depths and continental incline ravines. Scripture, GoogleEarth, Earth tomography studies and prominent creation theories were resources. Key breakthroughs included: 1) realizing thick continental crust prevailed in antediluvian earth, 2) clues from Scripture indicated some major flood events were not recorded, 3) molten seafloor material flowed toward the center of the Pacific even as the Atlantic spread and 4) Necker Ridge was ejecta. The study identified massive accretion by earth as the only satisfactory explanation to account for seafloor features formation. This discovery provided answers to Flood mysteries: A "standing low high tide" protected Noah as 71% of earth's crust was either destroyed or forced into the mantle. Spreading accreted mass concentrated global flood water into 29% of earth's surface, tripling flood depth, as huge volumes of sediments scraped from the tops of diving plates were swept up and deposited over surviving continental crust. Constrictive forces caused orogeny by direct shock, base uplifting, tidal "pinching," gravitational sliding, area slumping and volcanism under extremely deep water. Heavier molten materials flowed under, lifted, separated, and transported continents and later isostatically sank seafloors.

Organelle DNA Lineages, a New Molecular Baraminology Tool

Matthew Cserhati

The genomes of cell organelles, i.e. plastids and mitochondria can be used in molecular baraminology analysis, despite their small size compared to the nuclear genome. Apparently, the genome length, the DNA sequence and the GC% of organelle genomes are all conserved within a kind. Besides a few translocations, the gene order of the mtDNA is also generally conserved.

I hereby present the Organelle DNA Lineages (ODL) software, written in R version 4.0.3, available at github.com/csmaty/odl. The user needs only to download a list of species names and accession numbers from the NCBI website to run it. The software downloads the gene annotation and mtDNA sequence from NCBI for each species, and does a pairwise comparison between all species pairs in the study. The software compares the gene order and organelle sequence similarity for each species pair, and creates two heatmaps displaying baraminic relationships based on two clustering schemes. These include clustering according to

gene order similarity and clustering according to mtDNA sequence similarity. The software also creates a genome map showing the gene order for each species, grouped according to clusters. These clusters correspond to putative baramins.

This software has been used to map the gene order of ten putative cephalopod species. These include Argonauta, Nautilus, Octopodidae, Sepiidae, and six squid baramins, depicted in the figure below. This software can be used in future molecular baraminology studies to study other groups of organisms.

Pinniped Molecular Baraminology

Matthew Cserhati and Emory Moynagh

Pinnipeds are a group of semi-aquatic animals which live on land, but hunt for food in the water. As such, they constitute an apobaramin, similar to bats, which are the only flying mammals. Differentiating between seals (Phocidae), sea lions, fur seals (Otariidae), and walruses (Odobenidae) is therefore an interesting task for baraminology. A morphology-based baraminology study showed discontinuity between phocids and all other pinnipeds. Hybridization results also show that many different phocid genera are capable of interbreeding.

Using a gamut of molecular baraminology tools, the mitochondrial DNA, whole genome sequences and proteomes of several dozen pinniped species was studied. The analysis of mtDNA sequence similarity shows that Phocidae, Otariidae and Odobenidae form their own holobaramins. The whole genome analysis shows discontinuity between Otariidae and Phocidae and also Odobenidae. However, discontinuity between Odobenidae and Phocidae is not so clear. Looking at differences in gene content shows discontinuity between Otariidae and the other two pinniped groups. Discontinuity also exists between Odobenidae and the majority of phocids, except for *Leptonychotes weddelli*. However, a closer examination of orthology groups unique to *L. weddelli*, *Odobenus rosmarus* and the outlier species, *Mustela erminea* show that *L. weddelli* shows continuity with phocids, whereas *O. rosmarus* shows discontinuity with this group.

Ultimately, the morphological evidence, hybridization data and the results from the molecular baraminology analyses support three separate pinniped holobaramins at the level of the family. There also appear to be several phocid lineages in the subfamily Monachinae, based on mtDNA analysis, such as *Lobodon*, *Mirounga*, and *Monachus*.

Quantum Biology and the Origin of Life

Mary Beth De Repentigny

Any naturalistic explanation of how life began needs a self-replicating molecule to initiate the evolution of living organisms. According to McFadden and Al-Khalili, two major researchers in the burgeoning field of quantum biology, any proto-replicator molecule in the primordial soup of the classical world would be stuck in one of the estimated 2^{64} possible molecular configurations that cannot replicate itself. However, a proto-replicator in the primordial soup of the quantum world could exist in all of these 2^{64} possible configurations simultaneously as a quantum superposition. Being able to continuously repeat the search for self-replication, a quantum proto-replicator would presumably have made the emergence of life more likely by providing an efficient search strategy to find the impossibly rare structure of a self-replicating molecule.

However, transferring the successful explanatory power of quantum mechanics to the problem of the origin of life breaches the bounds of science. McFadden and Al-Khalili have cast off the burden of evidence in this area and spun a narrative fallacy that the wider culture may readily accept. In response, creation scientists must emphasize that a proper scientific hypothesis should be consistent with the facts. This review shows that quantum biology as applied to the origin of life is fraught with technical roadblocks, making the idea nothing more than the wishful thinking of those looking to quantum mechanics to do the impossible task of creating life from non-living materials.

Origin of the Laws of Nature

Don DeYoung

The ultimate origin of the physical laws of nature are seldom discussed in science circles. Yet, the regularity of these laws is assumed and depended upon in every scientific endeavor. Some have attempted to explain a spontaneous origin for physical laws, and six approaches are described and shown to be deficient. In contrast, Biblical creation provides a refreshing and credible alternative to secular thinking. Several physical laws will be illustrated with audience participation.

Homo erectus: Human or Ape? The Answer May Lie With Ancient Tooth Proteins

Anne Habermehl

Creationists have flip-flopped on whether or not *Homo erectus* were human, going back at least as far as the 1960s. Clearly, this lack of agreement shows that the distinction between humans and apes has not been all that obvious. DNA testing to solve the debate has not been possible because, although scientists have recovered DNA from Neanderthals and Denisovans, they have none from *H. erectus*. Opinions on *H. erectus* have therefore been based largely on subjective evaluation of the fossils. This standoff on the status of *H. erectus* may soon end, however, because a new science called paleoproteomics (analysis of ancient proteins) is expected to shed light on the subject. Two years ago scientists announced that they were analyzing ancient proteins from tooth enamel; and because tooth enamel protein survives both warm climate conditions and long periods of time well, they could now analyze much older specimens than before. They have shown that tooth enamel protein is identical in modern humans, Neanderthals and Denisovans; if *H. erectus* were also human, they should have tooth enamel protein identical to that of those three groups. Scientists are now working on analysis of *H. erectus* tooth enamel proteins, and anticipate results in the not-too-distant future. We can expect that paleoproteomics will settle the status of *H. erectus* once and for all.

Improving Young-Earth Ice Sheet Computer Models

Leo (Jake) Hebert, III

In 1993 Dr. Larry Vardiman of the Institute for Creation Research published a simple one-dimensional mathematical model of the rapid formation of a post-Flood ice sheet. Unfortunately, creationists have since done little additional work in ice sheet modeling. Of special interest is a comparison of creationist predictions of annual layer thicknesses to predictions from secular models: creation models predict much thicker annual layers than do uniformitarian models, and volcanic tephra layers within deep Antarctic cores already favor the creation interpretation. I recently used a simple computer code to estimate the thicknesses of annual layers in Vardiman's model. However, these preliminary efforts were crude, and there is a need for more rigorous calculations.

Ice sheet behavior can be modelled, absent the usual dubious uniformitarian assumptions, by solving the stress balance equations for parcels within an ice sheet. The simplest possible example of this approach is the Mahaffy (1976) model, which is demonstrated using a clever technique by mathematician Ed Bueler. The more sophisticated Blatter-Pattyn model is also discussed, as are ways that creationists could use these techniques to more rigorously estimate annual layer thicknesses in an ice core. Finally, limitations of and realistic expectations regarding these computer models are discussed.

Model Building and the Future of Creation Science

Robert Hill

Model building has been key part of the modern creation science movement at least since the publication of *The Genesis Flood* by Whitcomb and Morris. This was not the only book about origins from a biblical perspective available to readers at the time. However, *The Genesis Flood* launched the modern creation movement because it presented a positive creation model rather than just listing errors with evolution and standard geological interpretations. This talk will discuss the importance of models to science. The examples of current models in creation science will be reviewed, as well as new models being developed. Finally, the future of creation science will be considered, how model building will play a key role in future creation science, and how the Creation Research Society will be a leader in the future of creation science.

Revisiting the Comet Argument

Robert Hill and Danny Faulkner

Comets have been used as a young solar system argument by creationists for many years. Evolutionary astronomers have proposed Kuiper Belt Objects and the Oort Cloud to solve the problem of comets. We will review the observational evidence for Kuiper Belt Objects and for objects that exist in the Oort Cloud. The Object 2014 UN271 is outgassing, which is comet-like behavior. It also has an aphelion distance comparable to the range of distance for the Oort Cloud. Possible creationary interpretations will be presented.

Creationeering™: Joining Science, Engineering, and Business Entrepreneurship to Fulfill the Dominion Mandate on the Earth as Commanded in Genesis 1:26–28

Mark Horstemeyer

Creationeering™ is a new paradigm, or worldview, that integrates science, engineering, and business practice for technological entrepreneurship from a biblical basis. It is a paradigm that subsumes “intelligent design” along with other engineering attributes and business practice. Furthermore, Creationeering™ distinguishes itself from Creation Science in that the former includes the “creation process” while the latter is limited to the discovery of existing physical phenomena. The systems engineering steps of Creationeering™ include the following: design, analysis/synthesis, procurement/making, logistics, assembly, performance/function, sustainability, and death/recycling. The business aspects include the following: human personnel, finances, legal, sales/marketing, and management. The eight steps in engineering and the five aspects of business comprise the paradigm of Creationeering™. God’s account of the Creationeering™ process is presented with respect to the creation of the cosmos, and Moses’ account of the Creationeering™ process is presented with respect to the tabernacle. Finally, a modern example of the common automobile is discussed to bring clarification regarding Creationeering™.

Mathematical and Physics Proofs and Evidences of God’s Existence

Mark Horstemeyer

Three different cases are presented for the existence of God: One mathematical proof from Gödel, one mathematical and physics proof from the work of Ticho Teney, and one strong evidence is that of a Pareto Frontier in multi-objective design optimization. Gödel’s mathematical proof is a formalization of Saint Anselm’s ontological argument for God’s existence, given by the following: “God, by definition, is that for which no greater can be conceived. God exists in the understanding. If God exists in the understanding, we could imagine Him to be greater by existing in reality. Therefore, God must exist.” The PhD work of Ticho Teney combined the different equations of Hooke’s Law and Einstein’s General Theory of Relativity. In order to solve a boundary value problem and to define the stress state of any entity in the cosmos, one much then appropriate Cauchy’s Law, which leads to the mathematical and physics proof of God’s Hands operating on the outside of the space-time-matter continuum to control

things within the space-time-matter continuum. Finally, a multi-objective design optimization algorithm is used to create a Pareto Frontier, which demands multiple possible solutions in the set of real solutions. As such, intelligence outside of the multi-objective system is required by definition to make the final choice of the engineered solution.

Reverse Engineering Methods Can Provide a Systematic Methodology to Conduct Creation Science

Mark Horstemeyer and Tate Fonville

We present the formal process of reverse engineering as a method to conduct Creation Science research. Since the Young Earth Creation (YEC) does not believe that everything has evolved over long periods of time by random chance events but was indeed engineered by the Creator. The systems engineering process of a structure, system, or software tool comprises the following steps: design, analysis, procurement/making things, logistics, assembly, performance/function, sustainability, and death/recycling. This can be considered the forward engineering process although engineering requirements flow backwards from death/recycling to sustainability to performance/function to assembly to logistics to procurement/making things. Once these requirements are defined then the design and analysis steps can be used to optimize the forward engineering steps. Once the backward and forward engineering steps are in place, the engineered structure/system/software can be used in its performance environment to achieve its design objectives. Sometimes, engineers will not know the sequence of the history of a structure/system/software tool, so they will have to “reverse” engineer the particular structure/system/software tool in order to determine the design objectives, constraints, and operational variables. Different methods to reverse engineer a structure/system/software include fault tree analysis, accident reconstruction, and forensics engineering. We discuss these different methods in the context of Creation Science.

Toward a More Biblical Cosmology

D. Russell Humphreys

Three clues in Genesis chapter 1 point to the speed of light in the heavens being trillions of times greater during the first four days of creation than it is today. Those same days on earth were of ordinary length, according to abundant clues in chapter 1 and the context of Exodus 20:11. According

to general relativity and experiments, the “speed of time” is directly connected to the speed of light. So, the speed of light on earth during creation week must have been what it is today. But the high speed of light in the heavens means that billions of years’ worth of events must have occurred out there before the end of the fourth day on earth. Because we observe the speed of light in the nearby heavens today as being what it is on earth, the speed of light in the heavens must have dropped at some time from being high down to today’s value. I propose that this change happened suddenly throughout the cosmos near the end of the fourth day. Such a change would mean that we would see no difference between things closer than 6,000 light-years and things beyond that distance. The interface would be entirely transparent to us. Yet we could see the cosmos billions of light-years away and having an apparent history of billions of years, allowing the heavens to declare the glory of God (Psalm 19:1).

Has God Proved that He Cares for Wildlife? Doxological Biodiversity & Providential Ecology Exhibited in Job 38:39–39:30

James J.S. Johnson

Many important inquiries in creation apologetics can researched, either by methods of empirical science or by methods of forensic science (or both). As this study shows, doxological biodiversity and providential ecology can be illustrated and analyzed by careful review of Job 38:39–39:30, in conjunction with empirical science principles, with results that include proving God’s providential care for wildlife (and even domesticated beasts), shown by analyzing empirical observations of lions, ravens, wild mountain goats, cervids, wild donkeys, rhinoceroses, ostriches, horses, hawks, and eagles, informed by Biblical Hebrew word studies. This study also clarifies how proving empirical science facts differs from proving forensic science facts, a distinction all-too-often ignored or misunderstood by evolutionists and creationists alike. Moreover, when attempting to explain facts about God’s creation, evolutionist assumptions ubiquitously violate both empirical and forensic science standards. Furthermore, evolutionists avoid applying basic forensic evidence rules when researching past events, because evolutionists invalidly substitute uniformitarian assumptions as illegitimate replacements for reliable eyewitness testimony—routinely producing serious error. Contrastingly, the Bible demonstrates that some true facts are learned from reports given by reliable eyewitnesses (consistent with forensic science), while other true facts are learned by present-day observations (consistent with empirical science). Yet depending upon

relevant contexts, both types of science are useful for proving true facts (and for disproving falsities). Consequently, creationists should carefully distinguish between empirical science and forensic science, so that proper proving of evidentially important facts (about God and creation) can be both practiced and promoted—especially in creation apologetics contexts.

Three Lineages Descending from Noah were found in Y Chromosome Variant Databases

Marshall Jordan

Because all men alive today have descended from Noah within the last 4500 years, their Y chromosome genetic sequence should be identical to Noah’s except for accumulated mutations. Evidence for this common descent in large Y chromosome variant databases may be obscured by reference bias. Reference bias occurs because the reference genome against which variants are called is not Noah’s sequence, but the sequence of a modern man at many positions in the sequence. In this study an algorithm was developed which identified and corrected these biased variants, allowing identification of the original lineages descending from Noah. The method was applied to two large, open access databases available online and three patriarch lineages descending from Noah were found. The lineages were characterized by common variants corresponding to the major Y chromosome haplogroup markers of the deep branches of published phylogenetic trees. The three lineages could not be conclusively assigned to Noah’s three sons, who may not have had any mutations on their Y chromosomes. Homoplasmy and back mutation did not hide the patriarch variants characterizing the lineages because the variants occurred when the male population was very small, within a few generations of the Flood. Applying this method to Y chromosome genetic data in the light of the record of Genesis 10 and 11 may further our understanding of human migration from the Babel dispersion.

The Genesis Flood as the Mechanism for Amber Formation

Joseph Kezele

An examination of some aspects of amber chemistry, amber distribution, inclusions and geology is done to see if a straightforward explanation can be developed to answer questions that secular models do not adequately address. A survey of published articles revealed that: resin chemistry

has enough variables to make it difficult at times to correlate source species with current amber specimens; the existence of terrestrial, freshwater and marine organisms, as well as air bubbles entrapped in amber, indicate a marine environment; that log mats of fractured trees provide an adequate source of resin and for mixing of these organisms from widely different ecological zones; elevated oxygen levels in bubbles in amber are consistent with but do not prove the existence of elevated atmospheric oxygen in the pre-Flood world compared to present atmospheric oxygen levels; an aqueous environment is necessary for resin to remain in a liquid phase for adequate time for entrapment to occur; burial is considered necessary for resin to be converted into amber; and amber specimens are largely associated with coal deposits. A final conclusion is that only the Genesis Flood can account for the world-wide phenomena described in the scientific literature.

Exploring Arizona's Transition Zone

Nathan Mogk

Arizona's Central Highlands is a beautiful, complex, and varied landscape where the imprints of Earth's history from Creation onward are laid bare in the rocks. While often overshadowed by the Grand Canyon, this Transition Zone between the Colorado Plateau and the low deserts provides numerous opportunities for research on the most pressing questions in Flood geology. Three features in the Transition Zone help to constrain the Flood terminal boundary throughout the entire region, and in relation to late stage Basin and Range faulting, Colorado Plateau uplift, and the deposition of the ubiquitous valley fill deposits. The first is Granite basin, a makhtesh-like feature associated with a prominent Gila river transverse drainage. The second is the gravels associated with the confluence of the Verde and Salt rivers which show that drainage integration was simultaneous and subsequent to basin formation. Both of these features indicate that the bulk of valley fill deposits were deposited during the Flood. Several alternative scenarios are addressed. Finally, the Verde formation which constitutes the valley fill deposit in the Verde Valley shows features indicative of both Flood and post-Flood deposition, which provides interpretive challenges and is subject to ongoing investigation.

Flood Log Mats Provide Reasonable Answers to Geological Challenges

Mike Oard

There are a few hundred challenges left in geology that need to be answered within the creation science framework. The Flood and the post-Flood Ice Age were unique catastrophic events that can unlock these mysteries. Log mats during the Flood can provide reasonable answers for many of these challenges. These challenges include coal, polystrate trees, multiple layers of polystrate trees such as those in Yellowstone National Park, the peculiar mix of palyflora from different climates and environments, amber, insects in sedimentary rock, insects in amber, and some biogeographic challenges.

Implications of Increased Cosmic Rays during the Flood and Early Ice Age

Mike Oard

Measurements of in situ Be-10 during the Flood and early Ice Age show values significantly higher than expect in 6,000 years of biblical earth history. One potential explanation for high Be-10 concentrations during the Flood is that accelerated radiometric decay gave off neutrons that can form Be-10. However, it appears that this can only be part of the explanation, since atmospheric Be-10 was very high in ice cores during the Ice Age. The only way to explain such high values seems to be increased cosmic rays during the Flood, rapidly tailing off during the Ice Age. This suggests a nearby supernova or supernovae during the Flood.

Several implications follow from increased cosmic rays. Because of several complications, it is impossible to directly transpose secular Be-10 measurements into post-Flood time. It is possible that increased cosmic rays could cause or partly cause accelerated nuclear decay during the Flood and even after the Flood. Evidence for the latter is in another cosmogenic nuclide dating method: the ratio of Al-26/Be-10. This ratio is about seven today, but when measured in buried sediments, it is around 3 to 4. Since the half-life of Al-26/Be-10 is one to two million years, accelerated radionuclide decay continuing after the Flood seems to be the only way to account for these ratios.

Carbon-14 is another cosmogenic nuclide. C-14 dates within 3,000 years BP are generally similar for the uniformitarian and creation science timescales. However, secular dates for Ice Age features, such as woolly mammoths, range

to the limit of C-14 of 50 ka. So, we need to explain why dates of 3 to 50 ka are given from 4,500 BP, the date of the Flood, to 3,000 BP. Increased cosmic rays during the Flood and early Ice Age would result in a buildup of C-14 and thus explain the telescoping of C-14 dates to within 1,500 years after the Flood.

A third implication is that with accelerated radiometric decay after the Flood, we can telescope other dating methods into post-Flood time, such as the Uranium-Thorium dating of corals and caves.

The Role of Historical Science and Supernatural Causes in Biblically Based Scientific Studies

Rich Overman and Danny Faulkner

The Creation Research Society's statement of faith begins with "The Bible is the written Word of God, and because it is inspired throughout, all its assertions are historically and scientifically true in the original autographs." Hence, the Bible provides an authoritative source of information for scientific studies. This source material is in the form of descriptions of divine works and other events that occurred in the past. Many divine works are classified as miracles, but they can still leave effects that can be studied in the present (i.e. the original creation). Miracles have been categorized into Grade A, which seem to involve the suspension of physical processes or grade B in which God directs physical processes. In many cases, these historical events or miracles have left effects that can be studied in the present (i.e. the global flood). This paper addresses the role of historical events (e.g. historical science) and miracles within a general biblical scientific method. Examples, such as Dr. D. R. Humphreys work on magnetic fields and Dr. T. L. Clarey's work on Flood geology are used to illustrate biblically based scientific techniques.

Devolution of the Serpent Lineage: Evidence that Theropod Dinosaurs are the Ancestors of Modern Snakes

Michael Rudy

If the curse upon the serpent in Genesis 3:14–15 was pronounced upon a large, four-limbed creature then it becomes far more consequential. Furthermore, the Bible does not specify whether this curse happened instantly or whether it occurred over many generations of the serpent lineage. Here

I present genetic, fossil, skeletal, and historic evidence that theropod dinosaurs (like *Tyrannosaurus rex*) were the ancestors of modern snakes. Genetic analysis of snakes indicates that devolution of the serpent lineage involved changes in Hox gene expression and loss of sonic hedgehog (SHH) expression; leading to elongation of the thoracic region and loss of the otic capsule, forelimbs, and hindlimbs. SHH signaling defects can also be seen in the underdeveloped forelimbs of T-rex. Fossil evidence from Eupodophis and Haasiophis indicate that ancestral snakes were similar to T-rex in pelvic and hindlimb structure. The presence of cervical ribs and a split mandible in both T-rex and snakes further support this link. Most importantly, every skull bone of Python reticularis can be matched to a similarly shaped bone in the skull of T-rex and differences are all associated with a rostral shift of ventral/midline structures and horizontal compression of the T-rex cranium. This work highlights the need to reinterpret the so-called maxillary, anteorbital, and orbital fenestrae as the pit organ, eye socket, and venom gland respectively (a reinterpretation which is supported by further fossil and skeletal evidence). Taken together, this work provides a weight of scientific evidence indicating prophetic fulfillment of the curse upon the serpent lineage.

The Possible Origin of Parasitic Nematodes

Frank Sherwin

Nematoda is part of the Ecdysozoa of protostome animals. Three groups of nematodes provide a fascinating look into the possible transition from free-living to parasitism in a short period: the suborder Tylenchina, and the families Rhabdiasidae and Strongyloididae. The two aforementioned families may produce parasitic or free-living populations, depending on environmental conditions. Some species of the Rhabdiasidae undergo a heterogonic life cycle. Strongyloides species can undergo homogonic parasitic life cycles or maintain constant free-living generations. Tylenchina is composed of many species of tiny worms with assorted life cycles and feeding mechanisms. Alternation between parasitic and free-living generations is found in several species of Tylenchina. Exaptation is a characteristic whereby a trait created/developed for a biological role is later used for another (parasitism). Preadaptation to parasitism and opportunism should also be considered. In answering the question of the origin of parasitism in people and animals after the Fall, these three suborders may provide clues as to how roundworms (and perhaps protozoa and ectoparasites), made the transition from free-living to obligate parasitism.

Hydraulic Evaluation of a Dam Breach Hypothesis for Grand Canyon Formation

Christian A. Smith and Timothy A. Smith

Various proposals exist for formation of Grand Canyon. The authors evaluated the efficacy of a dam breach formation hypothesis to explain the origin of Grand Canyon. Previous research was reviewed on hydraulic mechanisms of surficial destruction, characteristics of dam breach failures, and topographic and geologic features surrounding the destroyed Grand Canyon corridor. Subsequent to this review, one-dimensional finite difference unsteady hydraulic modeling was performed for the destroyed corridor somewhat above the level of the narrow part of the incised canyon rim (approximately 1100 meters or 3600 feet of elevation). A failure height of 518 meters (1700 feet) was selected, given a low overflow elevation of 1713 meters (5620 feet) north on the Kaibab Plateau. This height and a failure open area smaller than the Kaibab canyon mouth yielded an estimated failure flow rate on the order of 15.3 million cubic meters per second (540 million cubic feet per second). Routing these flows through the destroyed canyon corridor produced velocities on the order of 6 to 15 meters per second (20 to 50 feet per second). Further, unsteady two-dimensional implicit finite volume modeling of the shallow water equations was applied to the Colorado Basin to enhance understanding of the potential flow impact across the basin. The authors concluded a dam breach is still a reasonable and appropriate, though not certain, mechanism for Grand Canyon formation.

This suggests something in the environment during Shem's developmental years fixed his potential lifespan, and subsequent environmental changes after the Flood had limited effect on his adult body. Radiocarbon incorporation into the genetic material of key organs, particularly the brain, during pregnancy and childhood, provides a mechanism for fixing maximum longevity based on the radiocarbon level during development. Modern radiocarbon decay causes genetic damage to approximately 400 million brain cells and 30 billion other cells over a typical 80-year human lifetime. This genetic damage could play a key role in our aging process. But if environmental radiocarbon levels were very low immediately after the Flood and gradually increased to modern levels, that could explain how Shem incorporated little radiocarbon during his childhood and thus aged slowly, whereas subsequent generations incorporated significantly more radiocarbon during development and aged much more rapidly.

This theory requires that there is little or no radiocarbon turnover during adulthood in the DNA in critical organs such as the brain—a fact only recently confirmed. Unlike other theories of Biblical longevity, this radiocarbon theory is testable, and might even play a role in the prophesied restoration of extreme longevity described in Isaiah 65.

The Mystery of Methuselah: Could Radiocarbon Incorporation into DNA During Childhood Explain the Unusual Longevity Patterns in Genesis 5 and 11? A Testable Theory with Prophetic Implications

Chris Williams

The Genesis 5 and 11 chronologies contain perhaps the most detailed scientific data in the Scriptures. Yet previous aging theories, including genetic entropy (inherited germ line mutations) or various post-Flood environmental changes fail to explain the rapid and strange pattern of decreasing longevity, including Shem possibly outliving his ninth generation descendent, Abraham.

Instructions to Authors

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Electronic submissions of all manuscripts and graphics are preferred and should be sent to the editor of the *Creation Research Society Quarterly* in Word, WordPerfect, or Star-Office/Open Office (see the inside front cover for address). Printed copies also are accepted. If submitting a printed copy, an original plus two copies of each manuscript should be sent to the editor. The manuscript and copies will not be returned to authors unless a stamped, self-addressed envelope accompanies submission. If submitting a manuscript electronically, a printed copy is not necessary unless specifically requested by the *Quarterly* editor. Manuscripts containing more than 35 pages (double-spaced and including references, tables, and figure legends) are discouraged. An author who determines that the topic cannot be adequately covered within this number of pages is encouraged to submit separate papers that can be serialized.

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4. Body of the text. Two types of headings are typically used by the *CRSQ*. A major heading consists of a large font bold print that is centered in column, and is used for each major change of focus or topic. A minor heading consists of a regular font bold print that is flush to the left margin, and is used following a major heading and helps to organize points within each major topic. Do not split words with hyphens, or use all capital letters for any words. Also, do not use bold type, except for headings (italics can be occasionally used to draw distinction to specific words). Italics should not be used for foreign words in common usage, e.g., "et al.", "ibid.", "ca." and "ad infinitum." Previously published literature should be cited using the author's last name(s) and the year of publication (ex. Smith, 2003; Smith and Jones, 2003). If the citation has more than two authors, only the first author's name should appear (ex. Smith et al., 2003). Contributing authors should examine this issue of the *CRSQ* or consult the Society's web site for specific examples as well as a more detailed explanation of manuscript preparation. Frequently-used terms can be abbrevi-

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Margulis, L. 1971a. The origin of plant and animal cells. *American Scientific* 59:230–235.

Margulis, L. 1971b. *Origin of Eukaryotic Cells*. Yale University Press, New Haven, CT.

Hitchcock, A.S. 1971. *Manual of Grasses of the United States*. Dover Publications, New York, NY.

Walker, T.B. 1994. A biblical geologic model. In Walsh, R.E. (editor), *Proceedings of the Third International Conference on Creationism* (technical symposium sessions), pp. 581–592. Creation Science Fellowship, Pittsburgh, PA.

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Submission of letters regarding topics relevant to the Society or creation science is encouraged. Submission of letters commenting upon articles published in the *Quarterly* will be published two issues after the article's original publication date. Authors will be given an opportunity for a concurrent response. No further letters referring to a specific *Quarterly* article will be published.

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Occasionally, the editor will invite individuals to submit differing opinions on specific topics relevant to the *Quarterly*. Each author will have opportunity to present a position paper (2000 words), and one response (1000 words) to the differing position paper. In all matters, the editor will have final and complete editorial control. Topics for these forums will be solely at the editor's discretion, but suggestions of topics are welcome.

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Creation Research Society

History—The Creation Research Society was organized in 1963, with Dr. Walter E. Lammerts as first president and editor of a quarterly publication. Initially started as an informal committee of 10 scientists, it has grown rapidly, evidently filling a need for an association devoted to research and publication in the field of scientific creation, with a current membership of over 600 voting members (graduate degrees in science) and about 1000 non-voting members. The *Creation Research Society Quarterly* is a peer-reviewed technical journal. It has been gradually enlarged and modified, and is currently recognized as one of the outstanding publications in the field. In 1996 the CRSQ was joined by the newsletter *Creation Matters* as a source of information of interest to creationists.

Activities—The Society is a research and publication society, and also engages in various meetings and promotional activities. There is no affiliation with any other scientific or religious organizations. Its members conduct research on problems related to its purposes, and a research fund and research center are maintained to assist in such projects. Contributions to the research

fund for these purposes are tax deductible. As part of its vigorous research and field study programs, the Society operates the Van Andel Creation Research Center in Glendale, Arizona.

Membership—Voting membership is limited to scientists who have at least an earned graduate degree in a natural or applied science and subscribe to the Statement of Belief. Sustaining membership is available for those who do not meet the academic criterion for voting membership, but do subscribe to the Statement of Belief.

Statement of Belief—Members of the Creation Research Society, which include research scientists representing various fields of scientific inquiry, are committed to full belief in the biblical record of creation and early history, and thus to a concept of dynamic special creation (as opposed to evolution) both of the universe and the earth with its complexity of living forms. We propose to re-evaluate science from this viewpoint, and since 1964 have published a quarterly of research articles in this field. *All members of the Society subscribe to the following statement of belief:*

1. The Bible is the written Word of God, and because it is inspired throughout, all its assertions are historically and scientifically true in all the original autographs. To the student of nature this means that the account of origins in Genesis is a factual presentation of simple historical truths.

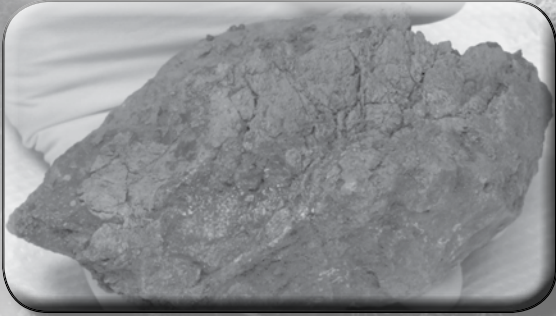
2. All basic types of living things, including humans, were made by direct creative acts of God during the Creation Week described in Genesis. Whatever biological changes have occurred since Creation Week have accomplished only changes within the original created kinds.

3. The Great Flood described in Genesis, commonly referred to as the Noachian Flood, was a historical event worldwide in its extent and effect.

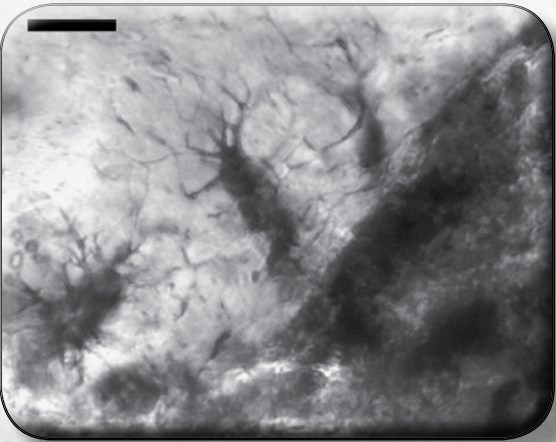
4. We are an organization of Christian men and women of science who accept Jesus Christ as our Lord and Savior. The act of the special creation of Adam and Eve as one man and woman and their subsequent fall into sin is the basis for our belief in the necessity of a Savior for all people. Therefore, salvation can come only through accepting Jesus Christ as our Savior.

iDINO II

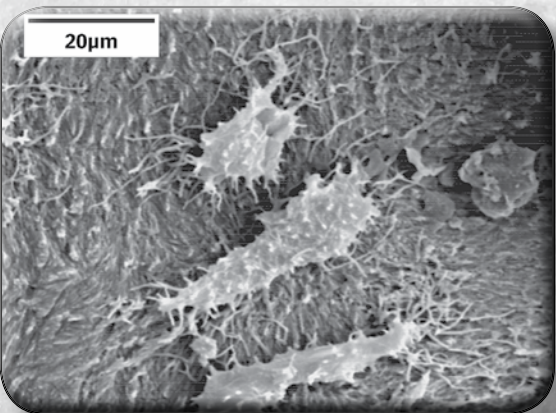
Investigation of Dinosaur Intact Natural Osteo-tissue



A fragment of the *Triceratops* brow horn.
Fragments, such as this one,
still contain tissue and cells.



Microscopic examination of tissue
extracted from a *Triceratops* horn
reveals bone cells still present.



Electron microscope picture of
intact bone cells still in tissue
extracted from a *Triceratops* horn.

How can pliable, stretchable tissue survive inside dinosaur fossils for over 65 million years?

How can this tissue still contain intact cells and even dinosaur proteins?

How can this fragile biological material survive for so long?

The answer to these questions directly challenges the current, evolutionary-biased, geologic timescale.

The Creation Research Society began its iDINO research initiative for the purpose of studying soft tissue in dinosaur fossils. The first phase of the project detected pliable, unfossilized tissue in a brow horn of a *Triceratops*. Within this tissue were intact osteocytes (bone cells). Some results from the iDINO project have been published in a technical microscopy journal and presented at an international microscopy conference. The Spring 2015 issue of the *Creation Research Society Quarterly* also features a special report of the iDINO project. Plus, to further spread the important information about soft tissue, the Society is developing a video (Echoes of the Jurassic).

The **second phase** of the project (iDINO II) will look more extensively at the process of tissue preservation. Evolutionists have offered various theories of how this tissue could survive for millions of years. iDINO II will methodically investigate these preservation claims, assessing their plausibility.

The iDINO results have already provided a strong challenge to the evolutionary worldview. More extensive and detailed examination may provide even stronger evidence that the age of dinosaur fossils is far less than 65 million years. To this end, the Society continues to seek those willing to fund this project with either one-time gifts or monthly donations.

For more information contact us at (928) 636-1153 or crsvarc@crsvarc.com.

Also visit <http://tinyurl.com/nphm2c4> for project updates and details.



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