

EDITORIAL

POLYPHYLY AND THE CAMBRIAN EXPLOSION

Perhaps the most compelling feature of the fossil record is the sudden appearance of a wide diversity of fossils at and near the base of the Phanerozoic sediments. This sudden appearance is called the Cambrian Explosion, and has been the subject of much comment and analysis.

First appearances of phyla and classes of metazoans (multi-cellular animals) are not distributed evenly throughout the geologic column, but are largely clustered at the lower end of the Phanerozoic, predominantly from the uppermost Precambrian to the Ordovician, peaking in the Cambrian.¹ First appearances for orders also peak in the Cambrian and Ordovician, but are more broadly distributed. In contrast, first appearances of families, genera and species are relatively low in the Cambrian, and generally increase through the geologic column.² The increase is especially marked from the Cretaceous to the top of the column. This means that the Cambrian fossil record consists of a relatively small number of species with widely varying anatomical designs, or body plans. As one moves upward through the column, the fossil families, genera and species differ from level to level, but the higher taxonomic categories tend to remain the same. What does this mean?

Most scientists read the geologic column as a record of history, in which the Phanerozoic portion extends over some 540 million years. Viewed from this perspective, the Cambrian Explosion is most easily explained as the result of a polyphyletic origin for life. But, oddly enough, the scientific community seems to resist this interpretation. The reason seems not to be scientific, but philosophical and historical.

According to standard evolutionary theory, all organisms derive from a single ancestral species. Darwin's famous book³ is noted for having only one illustration – the familiar monophyletic evolutionary tree, showing all living organisms linked to a single ancestor. The structure of this tree shows diversity first increasing at low taxonomic categories, eventually building to diversity at higher taxonomic categories. Evolutionarily speaking, this pattern

seems inevitable — small changes add up, eventually producing new species, then new genera, families, orders, etc. Unfortunately for the theory, this description is the opposite of the actual pattern in the rocks. The greatest morphological differences appear in the lower Phanerozoic rocks, while the rest of the fossil record consists largely of variations of familiar themes.

Molecular studies of living species impact the interpretation of the Cambrian Explosion. Several phyla are soft-bodied and/or microscopic, and absent or very rare as fossils. Viewed solely from the fossil record, these phyla might have originated much later in geologic history than the phyla that are found in the Cambrian sediments. But molecular phylogenies are interpreted as showing that the soft-bodied phyla are of similar age as those with a good fossil record.⁴ Thus, the Cambrian Explosion includes not only those phyla with fossils in Cambrian sediments, but also the other phyla with poor fossil records.

If the Phanerozoic is to be read as a record of extended history, what does the Cambrian Explosion tell us? One possibility is that the fossil record is woefully inadequate to trace the origins of the higher taxa. But this explanation has some serious implications. How can the fossil record be trusted to tell us anything if it is so poor that we cannot trace even the major stages in the evolution of higher taxa? And what evidence is there that the fossil record is that poor? Is there anything beyond the presupposition of monophyly that suggests such an incomplete record?

No one would claim the fossil record is perfectly complete, but it does not seem to be bad enough to explain the Cambrian Explosion in terms of monophyly. Fossils of soft-bodied organisms are famously found in Cambrian Preservat-Lagerstätten such as the Burgess Shale and the Chengjiang locality in China. Fossil bacteria are reported from both Precambrian and Phanerozoic rocks. Why would depositional conditions favor preservation of bacteria in both Precambrian and Phanerozoic rocks, but soft-bodied multicellular organisms only in the Phanerozoic and uppermost Precambrian?⁵ The fossil record is obviously incomplete, but there is no evidence it is so incomplete it would not preserve fossils of soft-bodied organisms for half their supposed geologic history.⁶

Perhaps polyphyly is an idea that deserves greater consideration by the scientific community. The idea has been mentioned a few times,⁷ but does not seem to have been seriously discussed within the mainstream scientific community.

A counterargument against polyphyly is that biomolecular similarities indicate common ancestry and monophyly. For example, the genetic code and metabolic enzymes are similar in nearly all living organisms. However, there are significant differences in the details of the cellular processes in different groups of organisms.⁸ Scientists have become so acutely aware of anomalies in molecular phylogenies that they have even considered abandoning attempts to reconstruct the root of the evolutionary tree, with the explanation that lateral gene transfer has confused the situation beyond recognition.⁹ In addition, the origin of the genetic code has no plausible naturalistic explanation.¹⁰ This may be a good time to make some changes in thinking.

Creation theory offers reasonable explanations for both the Cambrian Explosion and the origin and ubiquity of the genetic code. The taxonomic diversity seen in the Cambrian Explosion may be simply the result of preservation of various communities of marine organisms living on or near the floor of the sea. The basis for the association of the fossils is ecological rather than genealogical.¹¹ The absence of ancestors in the underlying strata is not due to a faulty fossil record, but reflects separate origins of the various groups. This proposition applies whether one reads the fossil record as extended history or as complex catastrophe.

Polyphyly implies that the genetic code has multiple independent origins, and is not the result of common ancestry. This suggests the concept of similarity by common design. Design may be the best explanation for the origin and ubiquity of the genetic code.¹² Common design seems eminently reasonable as an explanation of similar features in organisms that appear genealogically unlinked.

Is the fact that an idea is associated with creation theory sufficient reason to exclude the idea from consideration in science? It would be unfortunate if prejudice against a competing theory were so intense that an idea is rejected merely because it is part of that competing theory, even though it might be the best available explanation. Polyphyly is an important tenet of creation theory. In

this case at least, creation theory appears to provide the explanation that is most in accordance with the evidence from nature.

L. James Gibson

ENDNOTES

1. Erwin DH, Valentine JW, Sepkoski JJ. 1987. A comparative study of diversification events: the early Paleozoic versus the Mesozoic. *Evolution* 41:1177-1186.
2. Signor PW. 1994. Biodiversity in geological time. *American Zoologist* 34:23-32.
3. Darwin C. 1958. *The origin of species*. 6th edition, 1872. NY: Mentor Books. The diagram is found in Chapter 4; page number varies according to the publisher.
4. Ayala FJ, Rzhetsky R, Ayala FJ. 1998. Origin of the metazoan phyla: molecular clocks confirm paleontological estimates. *Proceedings of the National Academy of Sciences (USA)* 95:606-611.
5. Assuming the Ediacaran fauna are truly multicellular.
6. Foote, M., J.J. Sepkoski. 1999. Absolute measures of the completeness of the fossil record. *Nature* 398:415-417. See also the reference in Endnote 4.
7. Polyphyly has been suggested for life in general in: Schwabe C, Warr GW. 1984. A polyphyletic view of evolution: the genetic potential hypothesis. *Perspectives in Biology and Medicine* 27:465-485. Polyphyly has also been suggested for invertebrate phyla in: Willmer P. 1990. *Invertebrate relationships*. NY: Cambridge University Press, p 359. Such suggestions are much more rare than one would expect, given the state of the evidence.
8. Fox GE, Stackebrandt E, Hespell RB, Gibson J, Maniloff G, + 14 other authors. 1980. The phylogeny of prokaryotes. *Science* 209:457-463.
9. Doolittle WF. 1999. Phylogenetic classification and the universal tree. *Science* 284:2124-2128.
10. Di Giulio M. 1997. On the origin of the genetic code. *Journal of Theoretical Biology* 187:573-581. Many attempts have been made, for example: Alberti S. 1999. Evolution of the genetic code, protein synthesis and nucleic acid replication. *Cellular and Molecular Life Sciences* 56:85-93.
11. This does not imply denial of variation, or even speciation, among the Cambrian fossil groups, but emphasizes that the overall pattern of the fossils is not genealogical, but is related to ecology.
12. Design is not being proposed, but seems an obvious possibility. See, for example: Freeland SJ, Hurst LD. 1998. The genetic code is one in a million. *Journal of Molecular Evolution* 47:238-248.

ARTICLE

A BARAMINOLOGICAL ANALYSIS OF SUBTRIBE FLAVERIINAE (ASTERACEAE: HELENIEAE) AND THE ORIGIN OF BIOLOGICAL COMPLEXITY

Todd Charles Wood*

Assistant Professor,

Center for Origins Research and Education

Bryan College

Dayton, Tennessee

and

David P. Cavanaugh**

Harvest, Alabama

WHAT THIS ARTICLE IS ABOUT

The subtribe Flaveriinae (Asteraceae: Helenieae) includes a number of plant species sometimes called yellowtops, glowworts, and false broomweed. Different species of this subtribe differ in their chemical pathways involved in photosynthesis. Some species use a system known as C_3 photosynthesis, some use a system known as C_4 photosynthesis, and others display characteristics intermediate between the two. The authors apply a creationist research method known as baramnology to determine whether the species might have been created separately, or whether they may have descended from a single created ancestral species. They present a large amount of evidence that suggests the entire subtribe belongs to a single lineage which includes additional species not included in the study. The evidence also implies that the originally created ancestor used C_3 photosynthesis, and that the C_4 photosynthesis present in some species emerged since the creation. The characteristics of the intermediate species and the genetics of C_4 species support the hypothesis that latent genetic information may have been present in the ancestor, and activated during post-Flood diversification of the group, possibly through a mechanism called Altruistic Genetic Elements.

* Corresponding Author, Assistant Professor, Center for Origins Research and Education, P.O. Box 7731, Bryan College, Dayton TN 37321 wood@bryancore.org

** 27329 Alberta Drive, Harvest, AL 35749

INTRODUCTION

Creationists have long speculated whether the “created kind” can be approximated by a traditional Linnean classification level (Marsh 1976), with several creationists proposing that kinds may be equivalent to families (Jones 1972, Siegler 1978, Woodmorappe 1996). In general, these speculations are based largely on hybridization studies of vertebrates or on the lists of organisms in Leviticus. Although the family/kind approximation may be adequate for mammals and birds, for many other types of organisms this estimation may certainly be incorrect. Flowering plant families frequently contain thousands of species. For example, the Iridaceae contains 1500 species, the Melastomataceae 4000 species, and the Euphorbiaceae 7500 species (Cronquist 1981). The largest plant family is Asteraceae, with estimates ranging from 20,000 species in 1100 genera (Cronquist 1981) to 30,000 species in 2500 genera (Kim and Jansen 1995). While it is certainly possible that the Asteraceae could be a single created kind, its species diversity would be without parallel among the vertebrates. Thus, the magnitude of variation in the plants should be cause for skepticism in too quickly equating “family” with “created kind.”

As a preliminary case study of created kinds in plants, we present here a review of the taxonomy and phylogeny of the plants of subtribe Flaveriinae (Asteraceae). Wise’s (1992) method of baraminology evaluates additive and subtractive evidence separately in an attempt to approximate the complete membership of the created kind, or *holobaramin*. Additive evidence suggests that two species are genealogically related and is used to delineate *monobaramins*. Properly understood, monobaramins are simply a group of species which share a common ancestor; the group may be monophyletic or paraphyletic. By revealing a common developmental mode, the traditional hybridization criterion (Marsh 1976) is a source of additive evidence. Subtractive evidence suggests that two species or groups have a separate ancestry and is used to define *apobaramins*. An apobaramin is any group of species that are separated from all other species by a phylogenetic discontinuity; the apobaramin may contain one or more holobaramins. Novel biological features, such as flight in bats, are frequently used as subtractive evidences. Additive and subtractive evidence can also be evaluated together using the ANalysis Of PAttern (ANOPA) method, which is

effective in identifying significant continuity and discontinuity in phylogenetic data (Cavanaugh and Sternberg, in prep).

Currently, two different definitions of subtribe Flaveriinae exist. Flaveriinae *sensu stricto* includes only three genera, *Sartwellia* (4 spp., Turner 1971), *Haploësthes* (3 spp., Turner 1975), and *Flaveria* (21 spp., Powell 1978); while Flaveriinae *sensu lato* includes those three genera and the genera *Clappia*, *Jaumea*, *Pseudoclappia*, and *Varilla* (Karis and Ryding 1994). For simplicity's sake, herein we will use the strict definition of Flaveriinae with only three genera, referring to Flaveriinae *sensu lato* where necessary.

The plants of each genus of Flaveriinae prefer gypsiferous soils in arid climates. *Sartwellia* and *Haploësthes* are both found in overlapping ranges in New Mexico, Texas, and Mexico (Turner 1971, 1975). The range of *Flaveria* extends from the southwestern United States through Central America into South America and includes Florida and several Caribbean islands. Isolated *Flaveria* species are also found in Africa, India, and Australia (Bremer 1994, Powell 1978). Like all Asteraceae, the Flaveriinae reproduce by miniature flowers, which are aggregated into heads resembling larger single flowers, and one-seeded achenes (such as the familiar, striped shells containing the edible sunflower seeds). Unlike other Asteraceae, Flaveriinae contain large amounts of sulfated flavonoids, presumably as an adaptation to or consequence of the saline, sulfate-rich niches they occupy (Powell 1978).

The genus *Flaveria* is surprisingly diverse, containing annual and perennial species as well as woody and herbaceous species. Most remarkable of all, *Flaveria* is one of only a handful of genera that contain species that photosynthesize by the C₃ and C₄ pathways as well as various C₃-C₄ intermediates.

To review, the C₃ plants fix carbon dioxide into a three-carbon compound, 3-phosphoglycerate (3-PGA). This reaction is catalyzed by the enzyme ribulose 1,5-bisphosphate carboxylase/oxygenase (rubisco). 3-PGA then proceeds through a series of reactions known as the Calvin cycle, whereby CO₂ from the atmosphere is incorporated into sugars. True C₄ plants are characterized by the presence of Kranz anatomy, a ring of specialized bundle sheath cells (BSC) that surround the veins of the leaf. CO₂ is fixed in the regular mesophyll cells (MC) of the leaf into a four-carbon compound, oxaloacetate or malate, catalyzed by phosphoenolpyruvate carboxylase (PEPC). These four-carbon

compounds ultimately are transported to the BSC where they are broken down, releasing carbon dioxide, which is then fixed into 3-PGA by the enzyme rubisco (Figure 1). The advantages of C_4 photosynthesis include better nitrogen-use efficiency and lower photorespiration than in C_3 plants (Edwards and Walker 1983).

Although it may seem that this difference in biochemistry is sufficient to warrant the inference of direct divine design, the evidence is far from conclusive. There is no single C_4 pathway; to date, three different subgroups have been described based primarily on the different enzymes used to liberate the CO_2 from the four-carbon compounds transported

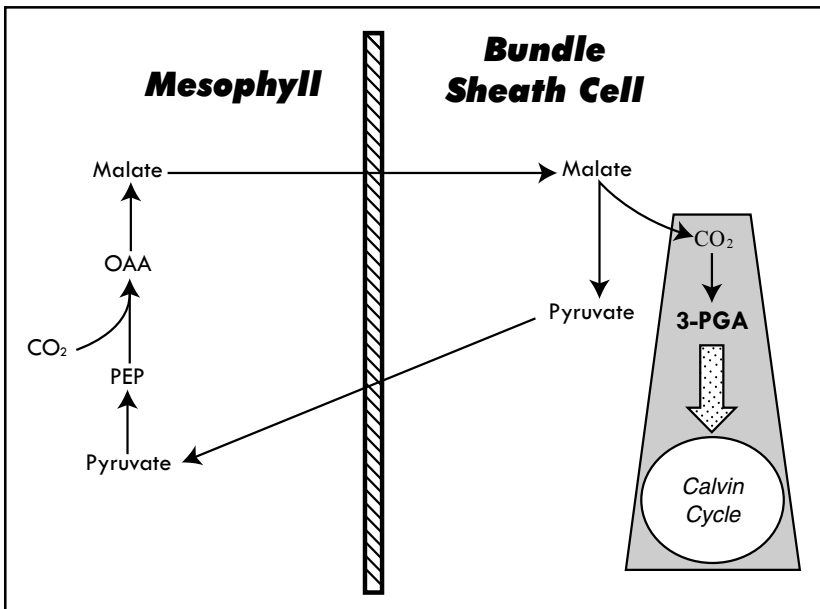


Figure 1. A simplified C_4 photosynthesis pathway of the NADP-ME type, as found in *Flaveria* species. CO_2 is fixed in the mesophyll cells by phosphoenolpyruvate (PEP) carboxylase yielding oxaloacetate (OAA). The OAA is converted to malate and then transferred to the bundle sheath cells (BSCs). The CO_2 is released in the BSC by NAD malic enzyme yielding pyruvate. The CO_2 is then fixed by rubisco yielding 3-PGA, which is delivered to the Calvin cycle for normal photosynthesis. The pyruvate is returned to the mesophyll for recycling into PEP. Note that in C_3 plants, the pyruvate cycling pathway does not exist. Only the reactions highlighted in grey occur in all leaf cells in C_3 plants. (Figure after Edwards and Walker 1983).

to the BSC. The different subgroups use PEP carboxykinase, NADP-malic enzyme, and NAD-malic enzyme to catalyze this reaction. Furthermore, 23 different species in seven different genera and five different families have been identified as exhibiting traits intermediate between C_3 and C_4 photosynthesis (Monson and Moore 1989). These intermediate traits can be limited to simple anatomical changes in the cells surrounding the BSC, or may include biochemical alterations such as compartmentation of enzymes into the rudimentary BSC. All C_3 - C_4 species possess a limited Kranz-like anatomy of specialized BSC that lack the thickened cell walls characteristic of true C_4 BSC (Monson et al. 1984). Many of the BSC of C_3 - C_4 species also concentrate organelles (mitochondria, chloroplasts, and peroxisomes) that contain enzymes critical to the C_4 pathway. In *Flaveria*, a limited C_4 pathway and enzymatic compartmentation has been observed in *F. ramosissima* (Monson et al. 1984). C_3 - C_4 intermediates typically undergo photorespiration less than C_3 species but more than C_4 (Moore et al. 1987).

An irreducibly complex system is “composed of several well-matched, interacting parts that contribute to the basic function, wherein the removal of any one of the parts causes the system to effectively cease functioning” (Behe 1996). Thus, any system of interacting parts that continues to function in a limited fashion without one of the parts cannot be irreducibly complex by definition. The existence of true intermediates demonstrates that the C_4 photosynthetic pathway is not irreducibly complex, for the C_4 phenotype can continue to function in a limited fashion even when biochemical parts of the underlying mechanism are absent. Because of this *reducible* complexity in C_4 photosynthesis, Behe’s design inference cannot be applied, and the question of direct divine design remains (Behe 1996). Thus, if it were shown that C_3 , C_4 , and C_3 - C_4 plants were members of the same holobaramin, the post-Creation origin of C_4 photosynthesis would be implied by the majority of C_3 species in Flaveriinae. Thus, *Flaveria* would be an excellent system to study the post-Creation origin of biochemical complexity.

RESULTS

Wise’s baraminology matrix (1992) consists of a series of questions designed to allow researchers to detect phylogenetic discontinuity. Unfortunately, many of the questions in the matrix do not apply to the Flaveriinae. For instance, there is no mention of the Flaveriinae in the

Scripture, nor could we find any reference to fossil Flaveriinae. Though the matrix cannot be used, the traditional baraminological practice of examining additive and subtractive evidence will be presented (Wise 1992; Robinson 1997; Robinson and Cavanaugh 1998a; Robinson and Cavanaugh 1998b).

Additive Evidence. Hybridization between the members of Flaveriinae is extensive. In the wild, only *F. floridana* and *F. linearis* readily hybridize (Monson 1989). The remainder of the crosses summarized in Figure 2 are the result of artificial hybridization studies conducted by Powell (1978). These hybrids are very good evidence for the assignment of monobaramin status to each of the Flaveriinae genera. Of 59 *Flaveria* interspecific crosses reported by Powell, 40 were suc-

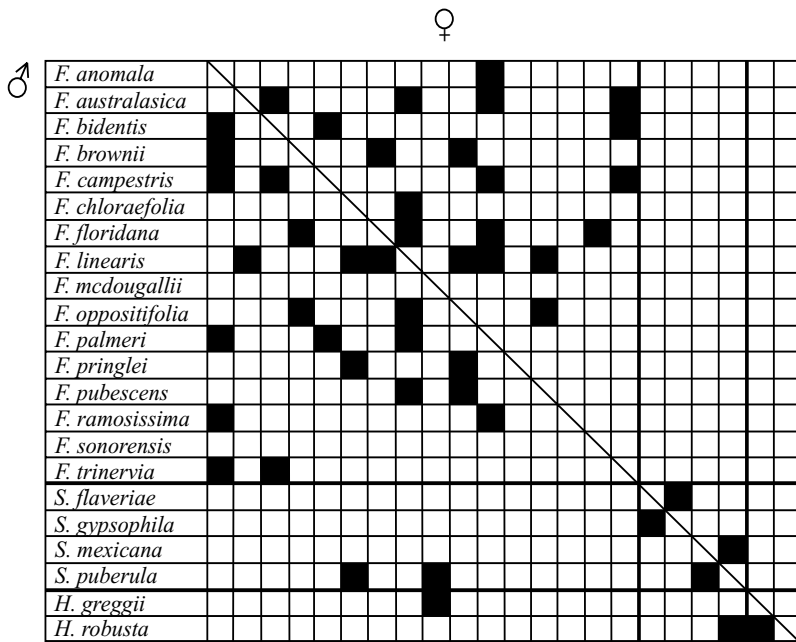


Figure 2. Known hybrids from subtribe Flaveriinae. Black squares represent known successful hybrids as described by Powell (1978). The diagonal line separates the male parent on the left from the female parent on the right. Artificial crosses of Flaveriinae species were conducted in a greenhouse. Crossability was determined by visually estimating seed-set, as described by Powell (1972). Fertility of the F_1 hybrids was not reported.

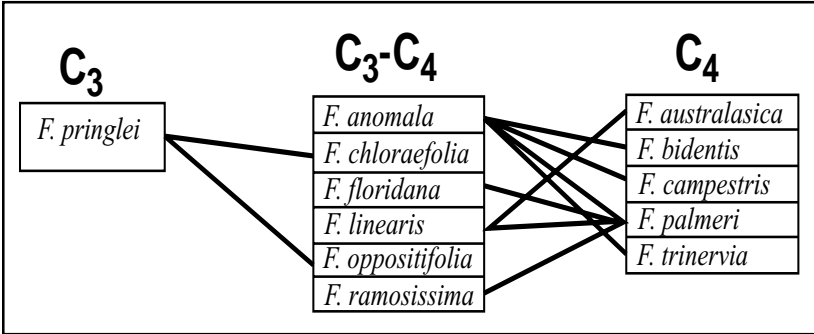


Figure 3. Successful hybridizations (represented by the dark lines connecting species names) between the photosynthetic types in *Flaveria* (based on data from Powell 1978). Connecting lines indicate successful hybridization. See Figure 2 for explanation of hybrid success.

cessful (Figure 2). Of the six possible interspecific crosses within *Sartwellia*, two were observed to be successful, and the two *Haploëthes* species were also successfully crossed. These crosses are strong indicators of the monobaraminic status of each genus of Flaveriinae.

Hybridization within genus *Flaveria* reveals a significant pattern of hybridization success versus photosynthesis type (Figure 3). At the time of Powell's experiments in the 1970s, no C_3-C_4 intermediates had been conclusively identified, although they were suspected to exist. Nevertheless, examination of the hybridization data reported by Powell indicates a clear hybridization success bias between the different photosynthesis types. No cross between a C_3 and C_4 species was directly successful, indicating that perhaps the different photosynthesis types may themselves constitute monobaramins. The monobaramin status of genus *Flaveria* is not necessarily called into question by this data, if one assumes associative hybridization in baraminic assignments (Scherer 1993). For instance, *F. pringlei* (C_3) crosses with *F. oppositifolia* (C_3-C_4) which crosses with *F. linearis* (C_3-C_4) which crosses with *F. palmeri* (C_4). Thus, gene flow between C_3 and C_4 species can be achieved.

Powell also attempted more than 30 intergeneric crosses, but only four were successful. Significantly, these four intergenetics unite the species of all three genera, including the *Flaveria* outlier from Grand Canyon, *F. mcdougallii*, which hybridizes with no other *Flaveria* species. Again, by assuming associative hybridization, gene flow can be

1996). Although this is a limited sample of the entire subtribe, it is sufficient to further establish the cobaraminic status of the C₃, C₄, and C₃-C₄ species. Of all the sequences, none are less than 93.2% identical. Most telling in this regard is the correlation of sequence similarity and hybridization potential (Figure 4). Three species (*F. anomala*, *F. floridana*, and *F. linearis*) can successfully hybridize with species that possess the most dissimilar sequences. Powell also noted that several *Flaveria* species have the ability to hybridize with very divergent *Flaveria* species, which he attributes to stronger reproductive barriers present in annual species than in perennial species (1978); of 40 successful interspecific crosses of *Flaveria*, only 5 are between an annual and perennial species. Further sequence analysis is necessary, particularly from specimens of *Sartwellia* and *Haploësthes*, before a full-sequence characterization of the Flaveriinae monobaramin can be made. Nevertheless, this sequence similarity certainly constitutes further additive evidence that the C₃, C₄, and C₃-C₄ *Flaveria* species are cobaraminic.

Subtractive Evidence. Unfortunately, subtractive evidence in the literature regarding subtribe Flaveriinae is scarce. No artificial hybridizations between a Flaveriinae species and a member of a separate subtribe have been reported; thus, the failure of hybridization gives no insights into reproductive isolation of the subtribe. Although the Flaveriinae possess 18 chromosomes universally, the predominant chromosome number for the tribe Helenieae is n=19, with other members of Flaveriinae *sensu lato* possessing 16 or 19 chromosomes (Lundberg 1996). The difference may be due to simple Robertsonian rearrangements, and in light of chromosomal rearrangements in mammals (Gibson 1984, 1986) and *Arabidopsis* chromosomes (Lin et al. 1999), it is unlikely that chromosome number will ever be a strong subtractive evidence. A phylogenetic analysis of Flaveriinae *sensu lato* has been conducted by Lundberg (1996). He found 12 equally parsimonious trees, all of which show a consistent clustering of the three genera *Flaveria*, *Sartwellia*, and *Haploësthes* apart from the other genera of Flaveriinae *sensu lato*. From the perspective of additive evidence, this is good reason to assign Flaveriinae the status of monobaramin, but Lundberg's dataset provides very poor subtractive evidence (see below).

No *gcsH* sequences from other members of tribe Helenieae are available for comparison to the known *Flaveria* sequences; however, a

comprehensive analysis of the entire Asteraceae family has been done using the chloroplast gene NADH dehydrogenase (*ndhF*) (Kim and Jansen 1995). Included in this phylogeny were two members of Flaveriinae *sensu lato*, *Jaumea carnosa* and *Flaveria ramosissima*, and a species from subtribe Pectidinae (*Tagetes erecta*) of the same genus as outgroup species used by Lundberg (1996). The *ndhF* phylogeny consistently shows *F. ramosissima* more closely related to *T. erecta* than to *J. carnosa* (82% bootstrap value) (Kim and Jansen 1995). In contrast, the morphological analysis of Lundberg showed the genus *Jaumea* more closely related to *Flaveria* than either are to *Tagetes* (Lundberg 1996). Thus, the subtractive evidence for apobaraminic status of Flaveriinae is ambiguous at best.

Analysis of Pattern. Cavanaugh devised the ANOPA method specifically to resolve problems associated with reducing the multidimensional variation in morphological data to only a few dimensions without loss of data (Cavanaugh and Stemberg, in prep). A detailed discussion of ANOPA is beyond the scope of this paper, but a brief description of the method follows (for more details, consult Cavanaugh and Stemberg, in prep). In 1D ANOPA, a morphological centroid is calculated from the means of all numerically encoded characters. Next, distances (termed a_0) from each taxon to the centroid are measured. In 2D ANOPA, an additional outgroup centroid is selected which is most distant from the initial centroid, and a “hyperline” is drawn between the two centroids [a hyperline is a one-dimensional line in multidimensional (>3D) space]. The hyperline serves as a line of reference to measure the distances t_0 (along the hyperline) and d_2 (from the hyperline) for each taxon. These multidimensional distances allow clustering patterns to be detected, including significantly similar species and significantly different species clusters. ANOPA is similar to discriminant analysis and principle components analysis in its ability to simplify highly complex, multidimensional datasets. Unlike discriminant analysis, ANOPA does not require any *a priori* categorization of the data points. ANOPA is also capable of recovering more information regarding the higher order pattern geometry without the loss of information as is incurred in PCA analysis. Of most significance to baraminologists is the fact that additive and subtractive evidence can be evaluated together in a single ANOPA analysis.

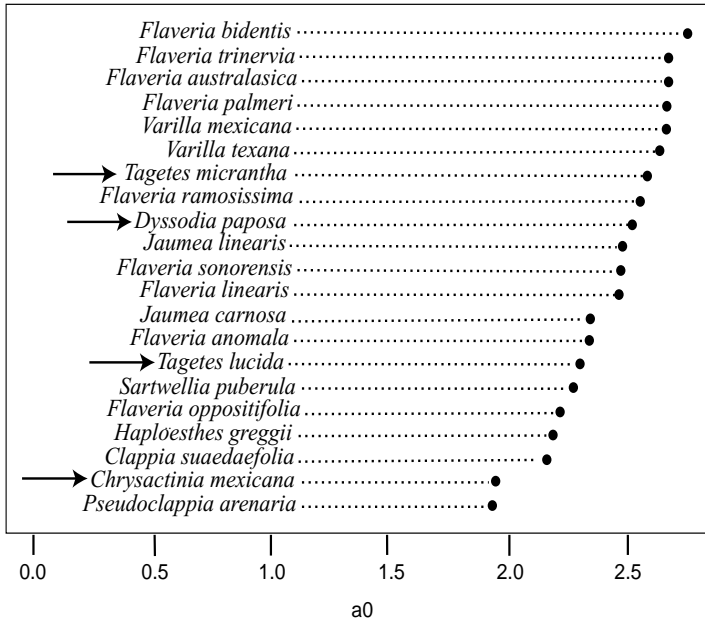


Figure 5. 1D ANOPA results for Flaveriinae and Pectidinae from the morphological data of Lundberg (1996). Outgroup species of Pectidinae are indicated with horizontal arrows. See results for explanation of axes.

To apply ANOPA to the Flaveriinae, we used Lundberg’s morphological data (1996). In addition to the *sensu stricto* Flaveriinae species discussed in this paper, Lundberg also included species from each genus of Flaveriinae *sensu lato* and four outgroup species from subtribe Pectidinae. The 1D ANOPA results (Figure 5) show no significant gaps between any of the species, including the Pectidinae. The 2D ANOPA results are very similar (Figure 6), with a slight gap between the C₄ *Flaveria* species and the rest. Most significantly, the outgroup Pectidinae are intermingled with the members of Flaveriinae *sensu lato*, and *Jaumea carnosa* is very close to *Sartwellia puberula*. Based on these results, we would conclude that all of these species form a homogeneous cluster.

The baraminological interpretation of the ANOPA results is far from clear. Whereas the additive evidence strongly supports the monobaraminic status of Flaveriinae, the ANOPA results do not support apobaraminic status of the same group of species. This would suggest that

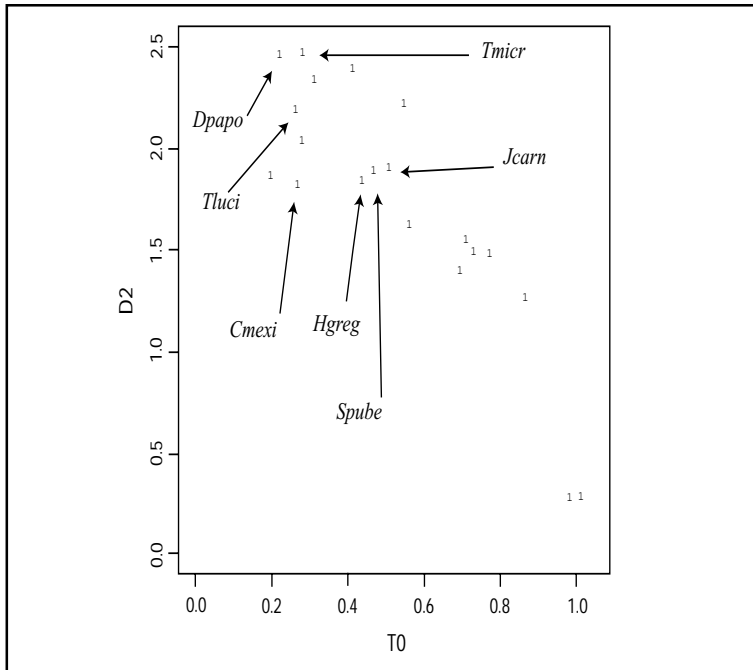


Figure 6. 2D ANOPA results for Flaveriinae and Pectidinae from the morphological data of Lundberg (1996). Species indicated are as follows: *Dyssodia paposa* (Pectidinae, *Dpapo*), *Tagetes micrantha* (Pectidinae, *Tmicr*), *Tagetes lucida* (Pectidinae, *Tluci*), *Chrystactinia mexicana* (Pectidinae, *Cmexi*), *Haploësthes greggi* (Flaveriinae, *Hgreg*), *Sartwellia puberula* (Flaveriinae, *Spube*), and *Jaumea carnosa* (Flaveriinae *sensu lato*, *Jcarn*). See results for explanation of axes.

Flaveriinae is probably a member of a larger holobaramin that includes at least the species of Flaveriinae *sensu lato*, and probably the species of Pectidinae as well. This would be consistent with the *ndhF* phylogeny that showed a close relationship between *F. ramosissima* and *T. erecta*. Unfortunately, the ANOPA results show no significant gaps between any of the species tested, thus it is not possible to establish the boundary of the apobaramin of which Flaveriinae is a part.

Summary. Although the additive evidence seems to support the monobaraminic status of Flaveriinae, as well as the monobaraminic status of *Flaveria*, *Sartwellia*, and *Haploësthes* individually, the subtractive

evidence is far more ambiguous. Further research is necessary to clarify the apobaraminic status of Helenieae and Flaveriinae *sensu lato*, before an identification of the extant holobaramin can be made.

DISCUSSION

We initiated this study to address two questions: First, can the holobaramin be approximated as the family for nonvertebrates? Second, have C_3 , C_4 , and C_3 - C_4 plant species descended from a common ancestor, thus implying the post-Creation emergence of biological complexity?

From our present analysis, we were unable to answer the first question definitively. We could not define any clear apobaraminic unit to which Flaveriinae belongs, allowing for the possibility that the entire family Asteraceae is a holobaramin. One observation in favor of this interpretation is the fossil record of the family Asteraceae. The family does not appear in the fossil record until the Oligocene and diversifies substantially by the Miocene (Bremer 1994, DeVore 2000). This Cenozoic appearance and diversification is similar to other post-Flood vertebrate baramins (Wise 1994, Wise 1995, Garner 1998, Wise 1999).

The second question regarding the origin of C_4 photosynthesis has been answered quite clearly. All of our evidence supports the view that all species of the *Flaveria* genus are members of a single monobaramin and therefore share a common ancestor. Since C_3 photosynthesis is the predominant type of photosynthesis for species of Flaveriinae and Flaveriinae *sensu lato* (Lundberg 1996), the most parsimonious interpretation is that the C_4 species have developed from C_3 ancestors. Based on this conclusion, the C_4 photosynthetic pathway is a biochemical pathway that has emerged in *Flaveria* after Creation and quite possibly post-Flood (considering the fossil record of the Asteraceae mentioned above).

Although the sequence data are insufficient to aid in identifying the apobaramin to which the Flaveriinae belong, the sequences can assist in understanding the monobaraminic divisions within *Flaveria* itself and the evolution of *Flaveria* species. A phylogeny of the genus *Flaveria* rooted by a homologous sequence from *Pisum sativum* (the garden pea) is shown in Figure 7. The phylogeny shows three distinct groups of *Flaveria* sequences, corresponding to the C_4 , C_3 , and C_3 - C_4 species groups. The phylogeny also shows that the C_3 - C_4 group branches between the C_3 and C_4 groups, and this may be explained by one of two hypotheses. First, the occurrence of C_4 and C_3 - C_4 intermediates group

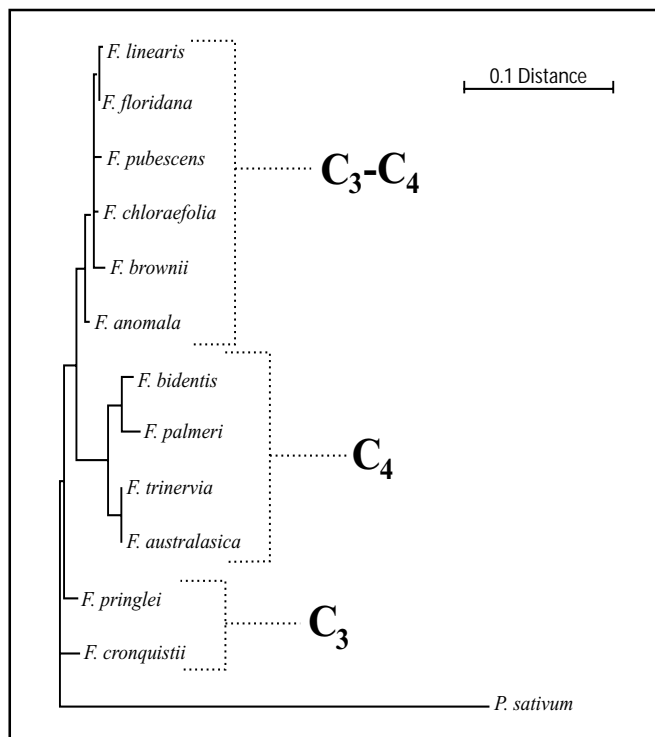


Figure 7. Fitch-Margoliash phylogeny of *gcsH* sequences from *Flaveria* and *Pisum*.

on two different branches implies that the modern C₃-C₄ species are not true evolutionary intermediates between the modern C₃ and C₄ species but that extant C₃-C₄ intermediates are the living descendants of a true evolutionary intermediate population. Alternatively, one may also conclude that C₄-like adaptations have arisen twice in the *Flaveria*, one producing the complete C₄ syndrome and one producing only a partial C₄ syndrome. To distinguish these explanations, we turn to the geography of the new world species of *Flaveria*. The distribution of the three photosynthetic types of *Flaveria* supports the hypothesis that the C₃-C₄ species are the descendants of the true evolutionary intermediates between the C₃ and C₄ *Flaveria* species. The C₃ *Flaveria* species and all species of *Haploësthes* and *Sartwellia* are restricted in range to Mexico and Texas, implying that the geographic origin of monobaramin

Flaveriinae is in this region. The C_3 - C_4 species of *Flaveria* are found in a restricted geographic band north of the C_3 species (Figure 8). Further north still, the C_4 species appear, from which they can then spread to a much broader range (Figure 8), including South America and the Australian *F. australasica*. It is likely that the C_3 - C_4 intermediates are occupying a limited range because of their physiology, while the C_4 plants are able to spread out much more readily because of their decreased photorespiration. Thus, when interpreted together, the molecular, morphological, biochemical, and geographic data all point to the evolutionary intermediacy of the ancestors of the modern C_3 - C_4 species.

Because the modern C_4 *Flaveria* species descended from ancestral species that were C_3 , the C_4 photosynthetic pathway must have arisen

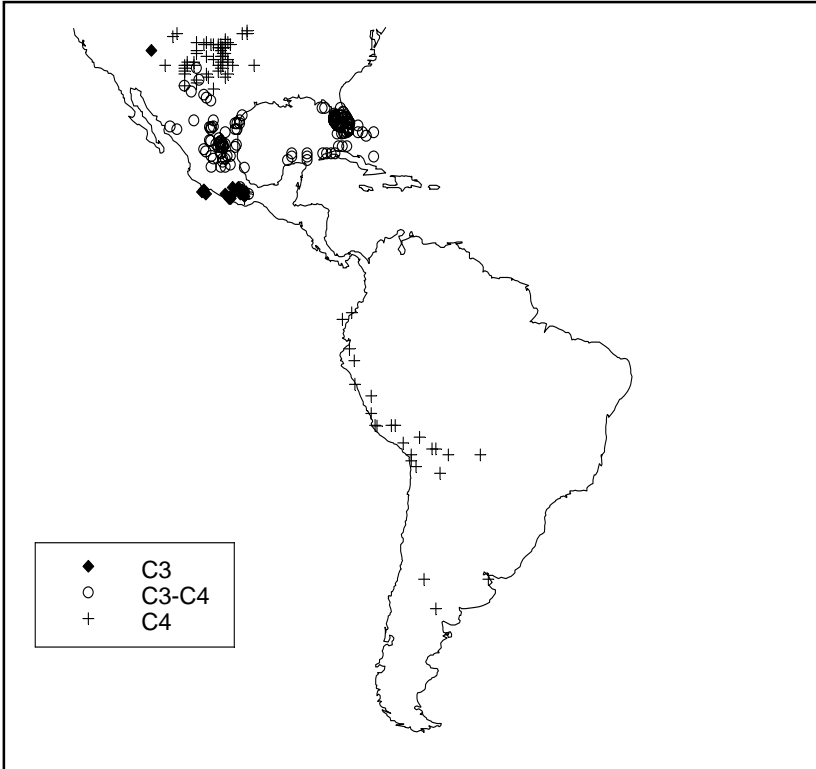


Figure 8. Geographic distribution of new world *Flaveria* species (Data obtained from Powell 1978).

after the creation of this holobaramin. Thus, one explanation for the origin of C_4 photosynthesis can be eliminated: direct creation by God. Superficially, the conclusion that C_4 photosynthesis has arisen since creation seems to deny the basic creationist belief that no increase in biological complexity has occurred, that all evolution has been degenerative (Nelson 1967, Morris 1974, Williams 1976, Davis and Kenyon 1993, Sarfati 1997, Sarfati 1999). Eliminating direct creation does not, however, leave gradualistic, accidental evolution as the only alternative explanation. The emergence of C_4 photosynthesis fits well with Wise's notion of diversification, a period of rapid speciation immediately following the Flood, which resulted in drastic changes within many holobaramins (Wise 1994, 1996). Recently, Wood has proposed a genetic model called the AGEing process that is capable of explaining numerous features of rapid post-Flood diversification (Wood, in prep). According to this model, intrabaraminic diversification occurs as a result of specially designed mobile DNA sequences called Altruistic Genetic Elements (AGEs). Hypothetically, AGEs are capable of activating or inactivating genetic potential already present in an organism's genome (Wood, in prep). Thus, C_4 photosynthesis could be designed without being directly created in its complete form. God could have made the genes necessary for C_4 photosynthesis in a latent state and allowed them to become activated at a later date by AGEs. The AGE-induced activation of latent genetic material explains the origin of C_4 photosynthesis better than evolution for the following reasons:

- 1) C_4 photosynthesis is a complex characteristic resulting from the interaction of three levels of biological organization: tissue anatomy, cell structure, and biochemistry. All C_4 plants possess specialized cells (BSC) in their leaves that house high concentrations of relevant organelles (Edwards and Walker 1983). Compartmentation also extends to important enzymes in the C_4 pathway, especially rubisco. This coordinated evolution is difficult to explain with a simple mutation/selection scenario; however, if the information necessary to produce each of these traits was already present in the genomes of the holobaramin, AGEs could easily activate it during the post-Flood diversification.
- 2) The previous reason would have much less force if it were not for the fact that C_4 photosynthesis is not limited to a single holo-

baramin. C_4 photosynthesis occurs in 16 different flowering plant families, two of which are monocots (Poaceae and Cyperaceae). While it is possible to imagine an evolutionary explanation of C_4 photosynthesis once, it is very difficult to explain the parallel evolution of very similar traits at least 16 different times. Further, the grass family Poaceae appears to have developed C_4 photosynthesis at least three times. All three types of C_4 photosynthesis (NADP-ME, NAD-ME, and PEP-CK), each of which display different physical arrangements of chloroplasts in the BSC (Edwards and Walker 1983), are found among the grass species. The AGEing process can explain this type of parallelism both within and between baramins by either true transposition of genetic material or by activation of originally created genetic material common to both holobaramins (Wood, in prep).

- 3) The fossil record of C_4 plants consists of several grass specimens from the Pliocene/Upper Miocene (Thomasson et al. 1986, Nambudiri et al. 1978), but $^{13}C/^{12}C$ ratios in fossil herbivores indicate the presence of C_4 grasses in the mid-Miocene (Morgan et al. 1994). A decrease in atmospheric CO_2 levels in the Upper Miocene is often cited as the selectional pressure responsible for the radiation of the C_4 grasses; however, if the C_4 grasses are already present during the deposition of the mid-Miocene sediments, the Miocene drop in CO_2 cannot have driven the initial emergence of the C_4 pathway in the grasses (Morgan et al. 1994). Thus, the CO_2 decrease merely serves to diversify a pathway that was already present in the grass population. The AGEing process predicts this type of phenotypic evolution prior to environmental selection for the AGE-induced trait (Wood, in prep).

If AGEing is indeed responsible for the expression of latent C_4 -specific genetic material in *Flaveria*, the various C_3 - C_4 intermediates would represent species that have not yet had the full suite of C_4 genes activated. Considering the potential for three apparently discrete levels of C_4 -like plants (anatomically C_4 , biochemically intermediate, and completely C_4), this would imply a minimum of three different genetic changes necessary for the C_4 trait to be fully expressed. Support for this theory is found in the genetics of C_4 photosynthesis (Sheen 1999). In particular,

C₄-specific genes are known to occur in C₃ species of *Flaveria* (Lipka et al. 1994). The primary differences between C₄-specific genes in C₃ and C₄ plants is the promoter region which controls the expression of the gene (Sheen 1999). Further research into the physiology of C₄ plants will no doubt shed new light on the source of these promoter differences in C₃ and C₄ species.

Regardless of mechanistic explanations, the presence of two very different kinds of photosynthesis in the same holobaramin highlights the elegant design that is so prevalent in the living world. Not only did God create organisms with what they needed at that time; He also provided an abundance of characteristics, which may or may not be immediately apparent, that would be necessary for survival in a world damaged by sin and ravaged by a worldwide Flood. From our narrow, utilitarian viewpoint, we may label a structure 'vestigial' or a strand of DNA 'junk,' but given the proper circumstances, these useless features may prove their value after all. The notion of AGE-activated latent genetic material could become a powerful explanation of apparently useless features of living organisms as simply the unexpressed abundance of a benevolent Creator.

ACKNOWLEDGMENTS

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METHODS

ANOPA. The cladistic data matrix of Lundberg (1996) was used for ANOPA analysis. Because ANOPA requires all data to be coded numerically, unknown character states were recoded as 0's with subsequent states increased by 1. Thus, a character state in Lundberg coded as ?, 0, and 1 is here recoded as 0, 1, and 2, respectively. A complete matrix of the transformed data is available from the authors on request. ANOPA was performed using standard methodology as described by Cavanaugh and Sternberg (in prep).

Molecular Phylogenetics. The sequence phylogeny was constructed from *gcsH* sequences obtained from GenBank (<http://www.ncbi.nlm.nih.gov>) for the following species: *F. anomala* (Z37524), *F. bidentis* (Z37517), *F. chlorae-*

folia (Z37520), *F. cronquistii* sequence A from Kopriva et al. (1996) (Z25854), *F. floridana* (Z37528), *F. linearis* (Z37521), *F. palmeri* (Z37529), *F. pringlei* sequence A from Kopriva et al (1996) (Z25855), *F. pubescens* (Z37530), *F. trinervia* (Z37523), and *Pisum sativum* (J05164). We omitted loci Band C from the C₃ plants for simplicity and because the source of the *F. pringlei* gcsHB is questionable (see discussion in Kopriva et al. 1996). Sequences were aligned with CLUSTALW v. 1.75 (Thompson et al. 1994) using default parameters. After trimming end-gaps, the final alignment consisted of 359 positions. Distances were inferred using the DNADIST program of the PHYLIP package (Felsenstein 1993). The phylogeny was constructed using the Fitch-Margoliash method (Fitch and Margoliash 1967) as implemented in the FITCH program of the PHYLIP package.

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ANNOTATIONS FROM THE LITERATURE

BEHAVIOR: DOMESTICATION OF THE FOX

Trut LN. 1999. Early canid domestication: the farm-fox experiment. *American Scientist* 87:160-169.

Summary. In 1959, the Russian geneticist Dmitry K. Belyaev began studying the behavior of captive foxes at a fur farm. Interested in the process of domestication, he experimentally selected foxes on the basis of their reaction to humans. Individual foxes that responded with fear were removed from the experiment, while those without fear were retained. Although Belyaev died in 1985, others have continued his experiment. Considerable variation has been noted, e.g., size, color, hair texture, floppy ears and curly tail. By the 6th generation, some foxes displayed behavior resembling domestic dogs — whimpering to attract attention and licking their keepers. This domesticated behavior increased to 1 pup in 6 by the 10th generation, and to 3 pups in 4 by about the 30th generation. These changes have been accompanied by a reduction in secretion of adrenal hormones, a reduction in basal levels of blood plasma corticosteroids, and an increase in serotonin levels. Other changes have occurred in morphology and reproductive behavior. In addition to foxes, the research group has also successfully domesticated river otters and Norway rats from wild-caught ancestors.

Comment. This experiment indicates that aggressive behavior has a genetic basis, and can be reduced rapidly through selection. This suggests that aggressive behavior might also become established rapidly if a world of peaceful coexistence became dominated by competition.

BIOGEOGRAPHY: DISAPPEARING DISJUNCTION

Wen J. 1999. Evolution of Eastern Asian and Eastern North American disjunct distributions in flowering plants. *Annual Review of Ecology and Systematics* 30:421-455.

Summary. Biogeographers have noted for many years that similar plants occur in eastern Asia and eastern North America, separated by

a distributional gap. About 65 genera of seed plants have disjunct distributions between eastern North America and eastern Asia. Explanations for these disjunctions, such as long-distance dispersal, have been based on the assumption that the similar species were each other's closest relatives. Molecular studies contradict this assumption and indicate that plants in eastern North America are generally more closely related to morphologically different plants in western North America than to morphologically similar plants in eastern Asia. The proposed explanation is that the disjunctions are due to multiple factors, including convergence, vicariance, and differential extinction. Molecular-clock studies suggest that the disjunctions studied originated mostly in the Miocene.

Comment. Disjunct distributions are one of the most interesting problems for biogeography to explain, and the large number of disjuncts in eastern Asia and eastern North America have elicited considerable discussion. Now we learn that the disjunctions may not be real. This illustrates the importance of a reliable taxonomy, and the difficulty in achieving it.

CHROMOSOMAL EVOLUTION: TETRAPLOID MAMMAL

Gallardo MH, Bickham JW, Honeycutt RL, Ojeda RA, Kohler N. 1999. Discovery of tetraploidy in a mammal. *Nature* 401:341.

Summary. The red viscacha rat, *Tympanoctomys barrerae*, is a member of the family Octodontidae, endemic to South America. The genome of *T. barrerae* has twice the amount of DNA found in its closest relatives. The number of chromosome pairs is 51, compared with 28 in the other species. The most reasonable explanation is that the red viscacha rat is tetraploid, but that some of the chromosomes have been lost. These appear to include the Y chromosome and one pair of chromosomes identifiable due to a secondary constriction.

Comment. This is the first report of a tetraploid mammal, and must represent a rare situation. It has been thought that tetraploidy might be lethal in mammals, but this discovery suggests that mammals may be subject to similar karyotypic processes as other vertebrates.

GENETICS: GENE DUPLICATION WITHOUT PSEUDOGENES

Cronn RC, Small RL, Wendel JF. 1999. Duplicated genes evolve independently after polyploid formation in cotton. *Proceedings of the National Academy of Sciences (USA)* 96:14406-14411.

Summary. Current evolutionary theory predicts that new genes may arise when genes are duplicated, producing extra gene copies that are free to mutate and evolve new functions. Alternatively, the extra gene copies may degenerate into functionless pseudogenes. A third possibility is that each of the gene copies may continue to function as before the duplication event. The relative frequency of these various fates is unknown. Polyploidy produces extra copies of every gene in the genome. Polyploids may form when two slightly different species hybridize. This has happened in cotton, and the ancestral species have been identified. Sixteen genes were studied in the polyploid cotton and its ancestral species. In nearly all the comparisons, the duplicated copies continued their original function. Although the gene sequences had diverged, there was no evidence that the rate of divergence was affected by the presence of duplicated gene copies. A high rate of divergence has been previously reported among duplicated highly repetitive DNA sequences, but there are no such reports from duplicated nuclear genes.

Comment. These results do not support the theory that gene duplication accelerates the process of pseudogene formation and evolution of new gene functions. Further studies are needed to see how widely these results apply.

GENETICS: INBRED VIGOR?

Visscher PM, Smith D, Hall SJG, Williams JA. 2001. A viable herd of genetically uniform cattle. *Nature* 409:303.

Summary. Inbreeding is generally considered harmful, due to accumulation of deleterious alleles. However, if inbreeding were combined with selection, deleterious alleles might be purged. Support for this idea comes from the Chillingham cattle, a feral herd of some 49 individuals living in a park in northern England. This herd is thought to have been isolated for at least 300 years, and is almost genetically uniform. The Chillingham cattle might provide a model for study of the bovine genome and the genetics of disease resistance.

Comment. This example suggests that inbreeding would not be harmful in a world without deleterious mutations. Small population sizes, such as after the creation or after the Biblical flood, would not necessarily cause genetic deterioration leading to extinction.

GENETICS: WHAT CAUSES PSEUDOGENES?

Satoh H, Inokuchi N, Nagae Y, Okazaki T. 1999. Organization, structure, and evolution of the nonadult rat beta-globin gene cluster. *Journal of Molecular Evolution* 49:122-129.

Summary. The beta-globin gene family has been characterized for both mouse and rabbit, but only incompletely for the rat. This study completes the description of the rat gene cluster by adding the embryonic globin gene sequences. The rat has three beta-globin genes expressed embryonically, in addition to the single adult gene. Two pseudogenes [non-functional degenerate genes] separate the embryonically expressed beta globin genes from the adult expressed gene. The mouse has essentially the same gene arrangement. Comparing the embryonic rat and mouse globin gene sequences shows that the functional rat genes are more similar to the corresponding mouse genes than to each other. In contrast, the rat psi-gamma-3 and mouse beta-h2 pseudogenes are more similar to functional genes of the respective species than to each other.

Comment. Similar gene arrangements are typically interpreted as inherited from a common ancestor. Similar location of pseudogenes in rat and mouse suggest possible inheritance from a common ancestor. On the other hand, the greater similarity of the rat pseudogene to the functional rat gene than to the mouse pseudogene suggests possible separate origins for the rat and mouse pseudogenes. More information is needed to clarify this situation.

Similar pseudogenes in humans and chimps have been argued as conclusive evidence for their common ancestry. The location of one or more pseudogenes between the embryonic and adult globin genes is a common feature of humans, chimps, rat, mouse, and rabbit. Could this be due to a common process of degeneration? Could it indicate a function in switching gene activity from embryonic globin forms to adult forms? These questions remain unsolved, and pseudogenes continue to present an interesting problem needing more study.

GEOLOGY: MISSOULA FLOODS OR FLOOD?

Shaw J, Munro-Stasiuk M, Sawyer B, Beaney C, Lesemann J-E, Musacchio A, Rains B, Young RR. 1999. The Channeled Scabland: back to Bretz? *Geology* 27:605-608.

Summary. The Channeled Scabland of Washington was originally described by Bretz as due to a catastrophic flood flowing from glacial Lake Missoula across the Columbia River Basalts to the Pacific Ocean. More recently, a series of floods has been proposed, extending over several centuries. This paper presents evidence indicating that there may have been only one flood, or a few, but that the water came from more than one source. Outflow from subglacial reservoirs of the Cordilleran Ice Sheet may have added to water from glacial Lake Missoula, providing sufficient water to cause the Channeled Scablands in a single flood.

Comment. The debate over the history of the Channeled Scablands provides an instructive example of the nature of science and the role of presuppositions in shaping scientific consensus. This paper adds one more chapter to the story.

MOLECULAR EVOLUTION: CAN EVOLVING PROTEINS RETAIN THEIR FUNCTIONALITY?

Bastolla U, Roman HE, Vendruscolo M. 1999. Neutral evolution of model proteins: diffusion in sequence space and overdispersion. *Journal of Theoretical Biology* 200:49-64.

Summary. A comparison of DNA sequences for homologous proteins shows a large peak at 8.5% sequence identity, which is within the range expected from a comparison of random sequences. The question that arises is whether proteins with such different sequences are connected by an evolutionary pathway of viable intermediates — a “neutral network.”

This question is explored with a model 36-amino acid sequence arranged in a lattice pattern. A single mutational step was taken at random, and the resulting sequence tested for whether it maintained its “phenotype,” which is analogous to its “viability” in real life. Sequences that passed the “viability test” were then mutated further. Results showed that only 6% of the sequences passed the “viability test”; 94% were rejected. Yet the small proportion of “viable” sequences

did form neutral networks in sequence space such that starting and ending points differed as much as would be expected from comparisons of random sequences. The implication is that protein function can be maintained while sequences evolve to the extent that the starting and ending sequences appear unrelated.

The model has some features that admittedly are biologically unrealistic. For example, the sequence is so short that all but two of the amino acids are on the surface of the protein. A larger number of “core” amino acids would impose greater constraints on viability of sequence changes. Other weaknesses of the model are that it considers mutations of amino acids rather than nucleotides, and does not address biological activity. However, the model does seem to provide a useful device for exploring the question.

Comment. Biologists have long been interested in the problem of viability of morphological intermediates during evolution. Less has been said about molecular intermediates, but the question is similar. The results reported by Bastolla et al. do not answer the question, but at least provide an interesting entry point into the subject. The suggestion that proteins can retain their function while undergoing major changes in amino acid sequence, if confirmed, might explain why gene duplications so rarely produce pseudogenes (see annotation on paper by Cronn et al.)

ORIGIN OF LIFE: MINIMAL COMPLEXITY

Kyrpides N, Overbeek R, Ouzounis C. 1999. Universal protein families and the functional content of the last universal common ancestor. *Journal of Molecular Evolution* 49:413-423.

Summary. Living organisms can be classified in three major groupings: eubacteria, archaea, and eukarya. Complete sequencing of the archaean, *Methanococcus jannaschii*, means that genomes of representatives of each of these groups are now available for comparison. Using the principle that shared features are ancestral, one can estimate the composition of the genome of the [hypothetical] last universal common ancestor. The number of genes shared by each of the three groupings is 324. These represent 246 unique biochemical functions. Since additional shared genes are known in other archaeans, this number represents a low estimate. This result indicates the last

universal common ancestor had a level of complexity similar to living unicellular organisms.

Comment. These conclusions have implications for origin of life theories. Scientists now have an improved basis for estimating the minimal complexity necessary in origin of life scenarios. Estimates of minimal complexity are similar to the estimate here for the “last universal common ancestor.” The degree of complexity required for even the simplest functioning cell is a strong argument for the role of intelligence in the creation of life.

PALEONTOLOGY: DINOSAUR DIVERSITY

Sereno PC. 1999. The evolution of dinosaurs. *Science* 284:2137-2147.

Summary. This paper reviews the fossil record of dinosaurs, from their first appearance in mid-Carnian (Upper Triassic) sediments to their last appearance in the Upper Cretaceous. A comprehensive, family-level phylogeny is proposed. Triassic dinosaurs are moderately diverse and include both major dinosaurian types, the Ornithischia and the Saurischia. Generic diversity waxes and wanes through the Mesozoic, reaching a maximum in the uppermost Cretaceous. Birds are linked to dinosaurs, with claims of feathered dinosaurs used in support. Dinosaurs exhibit several repeated morphological trends, e.g., increasing body size, increasing number of cervicals, increasing number of sacrals, reduction and loss of teeth, reduction of the forelimbs, etc. Dinosaurs are similar throughout the world in Triassic and Jurassic sediments, but show distinct regional differences in the Cretaceous. Biogeographic differences in dinosaur faunas seems more heavily influenced by local and regional factors than by the break-up of Pangaea into separate plates.

Comment. Dinosaurs have captured the public’s imagination, and this paper provides a valuable summary of their fossil record. Dinosaurs are notably diverse and geographically widespread at or near their first appearance in the fossil record. They have been reported from Upper Triassic sediments of North and South America, Morocco and India. Some twenty genera are known, representing ornithischians, sauropods and theropods. The failure of the dominant Mesozoic terrestrial vertebrates to exhibit phylogenetic relationships correlated with the break-up sequence of Pangaea may indicate a weakness in current interpretations of plate histories.

PALEONTOLOGY: DINOSAUR SKIN

Martill DM, Batten DJ, Loydell DK. 2000. A new specimen of the thyreophoran dinosaur cf. *Scelidosaurus* with soft tissue preservation. *Palaeontology* 43:549-559.

Summary. A fossil specimen from Great Britain with eight caudal vertebrae has been identified as a juvenile thyreophoran dinosaur. The surrounding sediments contain algal spores and bivalves that suggest the fossil came from Lower Jurassic marine sediments. Evidence of the skin is preserved, including osteoderms. Such excellent preservation of a terrestrial animal in a marine deposit is remarkable. The animal may have been washed out to sea soon after death, and sunk into the “soupy” substrate, where bacterial action contributed to mineralization of some of the skin tissue.

Comment. Taphonomy, the study of conditions of deposition and preservation of fossils, might provide important clues in improving our understanding of earth history. Data should be examined for possible trends in taphonomic conditions.

PALEONTOLOGY: FOSSIL RECORD AND PHYLOGENY

Benton MJ, Wills MA, Hitchin R. 2000. Quality of the fossil record through time. *Nature* 403:534-537.

Summary. This paper addresses the degree to which the fossil record faithfully records the history of life. It would seem obvious that older rocks are more likely to have been destroyed than younger rocks; hence, the quality of the fossil record should deteriorate as one moves downward through the geologic column. This question is tested by comparing the sequence of fossil taxa with the sequence of the branching of cladograms, where the cladograms are based on data independent of the fossil record. The results show that the degree of consistency between fossils and cladogram branching is roughly constant through the geologic column. In other words, cladograms based on Paleozoic taxa are no less consistent with the fossil record than are cladograms based on Mesozoic or Cenozoic taxa. This indicates that the fossil record, although undoubtedly incomplete, is, nevertheless, adequate for illustrating the history of diversification of living organisms.

Comment. One would expect the quality of the fossil record to increase as one moves upward through the column (the “pull of the

recent”). This paper suggests otherwise, unless the quality of the fossil record has little effect on construction of cladograms. If the quality of the fossil record is relatively uniform, the systematic pattern of morphological and genealogical gaps (fewer intermediates between higher taxa than between lower taxa) becomes all the more striking.

PALEONTOLOGY: THE INCOMPLETE RECORD

Brocks JJ, Logan GA, Buick R, Summons RE. 1999. Archean molecular fossils and the early rise of eukaryotes. *Science* 285:1033-1036. (Reaction by Knoll AH. 1999. A new molecular window on early life. *Science* 285:1025-1026.)

Summary. Archean rocks are dated as older than 2.5 billion years. There is some evidence of life in some of these rocks, but the rocks are frequently highly metamorphosed, and it has been difficult to identify the organisms. Samples of weakly metamorphosed rock from a drill core taken from northwestern Australia were analyzed and found to contain both hopanes and steranes. This extends the fossil record of biomolecules by a billion years. Hopanes are indicative of cyanobacterial activity, while steranes are derived from eukaryotes. These results indicate the presence of both bacteria and eukaryotes during deposition of these Archean sediments. They also indicate the presence of atmospheric oxygen needed for eukaryotes to produce the sterols from which the steranes were derived. These results tend to support molecular phylogenies that suggest bacteria and eukaryotes diverged long before the time suggested in the fossil record.

Comment. The presence of biomolecules unaccompanied by body fossils presents an interesting question. Why is there such a large stratigraphic gap between the biomolecules and the body fossils of the living eukaryotes that produced the molecules? Other examples of such gaps are known, although the size of the gaps is smaller. The role of depositional and taphonomic factors, including the possibility of infiltration of biomolecules into the rocks, is a topic worthy of further study.

PALEONTOLOGY: MIOCENE VERTEBRATE BURROWS

Meyer RC. 1999. Helical burrows as a palaeoclimate response. *Palaeogeography, Palaeoclimatology, Palaeoecology* 147:291-298.

Summary. Helical burrows were discovered many years ago in Miocene sediments of Nebraska. They appear to have been dug by *Palaeocastor fossor*, an extinct beaver. The burrows typically slope downward at about a 25-30 degree angle, and end in a straight, upward-sloping “living chamber” having an angle up to 43 degrees. The helical shape of the burrow is highly unusual, and it is not clear what advantage might be obtained from their peculiar shape. Calculations reported in this paper show that the helical burrows required removal of 36% to 61% more soil than would a straight burrow sloping at 43 degrees, dug to the same depth. The helical burrows do not seem to provide an advantage in closer packing of burrows within a colony, nor do they seem a good deterrent to predators. The entrance to the “living chambers” could be placed below water level to provide a refuge from predators, but the chambers lack venting. Perhaps the helical burrow shape helped conserve moisture in a dry climate. Helical burrows are also known from Permian sediments in South Africa. These burrows are thought to have been dug by *Diictodon galeops*, a therapsid. It has been suggested that the shape of the Permian burrows helped retain moisture within the living chambers. Perhaps the beaver burrows functioned in a similar way.

Comment. Burrows of terrestrial vertebrates present an interesting problem for creationists. One would not expect animals to be constructing burrows during a flood, and their presence strongly indicates that the surface was exposed to the atmosphere during the time the burrows were being constructed. This question has gotten much more attention than the question of whether the peculiar shape of these burrows might indicate some unusual environmental conditions. Perhaps future research will reveal that the answers to these two questions are related.

PALEONTOLOGY: NEANDERTHALS AND MODERN HUMANS

Krings M, Geisert H, Schmitz RW, Krainitzki H, Paabo S. 1999. DNA sequence of the mitochondrial hypervariable region II from the Neanderthal type specimen. *Proceedings of the National Academy of Sciences (USA)* 96:5581-5585.

Summary. Recovery of mitochondrial DNA sequences from a Neanderthal skeleton permits sequencing and comparison with modern human mitochondrial DNA. A previous sequence showed that Neanderthal DNA falls outside the range of variation among living humans. This second Neanderthal sequence confirms the previous report. The Neanderthal sequence is about four times as different as the range of variation among living humans. This is interpreted to mean that Neanderthals diverged from modern humans about 465,000 years ago, compared with about 150,000 years ago for the divergence of living humans. This supports the theory that Neanderthals are genetically distinct from modern humans, and became extinct without blending with modern humans.

Comment. Even if one accepts that Neanderthals did not contribute mitochondrial DNA to the living human population, this does not necessarily indicate that Neanderthals did not intermarry with anatomically modern humans. The familiar “mitochondrial Eve” hypothesis is based on the idea that all living humans can trace their ancestry back to a single female, but this in no way requires that there were no other females living at the time. Rather, only one ancestral female has a continuous line of female descendants, all other mother-daughter lineages having terminated. Thus, Neanderthals might have interbred with anatomically modern humans, but could be among the group without a continuous mother-daughter lineage extending to the present time.

PALEONTOLOGY: PERMIAN VERTEBRATE BURROWS

Groenewald GH, Welman J, MacEachern JA. 2001. Vertebrate burrow complexes from the Early Triassic Cynognathus zone (Driekoppen Formation, Beaufort Group) of the Karoo Basin, South Africa. *Palaios* 16:148-160.

Summary. Many living vertebrates dig burrows, but fossil burrows are uncommon. Several burrows of different types have been previously

identified in Permian sediments of the Beaufort Group. This paper reports a new type of burrow from Triassic sediments, also of the Beaufort Group. The burrows are branching and have terminal chambers. One burrow complex contained skeletons of 20 or more specimens of *Trirachodon*, a probably herbivorous mammal-like reptile. The cause of burial appears to be a flash flood.

Comment. These burrows are in sediments that creationists generally regard to have been deposited during the Genesis Flood. Such features seem to indicate constraints on the nature of Flood activity in South Africa during the construction of these burrows. A possible explanation might be that the area was not under water at the time, but sediment was being intermittently washed into the area from some source area. Sufficient time passed between sedimentary episodes, such as flash floods, to permit burrow construction by these animals, which were similar in size to prairie dogs.

PALEONTOLOGY: VERTEBRATES IN THE CAMBRIAN EXPLOSION

Shu D-G, Luo H-L, Conway Morris S, Zhang X-L, Hu S-X, Chen L, Han J, Zhu M, Li Y, Chen L-Z. 1999. Lower Cambrian vertebrates from south China. *Nature* 402:42-46. (Reactions: Janvier P. 1999. Catching the first fish. *Nature* 402:21-22; Zimmer C. 1999. Fossils give glimpse of old mother lamprey. *Science* 286:1064-1065.)

Summary. New fossil discoveries have confirmed the presence of vertebrates in Lower Cambrian sediments. The inch-long fossils were discovered in the area of Chengjiang, in Yunnan Province, China, an area famous for fossils in an excellent state of preservation. Two new genera of agnathan fish are described in this paper, *Myllokummia* and *Haikouichthys*. Both genera are considered more advanced than the living hagfish, but related to both the hagfish and lamprey.

Chen J-Y, Huang D-Y, Li C-W. 1999. An early Cambrian craniate-like chordate. *Nature* 402:518-522. (Reaction: Enserink M. 1999. Fossil opens window on early animal history. *Science* 286:1829.)

Summary. More than 300 specimens of a new chordate have been discovered in the Chengjiang region of Yunnan Province, China. The new find, named *Haikouella*, appears somewhat similar to *Yunnanozoon*, found in the same region in 1995, but is more vertebrate-like. The fossils were found in fine-grained silts, which preserved such

details as the heart, brain, fins, segmented muscles, and possible eyes. The fossils are up to three centimeters in length.

Comment. The sudden appearance of most animal phyla in Cambrian sediments is one of the most compelling features of the fossil record. Previous discoveries had suggested that chordates were included in the “Cambrian Explosion,” but this point has been debated. These newly discovered fossils should settle the case, not only for chordates in general, but also for vertebrates.

PHYLOGENY: DEVELOPMENTAL PROBLEMS

Lovejoy CO, Cohn MJ, White TD. 1999. Morphological analysis of the mammalian postcranium: a developmental perspective. *Proceedings of the National Academy of Sciences (USA)* 96:13247-13242.

Summary. Phylogenetic studies based on fossils have to rely on anatomical characters for which the underlying genetic basis is largely unknown. Increased resolution is often sought by subdividing characters into finer detail, without respect for whether the finer details are genetically independent. Research in vertebrate limb development has shown that patterning in the limb is determined at the cellular level, not the larger anatomical level. Thus, there probably is not a separate gene for each anatomical detail. Rather, anatomy appears to be the result of gradients of molecules that control rates of developmental processes. The authors propose that differences in traits between taxa be classified into five categories, based on the developmental genetics of the trait. This distinction could enhance phylogenetic studies by reducing the number of non-independent characters.

Comment. It has been known for a long time that increasing the level of anatomical detail may not increase phylogenetic resolution, but information has been lacking on the relationship between genes and structure. As this information becomes available, it should become easier to evaluate hypotheses of relationships among different species groups. It would be interesting to see whether this information might be useful in identifying groups with independent origins.

PHYLOGENY: DEVELOPMENTAL PROBLEMS IN HUMANS

McCollum MA. 1999. The robust Australopithecine face: a morphogenetic perspective. *Science* 284:301-305.

Summary. The robust australopithecines are considered a side branch in human evolution. Three species are grouped into a single clade, defined by a number of morphological synapomorphies, and sometimes classified in the genus *Paranthropus*. Resolution of relationships among the three species has been difficult, with the result that anatomical features have been more finely subdivided to increase the number of characters to be analyzed. However, these features may be correlated rather than independent. A model for the development of the face and skull is described in this paper, with the suggestion that the number of independent characters is actually only two, instead of the twenty that have been proposed. The three robust species show some significant morphological differences that might indicate separate ancestries for the East and South African forms.

Comment. This example illustrates the point made in the previous paper: that splitting morphological features more finely does not necessarily improve the accuracy of evolutionary relationships.

PHYLOGENY: GALAPAGOS TORTOISES

Caccone A, Gibbs JP, Ketmaier V, Suatoni E, Powell JR. 1999. Origin and evolutionary relationships of giant Galapagos tortoises. *Proceedings of the National Academy of Sciences (USA)* 96:13223-13228.

Summary. Darwin was much interested in the giant Galapagos tortoises, *Geochelone nigra*, when he visited the islands on his famous trip. However, their closest relative has not been determined. Based on mitochondrial DNA sequences, the closest living relative is the chaco tortoise, *G. chilensis*. Somewhat surprisingly, the chaco tortoise is relatively small-bodied compared to several other South American tortoises. However, fossils are known that appear plausible ancestors of the Galapagos giants. Giantism is thought to have preceded colonization of the Galapagos islands. The study may offer renewed hope for "Lonesome George," the last of the tortoises from the island of Pinta. He has failed to mate, despite numerous efforts to induce mating. Genetic analysis indicates his closest relatives are on the islands of

San Cristobal and Espanola, which are the farthest islands from Pinta. Perhaps a more suitable mate can be found on one of those islands.

Comment. It comes as no surprise to learn that size is not a reliable indicator of relationships. The unexpected geography of “Lonesome George’s” relationship reminds us not to take too much for granted, but we can all extend our best wishes to “Lonesome George” in perpetuating his race.

PHYLOGENY: THE HOATZIN IS A TURACO?

Hughes JM, Baker AJ. 1999. Phylogenetic relationships of the enigmatic hoatzin (*Opisthocomus hoazin*) resolved using mitochondrial and nuclear gene sequences. *Molecular Biology and Evolution* 16:1300-1307.

Summary. The hoatzin is a strange bird of uncertain relationships, living in South America. The young have claws at the wrist joint of their wings, used to climb among tree branches. The hoatzin has been classified with the pheasants, but recently has been proposed to be a cuckoo. Mitochondrial studies reported here indicate it is actually related to the turacos, which are otherwise restricted to tropical Africa. A hoatzin-turaco relationship has been proposed previously, but has not been generally accepted.

Comment. Identification of the hoatzin as a turaco adds another interesting biogeographical problem of a group restricted to Africa and South America. One might be tempted to explain this disjunction as due to separation of the African and South American plates, but this is an unlikely explanation. Turaco fossils are more widely distributed than are the living members of the group, and it is likely that the ancestors of the hoatzin came through North America. Extinction of the Eurasian and North American members of the group, perhaps due to climatic changes, would leave the hoatzin isolated in South America.

PHYLOGENY: IS THERE REALLY A TREE OF LIFE?

Doolittle WF. 1999. Phylogenetic classification and the universal tree. *Science* 284:2124-2128.

Doolittle WF. 1999. Lateral genomics. *Trends in Genetics* 15:M5-M8.

Summary. Phylogenetic trees based on different gene sequences often conflict in important ways. Conflict may be caused by inadequate

analyses or oversimple assumptions about rates of change, but these problems do not explain all the observed conflicts. It appears that genes have been commonly transferred from one species to another among the three great divisions of life, Archaea, Bacteria, and Eukarya. This process may be responsible for much of the confusion in attempts to trace their phylogenetic relationships. Thus, it may never be possible to portray phylogenetic relationships as a hierarchical tree with a single root. Instead, phylogenetic relationships may take the form of a net or web.

Katz LA. 1999. The tangled web: gene genealogies and the origin of eukaryotes. *American Naturalist* 154:S137-S145.

Summary. Eukaryotes are characterized by having a nucleus and a cytoskeleton. Hopes that eukaryotic DNA might have some identifying features have not been realized. Eukaryotic genes involved in information processing are more similar to archaean genes than to bacterial genes. Other types of eukaryotic genes, however, may be more similar to bacterial than to archaean genes. Still other eukaryotic genes are equivocal. The picture is emerging that eukaryotic genes might be chimeric, composed of material from different sources. Several hypotheses have been generated to explain the apparent chimerism of eukaryotic genomes. One such hypothesis is that most lateral transfers involved a few “donor” lineages that contributed genes to many recipient lineages. Other hypotheses invoke serial endosymbiosis, “you are what you eat,” or “genetic annealing.” The latter suggests an early explosion in the frequency of gene transfer, followed by a much lower rate. These hypotheses may be difficult to test, and to evaluate statistically. Better tools of analysis are needed.

Comment. The notion of lateral gene transfer is supported by evidence that seems convincing. However, the pattern of gene distribution among different organisms might be explained in part as the result of common design. It seems unsurprising that a Creator might design different species with different combinations of genes, thus providing for a variety of environmental interactions. Some of the conflicts in phylogenies might reflect separately created lineages rather than lateral gene transfer.

PHYLOGENY: LATERAL GENE TRANSFER

Jordan IK, Matyuina LV, McDonald JF. 1999. Evidence for the recent horizontal transfer of long terminal repeat retrotransposon. *Proceedings of the National Academy of Sciences (USA)* 96:12621-12625.

Summary. Mobile genetic elements are able to move within the genome of an organism, and are a leading cause of mutations. One class of mobile elements, the long terminal repeat (LTR) retrotransposons have been linked to mutations with major phenotypic effects. Movement of an LTR element is accomplished by reverse transcription of an RNA intermediate. Evidence presented in this paper indicates that LTR retrotransposons not only can move within the genome of an individual, but can also move from one species to another. An LTR element named *copia* is common in *Drosophila melanogaster*, but is patchily distributed among a distantly related species, *D. willistoni*. The best explanation is a recent cross-species transfer of this retrotransposon.

Comment. The origin and role of mobile elements are questions that potentially have far-reaching implications for understanding relationships among organisms. For example, shared patterns of inserted elements are claimed as the strongest evidence for an evolutionary relationship of whales and artiodactyls (e.g., cattle, pigs, hippos). Demonstration of cross-species transfer could weaken that claim, while evidence refuting cross-species transfer would strengthen it. Explanations of how mobile elements originated might shed light on the nature of the mechanisms involved in morphological changes since the creation.

PHYLOGENY: LIMITS TO CHANGE?

Wagner PJ. 2000. Exhaustion of morphologic character states among fossil taxa. *Evolution* 54:365-386.

Summary. This paper reports the results of efforts to determine if new character states are added continuously in evolutionary development of a lineage. If not, then character space might become saturated, and similar character states might appear repeatedly, frustrating efforts to determine evolutionary relationships on the basis of uniquely shared derived traits. Fifty-six taxa were analyzed, representing mammals, echinoderms, arthropods and mollusks. Results showed that character

space does tend to become saturated. New species tend to repeat previous character states rather than evolving new ones. This may explain why inconsistencies (homoplasies) are so common in phylogenetic studies, and also why long branches seem to tend to cluster together. Another implication is that phylogenetic studies may lack the precision needed to evaluate completeness of the fossil record.

Comment. The results reported here have important implications for constructing phylogenetic trees. On average, 75-80% of the potential character states were observed in fossils belonging to the taxa studied (ranging from genus to class). One implication is that cladograms become more unstable when living and fossil species are added together in the same study. Another is that diversification may involve different combinations of existing character states rather than addition of new character states. This is reminiscent of the creationist prediction of limits to change.

PHYLOGENY: THE SURPRISING SHARK

Rasmussen A-S, Arnason U. 1999. Phylogenetic studies of complete mitochondrial DNA molecules place cartilaginous fishes within the tree of bony fishes. *Journal of Molecular Evolution* 48:118-123.

Summary. Sharks and their allies comprise the cartilaginous fishes, which are usually regarded as the most primitive group of jawed vertebrates. Comparison of the complete mitochondrial DNA sequence of the spiny dogfish indicates it falls between the teleosts and non-teleost bony fishes on the phylogenetic tree. This implies that cartilaginous fish have lost the swimbladder and bony skeleton. In the tree, lungfish appear to be the most primitive jawed fish, and not the outgroup to amniotes (e.g., reptiles, birds, mammals). The altered phylogenetic tree changes the polarity of several traits used to analyze vertebrate relationships, and shows amniotes diverging outside the group of living fish.

Comment. Molecular phylogenies sometimes present unexpected results, but this result, if verified, is of more than ordinary interest. It is widely held that amniotes evolved from amphibians, which evolved from certain types of fish that have living relatives. This study indicates problems with the traditional scenario. In the proposed evolutionary tree, amniotes are not descended from any known group of jawed fish with living relatives. This could negate proposals that certain fossils

represent evolutionary transitions between fish and the ancestors of the amniotes, and require creation of a new evolutionary scenario for the evolution of jawed vertebrates.

SPECIATION: DEVELOPMENTAL GENES

Ting C-T, Tsaur S-C, Wu M-L, Wu C-I. 1998. A rapidly evolving homeobox at the site of a hybrid sterility gene. *Science* 282:1501-1504.

Summary. Homeobox genes are believed to have regulatory functions in development. They generally have highly similar sequences in different species. One homeobox gene, named Odysseus (*Ods*) has been found to differ significantly between two species of fruit flies, *Drosophila mauritiana* and *D. simulans*. Males resulting from crossing these two species are always sterile, and the *Ods* gene is thought to play an important role in the sterility. The gene responsible for the sterility was sequenced and compared among the two *Drosophila* species, the mouse *uncx4.1* gene, and the *unc-4* gene of the worm *Caenorhabditis elegans*. The two species of fly differ by 15 amino acids. This compares with a difference of 17 amino acids between *Drosophila* and the mouse, and only 7 amino acids between the mouse and *C. elegans*. Further comparison of the sequences of the two flies shows that the exonic sequences differ by eight times the intronic sequences. This is interpreted as due to strong selection on the gene. One potential selective force on this gene might be sexual selection for male hybrid sterility. If so, this gene may play an important role in speciation within fruit flies.

Comment. Homeobox genes are thought to be involved in switching genes on and off during development. The sequence consistency typical of homeobox genes is commonly interpreted to reflect conservation of gene function. This example of strong difference in homeobox sequence in two closely related species of *Drosophila* suggests that the relationship between homeobox genes and development is not so simple. This discovery is also important in indicating a possible molecular basis for speciation in these flies.

SPECIATION: RIFT LAKE CICHLIDS

Ruper L, Verheyen E, Meyer A. 1999. Replicated evolution of trophic specializations in an endemic cichlid fish lineage from Lake Tanganyika. *Proceedings of the National Academy of Sciences (USA)* 96:10230-10235. [See also Stiassny MLJ, Meyer A. 1999. Cichlids of the rift lakes. *Scientific American* 280(Feb):64-69.]

Summary. Lake Tanganyika has 49 endemic genera of cichlid fishes assigned to twelve different tribes, based primarily on morphological criteria such as tooth shape. One of these tribes is Eretmodini, with three genera and four species. Comparison of mitochondrial DNA sequences from these four species shows that six lineages are present rather than the four identified from morphology. Furthermore, morphologically different individuals are frequently more closely related genetically than morphologically similar individuals. It appears that similar tooth shape has evolved several times independently. Such parallel evolution has previously been reported in other cichlids.

Comment. The Rift Lake cichlids have become one of the classical examples of speciation. Studies such as this one have shown that genetically similar individuals may exhibit significant morphological variation, sufficient to be interpreted as distinct species. However, the number of alternative morphological states may be limited. In the present case, six different lineages produced only three different morphological states (interpreted as genera). It may be that the range of variation is limited within a species or group of species.

LITERATURE REVIEW

Readers are invited to submit reviews of current books or journal articles relating to origins. Please submit contributions to: ORIGINS, Geoscience Research Institute, Loma Linda University, Loma Linda, California 92350. The Institute does not distribute the publications reviewed; please contact the publisher directly.

TIME DEPENDENCY OF RADIOISOTOPE DECAY

*Reviewed by R.H. Brown
12420 Birch St., Yucaipa, CA 92399-4218*

RADIOISOTOPES AND THE AGE OF THE EARTH. Larry Vardiman, Andrew A. Snelling, and Eugene Chaffin (eds.). 2000. Santee, CA: Institute for Creation Research; and St. Joseph, MO: Creation Research Society. 676 p. Cloth, \$49.95.

This is an extraordinary book in many ways. It contains 47 pages of index, a 91-page glossary of specialized technical terms used in the book, and 56 pages of references to the professional scientific literature on the topics considered. A 66-page appendix outlines thirteen research projects for resolving critical questions raised in the text section. The topics considered in the book are treated at a high level of technical sophistication by seven specialists, each of whom has a recognized doctorate in the area of his expertise. The authors have endeavored to provide thorough and accurate presentations of the various models that have been developed in the effort to understand the radiochemical features of planet Earth's crust, together with a listing of the major associated references in the scientific literature. Highest quality printing and 73 excellent illustrations¹ contribute to a book of extraordinary value to the community of scholars. I rate Chapter 8 as essential reading for anyone who desires to understand radiohalos, and for anyone who wishes to make a presentation on radiohalos for the general public. Similarly I can designate Chapter 4 as priority reading for anyone who wishes to understand radioisotope age data.

Although the primary motivation for the preparation of this book is to foster development of compatible understanding of radioisotope data and the chronological specifications in the Bible, the book is a valuable resource for individuals who do not share this concern.

On page 215 there is an example of the hazards faced by individuals with even the best reputation for effort to maintain high scientific standards. In a discussion on the Kambalda volcanics of Western Australia, it is stated that “Although the whole suite yielded a good isochron ‘age’ of 2790 ± 30 Ma, the mafic and ultramafic samples alone gave an older best-fit ‘age’ of 2910 ± 170 Ma.” Since the range 2760-2820 is entirely enclosed within the range 2740-3080, these age determinations are actually in agreement. This statement on age difference is an exception to the general character of the book.

A more serious example of the extent to which conclusions may be influenced by an investigator’s initial bias is at the bottom of page 274: “... if there is one conclusive observation to be made, it is that the ‘ages’ derived from radioisotope systems can really only be regarded as maximum ages given the evidence of open-system behavior, mixing, inheritance, etc., ...” There are open-system processes that can reduce, as well as those that can increase a radioisotope ‘age’ characteristic. For example, heat could drive off argon, making the K-Ar ‘age’ younger than it was at the time of heating. Solution penetration could deposit potassium (or uranium), making the K-Ar (or the U-Pb) ‘age’ younger than it was at the time penetration occurred. A conviction regarding the age of the physical universe may prevent recognition of radioisotope age determinations that possibly have an unmodified relation to real time.

The reference to “dual ^{210}Po halos” in the third sentence on page 275 will cause confusion for some readers who are not acquainted with coalified-wood radiohalo phenomena. The ^{210}Po radiohalo has only one ring. The sentence would convey the author’s intent better if it read “Furthermore, the presence of both elliptical and circular ^{210}Po halos indicates that U infiltrated these strata at the time of, and soon after, deposition and rapid compaction.” This consideration is fully developed by the same author in a subsequent chapter (Chapter 8).

The data treated in RADIOISOTOPES fully indicate that Earth’s crust contains concentrations of radiogenic isotopes many orders-of-magnitude greater than could have accumulated in 6000 years at present

rates of radioactivity. The authors are organized as the RATE (Radioisotopes and the Age of The Earth) Group for investigation of the possibility that at some time(s) in the past radioisotope decay rates could have been orders-of-magnitude (possibly about five orders, which is 100,000 fold) greater than given by determinations made over the past century.

In the process of transformation (decay) the nucleus of a radioactive isotope ejects a particle that has kinetic energy inversely proportional to the half-life of its parent. For example, the three daughters of uranium that produce most polonium radiohalos, ^{214}Po , ^{218}Po , and ^{210}Po , have half-lives of 164 microseconds, 3.1 minutes, and 138.4 days, respectively; and emit alpha-particles (Helium-4 nuclei) with kinetic energy 7.69, 6.00, and 5.3 Mev, respectively. The air-equivalent distances traversed by these alpha-particles in dissipating their kinetic energy are 7.03, 4.67, and 3.87 cm, respectively.

To accommodate the observed abundances of fission-tracks and of radiohalos with postulated formation within a time-span in the order of 10,000 years, it must be presumed that radioisotope decay rates have been orders-of-magnitude greater than they are at present, without any significant difference in the energies of the particles ejected in the decay process. How can two isotopes of polonium be distinguished by related differences in their half-lives and the energies of the alpha-particles ejected in their decay, yet orders-of-magnitude changes in the half life of either of these isotopes be completely unrelated to the energy of its decay particle? This question is addressed in a theoretical chapter (Chapter 6). The author of this chapter concludes that reasonable changes may be postulated for energy relationships within the atomic nucleus that could produce orders-of-magnitude change in the decay probability (half-life) without significant change in the kinetic energy of the particles (fission products, or alpha particle) ejected in the decay. The appendix proposes research projects designed to seek for experimental confirmation of this speculation.

Exegesis that includes the entire physical universe in the creation account of Genesis 1:1 - 2:4 (see Table 1, p 338) mandates the troublesome theoretical considerations addressed in Chapter 6. Exegesis on the basis of modern concepts associated with the Hebrew terms *shamayim* (heavens) and *'eretz* (earth) comes readily. Vastly greater freedom in seeking harmony with radioisotope and astrophysical data

that has become available in the last century is obtained if exegesis is restricted to the definitions God, the Creator, gave for these crucial terms, as recorded in Genesis 1:8-10.² Elaboration of this consideration is available at: http://www.grisda.org/resources/rb_bibch.htm.

A discussion in RADIOISOTOPES regarding the initial geochemical makeup of planet Earth is conditioned by “the unequivocal Biblical statements that the Earth was in fact created before the Sun” (p 278). The highest commendation should be given to recognition of the significance inspired testimony (specifically, the Bible) has in the achievement of understanding the physical universe. There is danger of an unbalanced emphasis in the interaction between conclusions from properly conducted experimental observation and exegesis to determine the intent of inspired testimony. Only inspired testimony can convey assured knowledge concerning ultimate origins; but a study of related physical evidence (the RATE Group’s research programs, for example) may assist efforts to determine the intent of an inspired writer.

The first two chapters of Genesis have been accepted as a record of revelation received by an intermediary (probably Moses). Genesis 1: 1-2 provide an introduction to this record, and also a statement concerning the nature of planet Earth’s surface at the beginning of Creation Week. A conclusion to the basic account is given in Genesis 2:4a. The intervening verses outline what an observer on the surface of the planet would have seen step by step during the creation process. On Day 4 the “Heaven” (vs 8, KJV) created on Day 2 cleared sufficiently to make celestial objects discernable from the “Earth” (vs 10, KJV) created on Day 3. Since the Hebrew language does not have a pluperfect tense, the statement in verse 16 may be taken to specify either that the celestial objects were created by God *on* Day 4, or that the celestial objects previously created by God became discernable from the surface of planet Earth on that day. A personal judgment is required as to which interpretation best accommodates the testimony throughout the Bible, together with the accumulated astrophysical and geochemical data.

Significant inferences regarding the geological past may be drawn from helium concentration and the $^3\text{He}/^4\text{He}$ ratio in Earth’s atmosphere and crust, as discussed in Chapter 7. Individuals who are interested in helium considerations should also consult the article by R.H. Brown [1998. Unique enigmatic helium. ORIGINS 25(2):55-73; at: <http://www.grisda.org/origins/25055.htm>].

As I have already stated, this book provides a convenient survey of the radioisotope characteristics of planet Earth's crust, and ready access to their treatment in the scientific literature. I have a severe problem with the suggestion that these characteristics might be accounted for by a 100,000-fold increase in nuclear instability over a short time within the past 10,000 years. Changes in the energy relationships within atomic nuclei would be expected to occur in all matter, and not be confined merely to isotopes that are unstable at present.

Consequently, in addition to a 100,000-fold increase in the radiation and particle emission from the nuclei that are presently unstable, a corresponding release from many of the nuclei that are now stable would be expected. The cumulative increase would be many times 100,000 fold.

Organic life and the chemistry on which it is based would most likely be destroyed under such circumstances. Consequently the proposed increase in nuclear disintegration rates would be confined to the first two days of the Genesis 1 creation week (plus possibly a few hours of Day 3 before plant life was created). Therefore a postulation of higher decay rates over only the first two days is equivalent to a postulation that considers the radioisotope daughter features which presently characterize planet Earth to have been created in situ at the beginning, together with subsequent modifications of such. This alternative postulate does not involve either an increase in nuclear disintegration rates or development over long periods of time.³

ENDNOTES

1. The reader will need to consult the reference source in order to adequately understand some of the illustrations that are borrowed from the basic literature. Principal examples are Fig. 3, p 62; Fig. 8, p 81; and Fig. 10, p 164. The legends for these figures are incomplete.
2. The New International Version takes liberty to translate these terms differently in Gen. 1:1,2; 2:1,4 than in Gen. 1:8-10, imposing an interpretation that goes beyond straightforward exegesis.
The reader who wishes a broader treatment of exegetical considerations should consult "The Age of the Universe: What Are the Biblical Limits?", a 200-page book by Gorman Gray (2001. \$12 ppd. Morning Star Publications, 931 15th St., Washougal, WA 98671-1209. Telephone 1-888-667-6464).
3. If there is consideration of two creations, a primordial creation of the Solar System and a subsequent creation that fitted planet Earth with organic life, a development over long periods of time may intervene.

GENERAL SCIENCE NOTES

LOCAL CATASTROPHES, OR A WORLDWIDE DELUGE?

L. James Gibson
Geoscience Research Institute

The story of Noah and the flood has sparked intense interest and seemingly endless discussion for hundreds of years. The historical reality of a global deluge was accepted without question by most Christians until the beginning of the 19th century. Until the early 1800s, geological information was, more often than not, used as evidence of the biblical flood.

Belief in the traditional biblical account of the flood changed radically during the period from 1800 to 1850.¹ As geologists explored the sedimentary record and debated its meaning, the flood gradually became reduced from a catastrophic global deluge responsible for the stratigraphic column to a more tranquil flood responsible for only a surficial layer of “diluvium.” By about mid-century, the flood had been reduced to a local event that affected only humans. By the end of the century, it was even doubted that the flood affected all of humanity, and was restricted to the Mesopotamian Valley.²

Various factors were suggested as possible causes for a local flood. Rising sea level might have flooded the Mesopotamian Valley,³ or perhaps it was flooded by a tsunami generated by volcanic activity in the Mediterranean. Melting glaciers might have supplied water for a local flood.⁴ In an interesting repeat of history, new forms of these ideas have resurfaced recently, with some new twists.

The idea of inundation by rising sea level in the Persian Gulf has recently been revived by an international team of geologists.⁵ They attribute the rise in sea level to glacial melting, which is believed to have raised sea level more than 100 meters. As the Persian Gulf is only about 100 meters in depth, it would have been dry land during the height of the Ice Age. According to the proposal, it would have taken some 1000 years to fill the Persian Gulf, but the rising waters would have driven the inhabitants from their ancestral land and provided the basis

for stories that were handed down through the generations. It is not clear how seriously this theory will be considered. The gradual rise of sea level seems difficult to reconcile with the catastrophic event described in Genesis.

Another flood theory has been suggested by Glen Morton.⁶ Morton proposes that the biblical flood occurred when the Mediterranean basin was catastrophically filled during the Pliocene, some five million years ago. According to the Mediterranean flood theory,⁷ the Miocene collision of Africa and Europe sealed off the Mediterranean basin. The basin eventually dried up, leaving a deposit of salt on the basin floor. Then, at the beginning of the Pliocene, the dam broke, and Atlantic Ocean water poured through the strait at Gibraltar, cutting through the dam, and filling the Mediterranean in a hundred years or so. Morton's proposal is that the Mediterranean basin was populated by primitive humans in the form of erectines, or possibly australopithecines, and this accounts for the story told in Genesis. It is doubtful that this theory will become accepted, since australopithecines are not generally regarded as humans, and there is no evidence for the presence of either erectines or australopithecines in the area at the beginning of the Pliocene.

A more widely known flood theory was published in 1998 by William Ryan and Walter Pitman.⁸ Their theory is similar to that of Morton, except for the location and the timing. In their theory, the catastrophic filling occurs in the Black Sea, and occurred over seven thousand years ago. Because Ryan and Pitman have attracted considerable interest in their theory, presented in a video and a book written in a popular-style narrative, a more detailed review of their arguments follows.

In their book, Ryan and Pitman survey the history of flood exploration, beginning with the deciphering of cuneiform writing and ending with attempts to link the biblical flood to Woolley's discovery of a clay layer in the city of Ur.

The authors then lay out their own theory of a rapid inundation of the Black Sea basin when sea level breached the natural barrier separating the Black Sea basin from the Aegean Sea. They present evidence that the Black Sea was once a freshwater lake, much smaller than the present Sea. The argument is built from data collected from underwater currents, seafloor sediments, fossils, and paleomagnetism. Their conclusion is that about 7600 radiocarbon years ago, the lake was rapidly inundated with sea water, cutting a channel through the former barrier, and raising the level of the lake to that of the global ocean.

Archeological evidence, cultural legends, and considerable speculation is invoked to support a story of destruction of a lake-shore farming community due to sudden flooding of the Black Sea basin. The former residents migrated away from the Black Sea, scattering throughout Europe and southwestern Asia. Finally, the authors review the story they have created and compare it with ancient Mesopotamian flood legends.

I was struck by the story-telling ability of the authors – their book reads more like a novel than a scientific report. The personal stories of the authors add to the captivating writing style. The basic story line seems plausible. The Black Sea basin once held a freshwater lake, isolated from the sea by a narrow land barrier. The barrier was breached by the sea, presumably by rising sea level. Inflowing sea water cut through the barrier, creating the present connection between the Black Sea and the Mediterranean, and converting the lake into a brackish sea. This flood might well have made a lasting impression on any human inhabitants of the region. However, it is a long stretch to identify this event with the biblical flood.

Several features of this and other alternative flood scenarios are in conflict with the biblical flood description. Most obviously, the biblical flood ended, while the Persian Gulf, Mediterranean basin, and Black Sea basin each remain flooded. The biblical flood left no refuge for escape, and so killed all but eight of the human race. The other proposed flood locations are virtually surrounded by potential refuges, and the proposed floods would have killed at most a small proportion of the human population. The biblical ark landed in the mountains of Ararat, which is geographically distant from the Black Sea or the Mediterranean Sea. In the biblical story, the human population was given advance warning of the impending flood. An ark would be unnecessary to escape a local flood, since the population could simply migrate to a new area.

It seems clear that catastrophic floods have occurred on a scale not seen in modern history,⁹ and their stories are interesting and informative. However, these local floods do not explain important features of the biblical flood.

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