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Occasional Papers of the BSG

FRONTIERS IN CREATION RESEARCH

PROCEEDINGS OF THE SEVENTH BSG CONFERENCE

Roger W. Sanders
Executive Editor

Occasional Papers of the BSG

About the BSG: Founded in 1996, BSG: A Creation Biology Study Group is a society of researchers and scholars. The mission of the BSG is to develop and nurture a community of dedicated researchers committed to understanding the life sciences from a young-age creationist perspective through meetings and publications. Membership is open to any who share these goals. For more information, visit the official BSG website, http://www.creationbiology.org, or email secretary@creationbiology.org.

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OPBSG publishes peer-reviewed, original research or review papers of relevance to creationist biology. Acceptable topics include anything related to creationist biology, including philosophy, theology, and biblical studies. *OPBSG* is committed to constructive scientific research in creation biology; manuscripts that are primarily critiques of evolution will be referred to a more appropriate publication. All *OPBSG* issues are published and distributed electronically at http://www.creationbiology.org/opbsg/.

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Occas. Papers of the BSG No. 11, p. 1-11
www.creationbiology.org

Frontiers in Creation Research: Proceedings of the Seventh BSG Conference

Contents

From the President's Desk

Welcome to the 2008 conference of BSG: A Creation Biology Study Group. This has been a big transition year for us, with a new website that includes a whole new way of joining BSG and registering for our conferences. Our new online home is at creationbiology.org. I'd like to thank Tim Brophy and Stephanie Mace for helping with the website change.

This year, we're meeting for the first time with geologists who are looking to develop their own "study group," for the development of creationist geology. We hope to keep up these joint conferences for the foreseeable future to make it simple and affordable for those among us who wish to attend both conferences.

A few changes have been made to our usual way of doing things, in order to accommodate our geologist friends. Normally, our conference proceedings include a welcome from our host institution, an introduction to the conference theme (which I usually wrote myself), and a schedule of events. Since we're meeting at a hotel this time, we dispensed with the welcome letter, and we dropped the schedule in favor of a separated printed schedule. That will give us more flexibility in working out the joint conference details. I also replaced the theme introduction with this column, since there were more mundane things I wanted to talk about besides just "Frontiers in Creation Research." We will likely keep this streamlined form of the proceedings for future conferences.

Our last big change this year was our editorial manual and policies. In 2005, the BSG executive council charged our editor Roger Sanders with the task of developing a paper on peer review. As most of you know, we practice a tough peer review system that sets a high bar of expectation for our authors. Nearly everyone who submits is asked to revise their work in one way or another.

Such stringency leads to a minority of discontent, and we were surprised to find that creationists and Christians in general had given almost no consideration to the process of peer review itself. There were occasional items in creationist literature variously criticizing conventional peer review for excluding creationism or defending creationist efforts at peer review, but there was nothing that considered whether peer review itself had any value or justification in the Christian faith.

This was the question we took up at the 2005 BSG meeting, and I am pleased to report that we finally published the fruit of our work, "Toward a Practical Theology of Peer Review," in the new *Answers Research Journal* (http://www.answersingenesis.org/arj). Our basic conclusion was that God expects the best from us, and since peer review offers us a good way to achieve that in our scholarly work, we have a duty to practice and learn from peer review.

We concluded our paper with a series of recommendations for all creationist publications that would improve the peer review process. Our own *Occasional Papers of the BSG* actually had a lot of work to do to meet those recommendations. For example, *OPBSG* had no written editorial manual, no explanation of the job of the editorial board, and no policy on conflict of interest.

Stepping up to the plate again, Roger Sanders developed a new editorial manual which corrects all of these defects. The new editorial process is actually more complicated than the old one, but we believe it will be fairer and less prone to criticism or favoritism. Submissions are now assigned to a member of the editorial board, instead of going by default to the executive editor (Roger). The editor of each paper or abstract is now identified (you will see their initials at the end of the abstracts in these proceedings) so that readers know that *everyone* gets the same treatment in the peer review process. We built in safe guards to protect the integrity and authority of the editors' decisions, and we forbad coworkers editing each others' papers. We tried out the new system on this conference, and it's clear we have a few procedural bugs to work out. But I do want to publicly thank Roger for the work he's done on these important tasks. You can find our new editorial manual online at the *OPBSG* website (www.creationbiology.org/opbsg).

Our theme for this year's conference is "Frontiers in Creation Research." We chose it because it was neutral and would appeal to biologists and geologists, but it's also provocative. What *are* the frontiers of creation research? How do we decide what the frontiers are or should be? Most importantly, what *is* creation research? Or more properly, what is the point of creation research?

I've always understood the point of creation research to be encapsulated in the theme of the International Conference on Creationism: "Developing and systematizing the creation model

of origins." That means coming up with our own creation theories to explain the data that we see around us. Where did that mountain come from? How did that lizard get out to that island? Why are those fossils found only in that kind of rock? As I understand it, this is the goal of creation research.

Such a goal excludes other activities that creationists also engage in. Creation research does not necessarily entail improving the apologetic for young-earth creationism, although it could. Creation research also does not entail merely criticizing evolution, although good creation research will often contrast sharply with evolutionary hypotheses. There's nothing intrinsically wrong with these activities, but they are simply not the research focus that I and the BSG have chosen.

Criticizing other theories or creating apologetics is relatively easy when compared to the task of developing creationist models. Coming up with and testing our own theories is tough work, but I believe it is a crucially important task that will yield at least two benefits. First, it should help us to know our Creator better and prompt us to worship Him. He has revealed Himself in creation (Ps. 19, Rom. 1), and our study of creation glorifies Him and enriches us. Second, it takes us off the defense and puts us on the offense. There's no better refutation in science than a competing theory that works better. If we really want to change the culture, then that's where it will happen: A creation model that explains the data better than evolution.

What then are the frontiers of research? A frontier is the edge of exploration, but it also encompasses the idea of directionality. It doesn't mean only that we're doing research but that we're going somewhere with that research. We have a goal in mind.

For the past decade I have divided creationist biology research into five main areas: design, natural evil, systematics, speciation, and biogeography. Other biologists that I've shared my list with have confirmed that these five issues seem to be the biggest questions out there, from which all other questions flow. Creationist positions on problems specific to particular disciplines, like pseudogenes or tree rings, need these bigger issues resolved before satisfactory answers can be constructed.

Design encompasses not just arguments for design but theories to explain the broadest design features of this world. I'm beginning to suspect that a really good design theory will need to incorporate not just biology and theology but all other disciplines as well. I also used to think that design was just one of the five components, but I now see that design actually infuses through all five components. It may be the key to understanding all of biology.

Natural evil, the theme of our last conference, focuses on the effects of the Fall and the Curse. For my students, I summarize the issues with four P's: parasites, pathogens, predators, and poisons. Systematics covers the identification of the created kind and remains our most well-developed field. Speciation looks at how species change. There's been a lot of speculation and theorizing in this area but not much research. I hope that will change in the future. Biogeography is concerned with the distribution of organisms in the modern world and also in the world before the Flood.

Since I am not a geologist, I consulted Andrew Snelling, director of research at Answers in Genesis, to see if he had (or could make) a similar list for geology. He listed these five areas as frontiers in geology research: (1) getting the big picture of global geological sequences and patterns, (2) radioisotope dating, (3) a comprehensive Flood model, (4) chronology, particularly of the post-Flood, and (5) sorting the Precambrian into Flood and creation week deposits.

The "big picture" of geology would evaluate the suitability of the geologic column as a summary of the real strata of the earth and hopefully settle that issue. Though RATE made a valiant effort, there remains much to be done in the area of radioisotope dating. In particular, why does radioisotope dating fail in some cases but generally give a consistent pattern of dates?

With catastrophic plate tectonics (CPT) (Austin et al. 1994), the Flood model is probably the most advanced of these areas, but many questions are unanswered. In particular, how does CPT relate to the actual rock record that we observe? Post-Flood chronology should integrate the Flood model with radiometric dating, fossil sequences, archaeology, animal and human dispersal, ice cores, radiocarbon, tree-rings, and biblical chronology. Finally, Precambrian geology moves us closer to understanding the mystery of the pre-Flood world.

In addition to the issue of post-Flood chronology, I can also point out a few other areas where the frontiers of biology and paleontology intersect. First, how do we account for the orderliness of the fossil record during the Flood? At the BSG conference in 2004, Kurt Wise suggested that the fossil record of the Flood represented the deposition of strictly separated geographic provinces that existed before the Flood. If he's right, a comprehensive answer to the order of the fossil record requires elements of design, baraminology, biogeography, global stratigraphic patterns, and the Flood model.

Another very interesting area is something I'll call "diluvial blooms." Most creationists are familiar with large microfossil deposits, like the Chalk, where we find the physical remnants of microbes from the Flood in massive and pure layers. Recent advances in biogeochemistry have revealed even more biogenic layers, such as Cretaceous shale that appears to be the remains of an archaeal bloom (see Kuypers et al. 2001). Could it be that much of the Flood-generated rocks are not merely rocks but sediments altered and even generated by blooms of microbes? Answering this question again requires a good Flood model, a good understanding of global stratigraphy, and a creationist microbiology (which itself derives from the elements of creationist biology listed above).

These questions alone excite me, but the goal beyond them excites me even more. We're not just trying to answer some weird questions or refute the scoffers. Our goal is God Himself. We're trying to understand His creation, His design, which ultimately is a reflection of His very nature. What better goal could there be?

T.C. Wood
Editor: RWS

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Plenary Abstract

P1. Origins Research: A Better Worldview Yields Better Research Questions

L. Brand
Loma Linda University

There is a common worldview which leads to a two-level understanding of "truth": religion yields personal, subjective values and emotions, while science produces public, neutral, objective, reliable facts. In reality there is no such thing as a neutral search for truth. Everyone works within some worldview, although we are not always conscious of it. Two basic worldviews relevant to our discussion are a naturalistic view and a non-naturalistic view, either of which can exist in more than one version. A worldview is based on a set of assumptions, and these assumptions will have an inevitable influence on the research questions we ask, what we will notice in our research, and what data we collect. The assumptions will also influence, or even strongly control, our interpretations of the data.

For example, working within a naturalistic worldview does not allow asking whether the feature in question might be the result of design, and it exerts a strong bias against the conclusion that the feature does seem to require a designer. This worldview influence can exist in a more subtle form. For example a naturalistic worldview does not prevent a geologist from asking whether a given series of geologic deposits might have been deposited very rapidly, but experience indicates that this question is often not asked, because of entrenched biases.

The history of science shows that theories that we now consider false were able to generate significant scientific progress for centuries. However, the time is likely to come when scientific progress under a false paradigm or worldview will begin to slow down. The closer a paradigm is to reality, the more it should result in genuine scientific progress.

If we wish to objectively ask "what is truth in a given field?" we are far more likely to find the answer if we work in a worldview that is compatible with whatever is truth. Some scientists believe that a religious viewpoint cannot result in valid scientific research. However, abundant examples demonstrate that a religious (including biblical) worldview, when combined with high quality research procedures, can lead to productive research and suggest better research questions and hypotheses, with results publishable in the best peer-reviewed scientific journals. Examples will be given to illustrate this conclusion.

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Occas. Papers of the BSG No. 11, pp. 5-11
www.creationbiology.org

Contributed Abstracts

C1. Wolfram's Complexity Classes, Relative Evolvability, Irreducible Complexity, and Domain-Specific Languages

J. Bartlett
Independent Scholar

Stephen Wolfram observed four basic classes of complexity in his analyses of cellular automata based on their outcomes from a disordered initial state. Class 1 automata always arrived at a homogenous state no matter what their initial state was. Initial states in Class 2 automata have a finite sphere of influence for outcomes even if the computation was carried out an infinite number of steps. Class 3 automata are chaotic systems, where initial states do not have either a bounded sphere of influence nor do they produce predictable results. However, they do have stable statistical properties. Class 4 automata exhibit a hybrid of both the periodic behavior of Class 2 systems and the chaotic nature of Class 3 systems. More importantly, they are unpredictable both in their exact outcomes as well as well as in their statistical properties. These classes apply not only to cellular automata specifically, but to any type of programming language or system, for which the initial state is a program defined in a language.

Wolfram observed that the only types of systems known to be capable of universal computation were systems exhibiting Class 4 complexity. Therefore, while it may be possible to build a program on a Class 4 system which does not require its chaotic attributes, if a Class 4 automata is required for universal computation, then it is reasonable to suggest that a computation which requires a universal computer would also need to make use of the chaotic features which make it exhibit Class 4 complexity.

Because of the chaotic nature of Class 4 systems, there is not a smooth transition from changes in programming to changes in outcomes. Thus, systems which need to rely on Class 4 behaviors have great difficulty arising from natural selection because the chaotic mapping from the system's programming to the system's results prevents there from being a selectable path leading towards a solution. There is not yet a metric to measure evolvability in this way, though cyclomatic complexity may be a good starting point for research in this area.

In most programming systems, the most chaotic elements within those systems come from explicitly-controlled loops. Interestingly, while several evolutionary systems have been developed which utilize an underlying universal computer (such as Avida and GEMS), there have been no systems of which this author is aware where a loop control structure has been built from scratch using evolutionary algorithms, and the loop was required for the computation to be successful.

Such systems might still be evolvable, however. Many approach evolvability as an absolute measurement. However, the evolvability of a system depends both on the nature of the evolved system as well as the implementation language. A system may be complex in one language, requiring chaotic elements to implement it, while in another language it can be implemented using non-chaotic elements. While the complexity characterization of a system can determine its evolvability with regards to one implementation language, that does not prevent it from being more easily evolved via another language, such as a domain-specific language where features of the language are more closely mapped to the expected solution domain.

Therefore, a system which is unevolvable can be perfectly evolvable in another context. Therefore, designations such as "irreducible complexity" are relative designations, not absolute ones. Demonstrating the evolution of an "irreducibly complex" system would not invalidate either the concept or the designation, but rather point to a higher-level, domain-specific system which is guiding the evolution. Thus, "irreducible complexity" and similar ideas can be used as a detection method for higher-order evolutionary engines in operation within the genome. While further research is still required for an analytical method for detecting these systems, theory suggests that multiple, interacting feedback loops could only be evolved with the help of domain-specific systems.

Editor: RWS

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C2. Preliminary Observations on the Feeding Habits of Green Hydra, *Hydra viridissima*, and Their Relation to Natural Evil

J. Carr, Z. Williams, & T.C. Wood
Bryan College

One of the primary questions in creation research is that of natural evil: How did phenomena such as predation, parasitism, and disease come about in a creation that was originally described as "very good" (Gen. 1:31). Within this larger issue of natural evil, many smaller problems can be grouped, such as the origins of specific diseases or toxins. Previously, creationists have attributed many examples of natural evil to degeneration from a perfect state but Wood and Murray (2003, p. 157) argue that some instances of natural evil involve structures that appear designed. For example, cnidarian nematocysts, a class of organelles used for attack, defense, and locomotion, have a complex structure that appears very well designed. Nematocysts are hollow structures containing an inverted tubular thread. Upon reception of an external stimulus the thread is rapidly everted. Types of nematocyst threads include barbed penetrators which deliver toxins and threads which immobilize the target via entanglement or adhesion (Kass-Simon and Scappaticci, 2002). In summary, nematocysts are incredibly efficient, highly specialized structures that appear to be well-designed killers. How did they originate in a creation originally described as "very good?"

The answer may lie in mutualistic symbiosis, such as that found in the cnidarian *Cassiopeia xamachana*. It has been suggested that mutualistic relationships were typical in the original creation and that some pathological relationships may result from disrupted mutualism (Mace, Sims, and Wood, 2003). *C. xamachana*'s photosynthetic dinoflagellate symbionts have been shown to attenuate nematocyst toxicity (Radwan and Burnett, 2000). This led us to hypothesize that a similar inhibitory effect might be observable in green hydra (*H. viridissima*), a much smaller and simpler organism than *C. xamachana.* Like *C. xamachana*, green hydras contain an intracellular algae which is a mutualistic symbiont (Cook, 1972). To test our hypothesis, protocols for raising hydras and measuring toxicity must first be developed, which was the primary purpose of this study.

Hydras obtained from Carolina Biological Supply Company and Ward's Natural Science were observed over two months. Observations were made during feeding sessions. The hydras were fed with fresh *Artemia* (brine shrimp) larvae. Three different feeding patterns were observed: 1) immediate stinging and immobilization followed by ingestion; 2) immediate immobilization without ingestion; 3) no response to contact with *Artemia*.

The near instantaneous killing observed indicates that *Artemia* is too sensitive to hydra toxins for use in toxicity assays. Further studies are needed to develop toxicity assays for hydra. Assays similar to those in the *Cassiopeia* study mentioned above may be useful. Further experiments should also test nematocyst virulence in non-symbiotic brown hydras and aposymbiotic green hydras. While previous studies with *Cassiopeia* indicated that symbionts attenuate nematocyst toxicity, our results seem to show that symbiotic green hydras remain ravenous eaters. Thus, we would provisionally conclude that symbiosis alone is not sufficient to alleviate the 'natural evil' of green hydra nematocysts. As indicated above, additional controlled studies are needed to confirm our preliminary observations.

Editor: JWF

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C3. Where is the Garden of Eden?

J. Davis
Bryan College

Many assume Gen. 2:10-14 locates Eden in Mesopotamia, or that the material in 2:10-14 can no longer be used to locate Eden. While these ideas might be right, there are a number of problems.

With the first view, interpreters must divorce the normal Biblical meaning for Cush from Ethiopia or the eastern shore of the Red Sea to an unproven Cush in eastern Mesopotamia (see the detailed arguments of Albright 1922, pp. 19, 22; Skinner 1930, pp. 200-01, 61, Cassuto 1964, vol. 1, p. 117; Sailhamer 1992, p. 99, and Westermann 1994, p. 218). Ancient interpreters of the passage understood Cush as Ethiopia (see the LXX, Philo, Josephus).

With the second view, why did God include material in such detail? Moses wrote assuming that his audience would understand something, and they were a post-flood audience. Moreover, God knew of the coming flood when he created Eden. Why would he inspire material he could foresee would be meaningless to the majority of later readers?

An unexplored option for the resolution of this difficulty is that 2:10-14 means to connect Eden with the Promised Land/ Jerusalem/New Jerusalem (see Sailhamer 1992, pp. 99-100, 152; Beale 2005, pp. 5-31; and Tuell, 2000, pp. 171-89). It is easy to connect Eden and New Jerusalem in Revelation 21-22. Yet many interpreters fail to notice that it is a Jerusalem coming down to earth with the tree of life and a special river just like 2:10-14. One must ask, if God restores Eden to Jerusalem at the end of the Bible, how does that restoration relate to original Eden?

Extant Jewish literature connects Eden and Jerusalem (see e.g., 1 Enoch 25:3-5; Jubilees 8:19; and Testament of Dan 5: 12). Scholars see this connection in the OT: Ezek. 47:1-12, see Tuell 2000, pp. 171-89; Psalm 46:5-6 [4-5]; Zech. 14:8; Joel 4:18 [3:18]; the Hebrew of Ps 36:9 [8]; and Isa. 33:20-21. Other scholars connect Eden and the Tabernacle/Temple, e.g., Wenham 1986, pp. 19-25.

If canonically the "holy mountain of God" is Jerusalem (e.g., Ezek. 20:40), then Ezek. 28:13-14 identifies *ancient* Eden's location with Jerusalem.

What does this connection add to our understanding? It explains the boundaries of the Promised Land (Euphrates and the river of Egypt) because God is ultimately promising the restoration of Eden (see e.g., Ezek. 36:22-36, especially v. 35; so Sailhamer 1992, pp. 152-53). It explains an Eden-like Tabernacle and then Temple because these are the earthly copies of the Heavenly one to return (see similarly Cassuto 1964, pp. 117-18; Ezek. 47:1-12 and Revelation 21-22).

The chief unifying feature of this ancient view is connecting the place of the original sin with the place of its remedy in Christ. If Eden and Jerusalem are the same place, Christ becomes the center of it all. God veiled the location of Eden initially to progressively reveal its association with first the Promised Land, then the Tabernacle, then with Jerusalem. All of this draws the reader to realize a unity in the story focusing on Christ's redemption of Adam's sin at the ancient and future Eden. Such a unified view of the Bible gives God greater glory than the current consensus.

Editor: MR

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C4. The CT Toxin of *Vibrio cholera*, Its Structure, Function and Origin

J.W. Francis[1] & T.C. Wood[2]

[1]*The Master's College*

[2]*Bryan College*

The destructive effects of toxins are difficult to explain within the creation model because many toxins participate in complex, intricate, design-like mechanisms during their intoxication of cells. Cholera toxin (CT) is the most virulent toxin of *Vibrio cholera*, the causative agent of the pandemic disease cholera. CT, a heptameric protein which is part of the AB toxin family, attaches to cells and moves in an intricate retrograde fashion from the plasma membrane to the Golgi, ER and finally the cytoplasm of the intoxicated cell. In the cytoplasm, CT promotes the ADP-ribosylation of Gs-proteins. The ribosylated Gs protein causes adenylate cyclase to constituitively produce cAMP. This does not typically kill cells or tissues directly, but instead activates ion channels causing massive loss of ions and water from the cell.

Since creation theory predicts that CT once played a beneficial role within creation we have begun a research project to assess the beneficial roles CT may play or have played in ecosystems, and we have also begun to assess *Vibrio* genomes for evidence of genetic modifications of CT and functionally-related genes. Curiously, CT possesses many features which would suggest that it is highly functional within the lumen of internal organs of multicellular organisms and therefore may be uniquely fit for this environment. This appears to contradict in some ways our previous finding that *Vibrio cholera* appears to be fitter for the chitinous surfaces of aquatic arthropods, where it participates in the catabolism of chitin, than the human intestine (Francis, 2006). Our preliminary genetic analysis and analysis of the organisms which CT may encounter in the aquatic environment has led us to formulate several hypotheses regarding the ecological roles of CT. (1) CT may promote salt metabolism in some aquatic organisms. For instance, CT binds to the chitinous surfaces of the intestine of the blue crab where it has been postulated to promote salt excretion as the crabs move from low to high salt environments in estuarine waterways. This also suggests that *V. cholera* may possess multiple roles via its association with chitin. (2) CT may have originated in a symbiotic *Vibrio*. Our preliminary genetic analysis of the CT gene cluster show that it has a GC content and frequency of optimal codon usage consistent with its origin in *V. fischeri*, a *Vibrio* species which possesses some of the genes of the CT and related virulence factor gene clusters and is known for its symbiotic relationship with squid. In addition, part of the squid-*Vibrio* relationship involves a daily expulsion of excess bacteria and this is consistent with the action of CT on the mammalian intestine.

Furthermore, our analysis of the codon usage supports the hypothesis that the heat labile toxin of *E. coli* (LT) may have originated via lateral transfer from CT containing *Vibrio* in the environment of the mammalian intestine.

Editor: GP

Francis, J.W. 2006. The Role of Virulence Factors in the Establishment of Beneficial Ecological Relationships of *Vibrio cholera* and *Vibrio fischeri*. *Occasional Papers of the BSG* 8:14.

C5. Concurrency Patterns and Controls in Biological Systems

S. Gollmer

Cedarville University

Concurrency is a term that has its origin in the field of computer science. It is used to describe systems that have two or more processes operating at the same time with the potential of interaction between the processes. Early parallel computers used synchronized execution of code to increase computational speed and yet provide reliable interaction between processes. However, more flexible systems have been developed that allow processes to operate in an asynchronous fashion distributed over multiple computers. In this case, reliable interaction between processes becomes more problematic and, therefore, requires deliberate planning.

The book *Real-Time Design Patterns* by Douglass describes eight different architectural patterns for dealing with concurrency. Each of these patterns describes best practice methods of controlling and scheduling processes. This control not only ensures that asynchronous processes coordinate their efforts at critical times, but also ensures that shared resources are accessed

in a manner that does not corrupt the action of other processes.

Biological systems also demonstrate concurrent behavior. In the cell, transcription of DNA to RNA occurs simultaneously with multiple chromosomes and at multiple points within each chromosome. Subsequent translation of RNA can result in the construction of regulatory proteins, which in turn affect the DNA transcription processes. Regulation of these processes is coordinated to ensure an orderly growth and response of the cell to its environment. In multi-cellular organisms, each cell acts as an individual process, which is controlled to provide coordinated developmental differentiation and proper collective behavior for the benefit of the organism. The control of these processes is achieved through gene regulatory networks and signal transduction pathways. Mutations in proteins critical to these control mechanisms can lead to tumor growth, such as with p53 (Ventura et al., 2007) and the Ras family (Bos, 1989).

In this paper, a comparison is made between the Rendezvous Pattern and the role of p53 within the cell. The Rendezvous Pattern is used to hold up execution of a method until all reporting threads have satisfied a specific condition. This description is similar to the behavior provided by cell cycle checkpoints preceding S-phase and M-phase of which p53 plays a significant role. This research is still in its preliminary stage and needs to be expanded to include comparisons with other cell cycle checkpoints and critical regulatory elements in signal transduction pathways. Other concurrency patterns must be evaluated as to their usefulness in describing biological systems. These avenues of research will be pursued and progress will be reported at the time of the conference. Future research will expand this comparison to the developmental toolkit genes, such as the Hox genes.

It is anticipated that this comparison will provide insight into the different means employed by biological systems to control cellular and organismal processes. Although this study uses known biological control mechanisms, the context of architectural patterns may suggest additional mechanisms as yet unidentified in the biological literature. The complexity of these control mechanisms will also speak to the degree of plasticity available for biological systems to adapt to changes in the environment and in the genome.

Editor: TCW

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C6. The Hebraic Concept of Life and Death

D. Kennard

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The ancient Hebrew concept of life is especially showcased in word studies of *haya* and *nephesh* to indicate something that is: *vibrant, active, thinking, willing, accomplishing and moving* (Harris et al. 1980, Vol.1 p. 279). As such God, angels, humans, animals are alive and plants are not. The microbial are not discussed. Breath, thought, choices, accomplishments, and movement are indicators of life. Such evidences for life will be evaluated for their benefit in bio-ethical decisions. In the OT this concept of life has to do with existence before death, though in second Temple Judaism (5th centuryBC-2nd century AD; Freedman & Simon 1977; Wise et al. 2005) life begins to refer to an afterlife (Kennard 1992).

The ancient Hebrew concept of death is especially showcased in word studies of *mwt* and *sha'ol* to indicate the nonmoving corpse of what had been alive, and the metaphysical grave and cavernous place of the dead that houses the dead. There is simultaneity of lifeless corpse decaying and a metaphysical continuation of limited wholistic body in the place of the dead. Under the development of second Temple Pharisaism, this place of the dead separates into two different realms of Paradise and Hell (which view underlies the NT views of salvation and damnation; Freedman & Simon 1977; Wise et al. 2005). The Hebraic concept of death also includes a more active form in which in precarious times death reaches into this life and draws us down toward death, diminishing our present existence through illness and risk (VanGemeren 1977, Vol. 2, p. 887). When this encroaching death occurs, the place of the dead also encroaches into this life as well. Such a concept of death/life permits humanity being described as walking dead or wasting away in life. This walking death may have some relevance for God's promise in Genesis 2:17 for killing humans in the day that they sin in rebellion.

Editor: MR

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C7. The Oracle of Curse at the Fall of Creation

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God responds to human rebellion through His oracle of judgment in the Fall (Gen. 3:14–19). The problem I address is what the Bible declares about the consequences of the Fall: for animals, humans, and the rest of creation. **Method: tight exegesis of the "oracle of curse," namely Genesis 3:14-19,** with related passages it connects with.

First Conclusion: futility permeates all relationships: 1) intimacy with God breaks down (Gen. 3:8, 23–24), 2) humans are exhausted in their work now that the ground is cursed (Gen. 3:17–19), 3) marital relationship with tension between woman's quest for liberation and male dominance (Gen. 3:10, 16), 4) there is increased pain in child bearing (Gen. 3:16), 5) there is enmity between human and snake relationships (Gen. 3:15), 6) all beasts of the field are cursed but not as much as snakes (Gen. 3:14), and 7) snakes are cursed to crawl in the dust (Gen. 3:14).

Second Conclusion: blessing mingled with experiential evil. This futility leaves the blessings (be fruitful, multiply, fill the

earth, subdue, and rule) intact though diminished by their fusion with the experiential knowledge of evil, such as increased pain in childbirth and increased effort in accomplishing labor (Gen. 1: 28; 3:5; 9:1–7). Likewise, humans still retain the initial tasks like cultivating the ground but now in a manner that subjects them to futility with thorns and thistles and much labor (Gen. 3:17–19, 23). Even the extreme measures of God utilizing the waters of chaos to attack the sin dominated condition of the earth provides the remnant as preserved in blessing and work (Gen. 9:1–7, 20). Animal futility fits within creation futility in a more modest form, since the passages mostly address human futility.

Third Conclusion: Specifics of this **futility for animals** (as well as humans) are fleshed out by further metaphors: **death, no permanence, perhaps a reigning death condition, pain, and having life summed up as vanity** (Gen. 2:17; 3:14, 19–20; 4:8, 23; 5:5, 8, 11, 14, 17, 27, 31; word study of vanity in Eccl. and applied to Eccl. 3:18–22; Rom. 5:12–21; 8:18–23; Eph. 2:2–3). While these conditions are especially developed as definitely applied to humans, I will probe these passages to conclude in a more tentative manner (thus somewhat conjectural with some evidence) to work out the same conditions for animals.

Finally, **Resolution**: Isaiah 11 and second Temple Judaism leaves creation with a **generic hope for animals to return to a paradise condition in Kingdom**, as humans are redeemed specifically for co-reigning in Kingdom with everlasting life. There is no specific promise for salvation of a specific animal, as there are for humans.

Editor: JWF

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C8. The Creation-Evolution Literature Database (CELD)

S.R. Mace & T.C. Wood

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Expansion and growth of the creation model by scholarship depends on building on the foundation of the existing knowledge and conducting new research. Various databases, such as PubMed or GeoRef, offer access to conventional scientific periodical literature, but researchers interested in the creation/evolution issue must search a variety of publisher's websites looking for papers of interest. To remedy this difficulty, the Center for Origins Research (CORE) developed the Creation-Evolution Literature Database (CELD). CELD presently archives abstracts and citations from 56 publications, spanning the last 140 years. For items without an explicitly labeled abstract, CELD records the first paragraph (for longer items) or the first sentence (for short items). CELD includes all published items (articles, letters, commentaries, book reviews, etc.) from each periodical. CELD tracks major creationist publications (e.g., *CRSQ*, *Journal of Creation*, *Creation* magazine), as well as theistic evolution publications (e.g., *Science and Christian Belief*, *Perspectives on Science and the Christian Faith*), and publications on religion and science (e.g., *Zygon*). CELD currently contains more than 20,000 citations, approximately 40% of which also link directly to online content from the publishers' websites. Researchers can search CELD for authors, titles, abstract words, or keywords. The content of CELD reflects the content of the CORE library, with additional periodicals added as they become available. Early development of CELD emphasized archiving the scholarly literature rather than more popular publications. Consequently, CELD lacks a few significant titles, such as *Bible-Science News* and *Origins Research*, which will be added in the future. CELD can be accessed at the CORE website, www.bryancore.org/celd.

Editor: GP

C9. A Baraminological Analysis of the Landfowl (Aves: Galliformes)

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The landfowl (Aves: Galliformes) form a large (250 species, 70 genera) and cosmopolitan group of birds that have consistently been grouped together since the inception of avian taxonomy. We analyzed a published morphological (primarily osteological) dataset (Dyke et al., 2003) using baraminic distance and classical multidimensional scaling (MDS). The dataset consists of 102 characters from 60 extant landfowl and five extant waterfowl (Aves: Anseriformes) taxa. The landfowl taxa include three mound builder (Megapodiidae), five cracid (Cracidae), four guineafowl (Numididae), seven New World quail (Odontophoridae), two turkey (Meleagrididae), six grouse (Tetraonidae), and 32 phasianid (Phasianidae) genera (including Old World quails, peafowl, tragopans, pheasants, partridges, and allies). Both baraminic distance correlation analysis and multidimensional scaling suggest the possibility of four holobaramins within the landfowl order: Megapodiidae, Cracidae, Numididae, and the remaining Phasianoidea. Hybridization data (McCarthy, 2006), however, connects three of these provisional holobaramins (six of the currently recognized families). Considering both sets of evidence, we conclude that the landfowl are composed of two monobaramins: Megapodiidae and [Phasianoidea + Cracidae]. The five currently recognized families in the superfamily Phasianoidea have, until recently, been considered subfamilies in a more broadly conceived family Phasianidae, so it should not be surprising that they are members of the same monobaramin. Perhaps the most surprising result of this study then, is the inclusion of the Cracidae in the phasianoid monobaramin. A closer inspection of our data along with more recent phylogenetic analyses of the landfowl, however, suggest that that the Cracidae are more closely related to the Phasianoidea than once assumed. This study emphasizes the continued value of hybridization data

in baraminological research, illustrates the importance of using multiple lines of evidence when delimiting holobaramins, and is suggestive of the potential uses and limitations of statistical baraminology.

Editor: RWS

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C10. Lantana (Verbenaceae) as a Model to Study the Origin of Traits Exhibiting Natural Evil

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Many features of organisms related to protection, aggression, or nutrition inflict suffering or death on other species. They can be referred to as cases of "natural evil." In conventional biology, traits exhibiting natural evil are viewed as evidence of the lack of design, having arisen from previously adapted features co-opted for their present functions or by direct adaptation resulting from (further) natural selection. In contrast, creation biology views such features as evidence for design marred by the entrance of sin into God's perfect creation. Creation models proposed to explain them include: original design with transfer of function, fiat redesign, intrinsic degeneration (random loss genes), extrinsic degeneration (shift of habitat or co-symbiont), and mediated design (pre-programmed genetic elaboration) (Wood & Murray 2003, ch. 9-10). A research program is being developed to investigate the origin of such features. Because the author has extensive experience with the genus *Lantana* (shrub verbena in the family Verbenaceae), the present study evaluates whether this plant group has potential as a model system for use in a series of future studies. It has long been known that certain species of *Lantana* possess traits that can be classed as natural evil. These include prickles, triterpenes toxic to mammals, pungent surface oils toxic to insects, and aggressive weediness in areas where the natural species and/or hybrid strains are alien (Sanders 2001). It is significant that some species with these traits and others species that lack some or all of them can easily hybridize with each other. In fact, hybridization is extensive within taxonomic sections of *Lantana* (Sanders 2006). The author's original unpublished observations suggest that the prickles show incomplete dominance at one or multiple loci and are associated with variable proliferation of epidermal cells at the base of stiff surface hairs.

This information, plus the ease of culture and accessibility of *Lantana*, suggests that it is a good candidate with which to study the origin of traits exhibiting natural evil. The hybridization ability suggests both that *Lantana* is a monobaramin and that much of the underlying genetic basis of features can be determined. Further baraminological research is needed to determine the limits of the holobaramin to which *Lantana* belongs. However, morphological variation among similar genera suggests the holobaramin to be the family Verbenaceae or subfamily Verbenoideae, depending on the classification authority followed. Therefore, it is tentatively hypothesized that *Lantana* originated during a post-Flood period of rapid diversification of its baramin, precluding original design and fiat redesign in the origin of these features at the Fall. Aggressive weediness is clearly a case of ecological degeneration in modern history. It is not clear whether the prickles, triterpenes, and oils arose by genetic degeneration or pre-programmed mediated design. Variation and development of prickles make them amenable to genetic analysis and possible sequencing of the underlying genes. Review of the conventional literature on the biochemical pathways of the toxic triterpenes and oils in *Lantana* and related genera is needed, as well as identification and sequencing of the underlying genes. Assuming such data become available through the planned program or conventional publications, origin of these features during diversification by either random intrinsic degeneration or mediated design should become clear.

Editor: JWF

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C11. Baraminology and the Fossil Record of the Mammals

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Both the abundance of fossils and the severity of the Flood suggest that many non-terrestrial organisms were killed in the Flood. It is likely that not just terrestrial, but *all* baramins experienced a severe diversity bottleneck in the Flood. Thus whereas modern baramins have existed continuously since the Flood, most sub-baraminic groups originated *after* the Flood. This suggests a new baraminology criterion – called here "post-Flood fossil continuity criterion" (PFCC): high preservability baramins should have a continuous fossil record back at least to the Flood, and high preservability groups with a first-appearance in the fossil record substantially after the Flood are sub-baraminic.

The new criterion is here applied to the mammals. McKenna and Bell (1997) present known stratigraphic occurrences for all mammal taxa above the level of species (>1130 genera; >420 families; >220 super-family taxa) to the sub-system level in the Mesozoic and sub-series level in the Cenozoic.

Hybridization reports firmly establish that mammal baramins are more inclusive than genera, tribes, and even subfamilies. More complete baraminology studies usually place the mammal baramin at the level of the family or higher. Using the PFCC, the Flood/post-Flood boundary should post-date the first appearance of most families and pre-date the first appearance of most intra-family taxa. Among living taxa with a fossil record, and assigning sequential numbers to the sub-series, one standard deviation below the mean first-appearance are as follows: Upper Miocene for genera (n=648); Upper Oligocene for subtribes (n=130) and tribes (n=31); Lower Oligocene for subfamilies (n=162); Middle Eocene for families (n=140); and Upper

Paleocene for superfamilies (n=56). If mammal preservability was constant following the Flood, the PFCC places the Flood/post-Flood boundary between the Middle Eocene and the Lower Oligocene. If (as is more likely) mammal preservability rose with population following the Flood, the boundary is lower (*e.g.* the K/T boundary).

Some families previously identified as holobaraminic (Equidae; Camelidae) or monobaraminic (Canidae) could be holobaraminic by the PFCC. Some families previously identified as monobaraminic (*e.g.* Cercopithicidae; Canidae; Ursidae; Felidae) are, by the PFCC, sub-baraminic.

The PFCC suggests mammalian holobaramins may be identified with fossil superfamilies. This would place the Flood/post-Flood boundary closer to the K/T (Upper Paleocene) and extend many proposed holobaramins back to the Flood (*e.g.* caenolestoids; aplodontoids; geomyoids; cavioids; ursoids; phocoids; soriocoids; tapiroids; and anthracotherioids when hippopotamids are reclassified with them as suggested by Wood 2006). Such a superfamily assignment can be tested by baraminology studies on superfamilies with multiple living families (*e.g.* megatheroids; phocoids; soriocoids; non-hippopotamid suoids; cervoids).

The PFCC suggests groupings above the level of superfamily in 9 mammal groups (% families lacking a fossil record; % genera lacking a fossil record; % families with discontinuous fossil records): bibymalagasians (100%; 100%; n/a); primates (38%; 67%; 25%); bats (29%; 62%; 42%); Australidelphia (21%; 29%; 55%); pilosans (20%; 40%; 50%); Caviida (0%; 53%; 44%); cetaceans (0%; 50%; 36%); ruminants (0%; 10%; 0%); and proboscidians (0%; 0%; 0%). In all but the last two groups a poor fossil record might be at least a partial explanation. That the classification of some of these groups should be reconsidered is suggested by 1) classification bias for animals most similar to humans 2) the difficulty distinguishing humans from the primates (including with the PFCC); 3) the strong similarity among the bats; and 4) the geographical isolation of the Australidelphia.

Mace and Wood (2005) divide the whales into at least 4 holobaramins, and, with Cavanaugh and Sternberg (2005) and Wood (2006), separate the whales from the archaeocetes. Although these baraminology studies identify the whale baramins approximately along McKenna and Bell's superfamilies (as suggested by the PFCC applied to other mammal groups), the PFCC applied to whales suggests one holobaramin for all whales plus the archaeocetes.

Given the holistic holobaramin concept (Wood *et al.* 2003), the PFCC should be utilized only in concert with other criteria. Also, given its theory dependence, until tested, the PFCC should be employed cautiously.

Editor: RWS

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