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Number Five

Occasional Papers of the Baraminology Study Group

**A GRANDER VIEW OF LIFE
PROCEEDINGS OF THE FOURTH BSG CONFERENCE**

edited by
Roger W. Sanders

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Occasional Papers of the Baraminology Study Group

Editor: Roger Sanders, 1854 Greenwood Road, Weatherford, TX 76088, USA
Email: opbsgeditor@bryancore.org

Assistant Editor: Todd Wood, Center for Origins Research and Education, Bryan College, Dayton, TN 37321, USA

Editorial Board: Joseph Francis, Margaret Helder, Georg Huber, Richard Sternberg

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1. Develop a new view of biology that is consistent with the Biblical record.
2. Encourage high-quality creation biology and baraminology research.
3. Sponsor conferences and other appropriate activities to promote creation biology.
4. Develop a community of creation biologists who share these goals.

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A Grander View of Life: Proceedings of the Fourth BSG Conference

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Welcome

New Saint Andrews is honored to host this important conference. We are delighted to have Christian scholars with spiritual and intellectual backbone presenting the fruit of their labors in the life sciences here in Moscow. Scientists with biblical integrity are far too rare these days. Too many have sold their intellectual birthright for a mess of academic respectability or bowed the knee to the idols of our age—Modernism’s blind faith in secular Science or Postmodernism’s “dictatorship of relativism” (as Pope Benedict XVI has put it). This conference is a fitting testimony to a grander view of life from those who still trust the Lord of the sciences.

This conference is at the front lines of the conflict between belief and unbelief in our day. Life itself, as it were, hangs in the balance. For those who do not trust the Scriptures and deny the Creator, creation has become the fertile soil for pseudoscientific speculations and modern mythmaking. Darwin is their king, having driven out Zeus (to paraphrase Aristophanes), and a culture of death—from abortion to euthanasia—is their grim reward. For those who trust the Lord of life, creation reflects the boundless majesty of its Creator. Christ is our king and a glorious diversity of life, reflecting the unity and diversity of the Triune godhead, is our bountiful heritage. This conference affirms the grandeur of life and fosters a culture of life. We are honored to play a supporting role in the fight for “A Grander View of Life.”

During your stay in Moscow, we invite you to get to know New Saint Andrews better. Our College is a classical Christian undergraduate institution devoted to the pursuit of truth, beauty, and goodness in the light of God’s infallible Word. The College offers a curriculum and pedagogy rooted in the Biblical and classical worlds, refined by the Christian schools and earliest universities of Medieval Europe, and revered by colleges and universities in North America until the end of the 19th century. New Saint Andrews, like all the great colleges prior to their corruption by modern philosophies of education and their confusion of vocational-technical training for genuine education, offers one—and only one—academic program: the classical liberal arts and sciences. New Saint Andrews concentrates on the classical languages, literature, history, theology, philosophy, natural philosophy, and music of Western culture, which is where, in the providence of God, Christianity arose and grew to maturity. New Saint Andrews is therefore devoted to the study of

the West’s classical heritage from an uncompromising Christian worldview.

Our close-knit community of Christian scholar-colleagues shares a common biblical foundation, academic vision, and religious worldview. New Saint Andrews is defined by the character and common Christian vision of its faculty, united by its belief in the integration of all knowledge in Christ, and driven by its zeal for reformation in all of life under our Triune Creator and Redeemer. Our faculty community (not student enrollment) defines the size and scope of the College. Each year the New Saint Andrews faculty invites about 50 new students to join us in the pursuit of truth, beauty and goodness. Our classes—and the College—are small by design and distinguished by voluminous reading, lively discussion, and iron-sharpening-iron challenges.

The College is also part of a larger, vibrant church community in Moscow blessed with faithful families and gifted individuals. Moscow is a friendly college town with a lively downtown. Please enjoy the hospitality of our community and take the time to see some of the wonderful natural sights in our surrounding environment—from the rolling wheat fields of the Palouse to the deep canyons of the Snake River and its tributaries.

Again, welcome to New Saint Andrews and Moscow, and enjoy the 2005 Baraminology Study Group Conference. We hope you have a glorious conference and we look forward to getting to know you better.

Roy Alden Atwood
President

Introduction

The apostle John records a very peculiar instance in the life of Christ and his disciples. They were in Capernaum at the time, just after Jesus fed the five thousand and walked on the Sea of Galilee. These spectacular miracles undoubtedly added to Jesus' growing fame, something Jesus always seemed to spurn. The incident in question began at the local synagogue when Jesus claimed, "I am the living bread which came down from heaven. If anyone eats of this bread, he will live forever" (John 6:51). The people quietly sneered at this statement. After all, it was only Jesus, son of the carpenter Joseph, who had grown up in that neighborhood. Besides, how could "this Man give us His flesh to eat?" (6:52).

Knowing they murmured against Him, Jesus spelled it out for them, "Whoever eats My flesh and drinks My blood has eternal life, and I will raise him up at the last day." Knowing very well the tendency of human beings (and especially scholars) to try to allegorize religious statements that are hard to understand, Jesus continued, "For My flesh is food indeed, and My blood is drink indeed. He who eats My flesh and drinks My blood abides in Me, and I in him" (6:55-56). His words painted a grisly picture and left little room for allegory.

His disciples seemed to get the message, because John wrote that they murmured among themselves and "many of His disciples went back and walked with Him no more" (6:66). Jesus then turned to the twelve and said, "Do you also want to go away?" (6:67). Peter spoke up (as usual) with what I like to call a confession of desperation. He said, "Lord, to whom shall we go? You have the words of eternal life" (6:68). Jesus replied not by commending Peter's confession but by reminding them that one of the twelve was "a devil" (6:70).

Unfortunately, we've heard this story in so many sermons and Sunday school lessons that we've lost touch with the shock that these words invoke. Jesus demanded that His followers practice cannibalism on His own body! Like most Protestants, I'd *like* to think He was speaking metaphorically, and that through the regular practice of Communion, Christians consume symbols of His "flesh" and "blood." The other scriptural passages on communion would support that interpretation, but here there's something disturbingly persistent about Jesus' explanation, almost as if He wanted people to take Him literally. I won't pretend to understand just what He was trying to do or say.

Whatever Jesus meant, it's Peter's reaction that speaks most

deeply to me, probably because Peter is so human. To understand Peter, we have to remember that he left everything to follow Jesus (Mark 10:28). This was no passing infatuation, Peter was serious, committed follower of Christ. He *really* believed that Jesus was the Messiah, and he was usually the first of the apostles to say so. Now try to imagine his shock at hearing this bizarre teaching, "eat My flesh... drink My blood." If that wasn't bad enough, a bunch of his fellow disciples left because of it. As one of the most prominent of Jesus' followers, Peter must have tried to talk with those who left, at least to find out why they were going. I'm sure he got an ear-full about Jesus' apparently tenuous hold on sanity. So Peter's between a rock and a hard place: he wants to believe Jesus but Jesus is teaching some strange things. As if that wasn't bad enough, Jesus looked at Peter and said essentially, "Why are you still here? Aren't you going to leave too?" Why didn't Jesus try to console him? Why didn't He try to encourage him? This was a tough time for all the disciples, and all He said was "one of you is a devil."

I can totally understand the disciples who left, and I think I understand Peter. I think Peter knows that life with Jesus may not be easy or simple or even comprehensible, but it's incomparably better than life without Jesus. I think he recognized that Jesus rarely gives us the answers to life's confusion, but He never fails to give us Himself. "Where else can I go? You have the words of eternal life," said a befuddled and frustrated Peter. Where else indeed?

As a scientist, I want everything to make sense. I've been trained to find logical or empirical problems and to solve them. To accept the illogical or poorly-supported is the worst thing a scientist could do, and this training flows over into my life of faith. I want (as I imagine most Christians want) Jesus to make sense. I want the Bible to be rational. I don't want to be a fool for believing the unbelievable. I want to understand it all. I'm basically just like Peter.

Then along comes the God of the Bible, and He shatters those desires right at the start. He tells Abraham to sacrifice his promised son, Hosea to marry a hooker, Isaiah to walk around naked for three years, and Peter to eat His flesh. These are things the very same God told us NOT to do! It doesn't make any sense! God seems to relish using holy foolishness to confound our greatest secular wisdom (I Cor. 1:27). God wants us, like

Peter, to realize that the greatest value in this world is not logic, not even divine logic. It's God Himself.

As we gather here once again to celebrate science, I think it's very important for us to take a sobering look at the "hard sayings" that we struggle with. "In the beginning God created..." (Gen. 1:1). "God created ... after their kind" (Gen. 1:21). "In the day that thou eatest thereof thou shalt surely die" (Gen. 2:17). "Whatsoever Adam called every living creature, that was the name" (Gen. 2:19). "The serpent was more subtil than any beast of the field ... and he said" (Gen. 3:1). "All the days of Methuselah were nine hundred sixty and nine years: and he died" (Gen. 5:27). Who among us has the audacity to say that we truly understand these statements? These claims fly in the face of our most common experiences. A killer tree? A talking snake? A 969-year-old man? Why would anyone believe this?

Why? Because life with Jesus is better than life without. This is something that Charles Darwin never understood. After concocting an ingenious theory to explain living things without invoking divine intervention, Darwin tried to endow his theory with a little wonder. In 1842, he wrote,

There is a simple grandeur in the view of life with its powers of growth, assimilation and reproduction, being originally breathed into matter under one or a few forms, and that whilst this our planet has gone circling on according to fixed laws, and land and water, in a cycle of change, have gone on replacing each other, that from so simple an origin, through the process of gradual selection of infinitesimal changes, endless forms most beautiful and most wonderful have been evolved. (Barrett & Freeman 1986, p. 40).

I won't argue that evolution has a certain grandeur to it, but I will contend to my dying breath that life with Jesus is far grander. I admit that I still want to understand and explain the hard sayings of Genesis, which is why I'm here, but I also admit that I probably never will, at least on this side of heaven. I don't expect anyone in my lifetime to explain them either. Even if we could answer one question in Genesis, there are dozens more perplexing statements still on the list. That doesn't mean we should stop trying to understand, because in reality the quest to know truth is actually the quest to know Jesus, Who is the Truth. As we come together, we mustn't lose sight of the real reason we've come: to know Him. We may not be able to understand it all, but we know He's worth it. The reality of Jesus' presence infuses our research with greater purpose and gives us a much grander view of life than Darwin ever knew.

Todd Charles Wood
Assistant Professor
Center for Origins Research
Bryan College

Barrett, P.H. and R.B. Freeman. 1986. *The Works of Charles Darwin Volume 10. The Foundations of the Origin of Species*. New York University Press, New York.

Conference Schedule

Wednesday, June 15

2:00 p.m.
Registration opens

6:00 p.m.
Dinner

6:45 p.m.
Welcome from New St. Andrews College and Opening Prayer

Introductions and Announcements
Gordon Wilson
New St. Andrews College

7:00 p.m.
Plenary: "A Grander View of Research: Faith and Science as a Mutual Support System"
Leonard Brand
Loma Linda University

8:00 p.m.
Discussion

Thursday, June 16

8:30 a.m.
Plenary: "A Biblical View of Life: What Means this Text?"
Steve Boyd
The Master's College

9:30 a.m.
Discussion

9:50 a.m.
Break

10:00 a.m.
Student Papers

R1. Demme, "Does it Matter Where Spotted Owls Come

From?"
R2. Yong, "Investigating the Presence of Toll-like Receptors on the Cell Surface of Earthworm Coelomocytes"

10:50 a.m.
Research Papers Session I

R3. Anderson, "Genetic Analysis of Stress-directed Adaptive Mutations in Bacteria"
R4. Brophy, "Preliminary Results of a Cognitum Study Investigating the Traditional Tetrapod Classes"

12:00 noon
Lunch

1:30 p.m.
Plenary: “A Systems View of Life: A Grand Order in the Complexity of Life”
Steve Gollmer
Cedarville University

2:30 p.m.
Discussion

2:50 p.m.
Break

3:00 p.m.
Research Papers Session II

R5. Buggs, “Diversification by Polyploidy”

R6. Cavanaugh, “An ANOPA Study of Cetacean Sister-Group Relationships”
R7. Fouts, “Theodicy, Theistic Evolution, and the Question of God’s Care for the Animals”
R8. Gruenke, “Possible Post-Flood Genetic Changes in Humans that May Contribute to Reduced Longevity”
R9. Hennigan, “An Initial Investigation into the Baraminology of Snakes: Order Squamata, Suborder Serpentes”

6:00 p.m.
Dinner

7:30 - 9:00 p.m.
Poster Session

Friday, June 17

8:30 a.m.
Research Papers Session III

1:30 p.m.
Business Meeting

R10. Mace, “Statistical Evidence for Five Whale Holobaramins (Mammalia: Cetacea)”

R11. McGary, “Protein Interactions in Yeast Influence Protein Sequence Conservation”

R12. Standish, “A New Molecular Tool for Investigation of Inter and Intra Baramin Variation”

R13. Wise, The Nature of God as a Curricular Theme in Biology

10:15 a.m.
Break

10:30 a.m.
Plenary: “A Grand View of Nature: Creation and Evolution in the Galápagos Islands”
Todd C. Wood
Bryan College

11:30 a.m.
Discussion

12:00 noon
Lunch

Plenary Abstracts

P1. A Grander View of Research: Faith and Science as a Mutual Support System

L. Brand
Loma Linda University

Experience and a balanced understanding of the philosophy of science indicate how faith and science can be integrated into a search for truth. Many scholars have concerns about pitfalls that can cause problems when someone attempts to “mix science and religion.” Prominent among these are: 1) Science may disprove our Christian belief system; 2) The danger of returning to god-of-the-gaps thinking; 3) Religious explanations (“God did it”) may discourage scientific investigation; 4) We may hold religious positions that are ultimately not biblical, and scientific disproof of these positions will discredit our faith unnecessarily; and 5) Religion will introduce biases into our science. Solutions to these problems will provide the characteristics needed in a trustworthy method for integrating faith and science.

New scientific findings may challenge our understanding of some scriptural concept. This can lead to more careful study of the Bible, to be sure we are not reading something in between the lines. The reverse can also happen - scripture challenges a scientific interpretation. This can also lead to more careful, critical examination of the relevant science. In this process, the Bible and science can challenge each other in our minds, and lead to more careful study of both. A faith-based paradigm can open the researcher’s eyes to see things in a new way and ask questions that others are not asking. The role of science then is to test these new ideas, and determine if they will stand up to critical evaluation and peer review. If this is done right, the faith component does not compromise the scientific process in any way, but it can lead to scientific discoveries not likely to be made otherwise. Both science and religion benefit if scientists with different worldviews work on the same problems, as each will see things that the other is apt to miss.

P2. A Biblical View of Life: What Means this Text?

S. Boyd
The Master’s College

When properly understood the biblical texts that address matters normally considered to be the exclusive bailiwick of science furnish valuable information concerning the definition, taxonomy and hierarchy of life. That proper understanding is that these biblical texts are *vertical historical accounts*, *magisterial literary compositions* and *foundational theological treatises*. Apart from the first of these characteristics the pertinent texts could not admit a rigorous philological investigation to ascertain the biblical definition of life, the biblical perspective on taxonomy and the biblical perspective of the hierarchy of life, because if these texts are ahistorical myths, they cannot yield useful information to a scientist. On the other hand, if they are *historical narratives*, informed by this understanding, a careful philological study comprising primarily lexicography and syntax can yield significant results. But our understanding must be tempered by the second characteristic of these texts: they are *magisterial literary compositions*, and as such the first thing to note is that they must be read from the perspectives of their first readers. The author wrote his text with his first readers in mind. The author employed therefore a phenomenological perspective in his writing. He described the world as seen by the naked eye, as heard by the ear, touched by the hand, smelled by the nose and even tasted. Consequently, we should not expect the wording of a so-called “precise” scientific description or a discussion of life forms invisible to even our naked eye. Furthermore, texts mean what words mean, and words mean what the original readers would have thought them to mean. Ideas utterly unknown to them because they are based in modern thought would have been utterly foreign to the readers’ approach to the text. At the same time the second thing to note is that the author wrote from a divine perspective, writing about events absent of man or inaccessible to man. And finally, we must understand that these texts are *foundational theological treatises*. This does not disqualify them from being repositories of accurate scientific information. Nor does this preclude their literariness. Their genius is the balance of the three: real event, literary portrayal

and theological message. Only by applying all three can we know: what means this text?

P3. A Systems View of Life: A Grand Order in the Complexity of Life

S. Gollmer
Cedarville University

Design has been a key and yet elusive word in the areas of science and philosophy for many years. It seemed to reach its apex in 1802 with Paley's *Natural Theology*. However, in the wake of Darwin's *Origin* the recognition of design as part of a biological research paradigm has been greatly undermined. Design as expressed in *Natural Theology* is equivalent to that of a highly tuned machine. The parts are idealized and their relationships are synchronized and static. Although we see design of this type in nature, it has limitations when dealing with dynamic, complex interactions between components of a system. Component interaction can range from that of an organism within a biosphere to that of an organelle within the cell. Could there be a broader definition of design that can provide useful insights into the study of the creation and in turn become part of a fruitful research paradigm?

Here systems theory is used to develop a framework for defining design in a broader fashion. General systems theory, developed in the 1930s by Ludwig Bertalanffy, proposes the existence of properties or laws that describe the interactions between systems. These laws of interaction apply not only to biological systems, but also to social, political and mechanical systems. Cybernetics, a subdiscipline of systems theory, treats each component of a system as a black box. The black box interacts with its environment through inputs and outputs. Although the outputs of a component are dependent on its environment and internal state, it is possible to study component interaction without knowing the internal function of the component. This is a more holistic approach and provides a context from which to study adaptation, complexity and optimal design.

In recent years computer scientists have gained experience working with the design of complex systems. One fruitful approach to software design is Object Oriented Programming (OOP). In this approach complex programs are broken into smaller interacting components. By restricting the amount of interaction between components, the programmer is able to better anticipate the complexities of the system's behavior and, therefore, control and hopefully eliminate errant behavior. Out of OOP came the concept of design patterns, which are rules of "best practices" when solving certain software problems. Gamma et al. (1995) identified twenty-three such design patterns. Assuming these patterns capture the essence of design in a broader sense, a comparison can be made to biological systems.

From this comparison there is at least an analogous correspondence between OOP and biological systems. This gives confidence that design patterns provide a starting point for developing an inter-disciplinary language of design. As a research paradigm, a design language provides potential solutions to classes of biological problems. Although it does not prescribe the particular solution, it does restrict the number

of viable solutions for a well behaved system. As biologists are able to recognize and communicate design concepts effectively, new patterns can be discovered, which can benefit the OOP community as well as others.

As a specific application, systems theory and design patterns can be applied to the study of limits of variability in the creation. Thinking of an organism as a collection of interacting components, it is possible to differentiate between components exercising global control and those exercising only local control. Likewise a distinction can be made between components of interdependent function and components of peripheral function. Although the loss of a peripheral component is not lethal, it may reduce the ability of an organism to adapt to its environment. Assuming there has been a systemic degradation of each holobaramin since the fall, it may be possible to restore some of the adaptive capabilities of an organism by comparing current members of a particular holobaramin.

Gamma, E., et al. 1995. *Design Patterns: Elements of Reusable Object-Oriented Software*. Addison-Wesley, San Francisco.

P4. A Grand View of Nature: Creation and Evolution in the Galápagos Islands

T.C. Wood
Bryan College

Despite the reputation of the Galápagos Islands as nearly "sacred ground" to evolutionists, creationists have largely ignored them. Darwin's visit to the islands led him to reject species stasis and accept common descent, but the widespread belief that Darwin developed his ideas about natural selection from observations at Galápagos are false. Natural selection as an explanation of, for example, Darwin's finches came only in the mid-twentieth century. I recently completed a major review of Galápagos biology with particular attention to common ancestry and natural selection.

I analyzed eight groups of animals and plants, each with at least one species endemic to Galápagos, using baraminic distance and classical multidimensional scaling. The eight groups consisted of the cormorants (family Phalacrocoracidae), lava lizards (genus *Tropidurus*), a sunflower tribe (Asteraceae), the boobies (family Sulidae), the weevils (family Curculionidae), the penguins (family Spheniscidae), the iguanid lizards (family Iguanidae), and the turtles (order Testudines). Based on the results of these studies, I found that most groups contained at least one monobaramin, and I also identified seven holobaramins (the penguins, iguanids, and five turtle groups). At lower taxonomic levels within families, I did not find conclusive evidence of discontinuity using baraminic distance correlation. Only when examining families and their outgroups were discontinuities apparent (except for the curculionids which did not show evidence of discontinuity with outgroup taxa). These initial findings suggest that the baraminic distance correlation method does not indiscriminately identify any difference as a discontinuity.

Although adaptive radiation is frequently used to describe Galápagos organisms, it is poorly defined. To remedy this, I adapted five criteria from Carlquist (1974), two of which identify evidence of adaptation and three of which identify evidence of

radiation. When applied to six groups of Galápagos organisms frequently attributed to adaptive radiation, I find that only one, Darwin's finches, clearly show evidence of adaptive radiation. The sunflower trees of genus *Scalesia* could possibly be classified as an adaptive radiation, if the habitat diversity of the species were more well-known. The Galápagos tortoises, *Galapaganus* weevils, and the lava lizards show evidence of radiation but not adaptation, suggesting that radiation could occur without environmental adaptation (i.e. nonadaptive radiation). Because of a lack of research on native forms, the Galápagos prickly pears (*Opuntia* spp.) could not be identified as an adaptive or nonadaptive radiation.

These results imply that Darwin was correct when he inferred a common ancestor between mainland and island forms but that Darwin may have erred in attributing species diversity to natural selection. Future creationist research could focus on additional species found in the islands as well as more detailed studies of adaptive and nonadaptive radiation in the endemic species groups.

Carlquist, S. 1974. *Island Biology*. Columbia UP, New York.

Research Abstracts

R1. Does it Matter Where Spotted Owls Come From? The Importance of Life's Origins and History for a Christian Biodiversity Ethic

I. Demme
Independent Scholar

Modern species extinctions must be contextualized within the history of life and God's work of creation. Christian environmental ethics in turn must be contextualized within a historical and theological framework of creation, fall, and redemption.

A young-life theology of creation claims that extinction is a product of God's curse, and that all animal fossils were formed within human history. By contrast an old-life theology suggests that extinction is a normal and divinely orchestrated process of creation independent of human sin or divine curse.

Estimating the number of extinct species represented by fossils requires certain assumptions, which are affected by our theology of creation. The results of such estimations help us frame current extinction rates in the broader history of life. Using old-life assumptions, it can be estimated that 99.9% of all species that have ever lived went extinct before the creation or fall of man whereas young-life assumptions lead us to the conclusion that the majority of the species that have ever lived are still present today.

A biodiversity ethic which proceeds from a young-life theology of creation roots biodiversity preservation efforts in the work of redemption from nature's cursed state to an unfallen normative state of ecological harmony, while an ethic which proceeds from an old-life theology must see biodiversity preservation as a novel idea, and the Christian who holds to such an ethic must take care not to oppose God's work in creation by interfering with extinction processes (the normative state here of creation is in this view ecological balance and growth through extinction, rather than ecological harmony free from extinction).

In both cases, scientific research into the mechanisms and potential results of biological diversification will be very helpful in focusing preservation efforts and in furthering understanding of the role of diversity in God's creation.

R2. Investigating the Presence of Toll-like Receptors on the Cell Surface of Earthworm Coelomocytes

S. Yong, J. Francis, S. Stewart, and K. Reigstad
The Master's College

The earthworm immune system (EIS) is a focus of comparative immunological studies. Like other invertebrate systems, it displays a profound discontinuity with vertebrate systems because the specific immune system appears to be missing. Nonetheless, the EIS is efficient in protecting earthworms from soil pathogens, is involved in transplantation rejection, and can eliminate vertebrate tumor cell lines (Engelmann et al. 2005a). The major components of this innate immune system are the coelomocytes.

This study, which was undertaken by undergraduate biology students, represents a first attempt to assess the presence of Toll-like receptors (TLRs) on the coelomocyte surface. TLRs initiate the innate immune response and prime the adaptive immune response by recognizing various antigens on pathogen surfaces, called pathogen-associated molecular patterns (PAMPs) (O'Neill 2005). Hence, this could be a mechanism of defense of coelomocytes.

Coelomocytes from *Lumbricus* and *Eisania* worms were harvested and then labeled using fluorescent, monoclonal anti-human-TLR-2 antibodies, and non-fluorescent, polyclonal anti-TLR-2, 4, 6, and 9 antibodies. *Lumbricus* coelomocytes were labeled with fluorescent, monoclonal anti-mouse/rat CD-90 antibodies: a cell marker on *Eisania* coelomocytes. Recently developed monoclonal antibodies to EFCC1 and EFCC3 (cell surface markers specific for earthworm coelomocytes) were used as positive controls (Engelmann et al. 2005b). The non-fluorescent primary antibodies were labeled with either fluorescent anti-rabbit or anti-mouse secondary antibodies. Anti-TLR antibodies were established to be functional by obtaining positive results in human blood cell labeling. Anti-EFCC and anti-CD 90 antibodies were established to be functional by obtaining positive results on *Eisania* coelomocytes. Live adherent cell assays with fluorescent Lipopolysaccharide (LPS) were performed. Cells were viewed and photographed using a

fluorescent microscope.

We did not observe positive labeling of *Lumbricus* and *Eisinia* earthworm coelomocytes using monoclonal anti-TLR-2 or polyclonal anti-TLR-4 antibodies. The results from preliminary studies are negative labeling of *Eisinia* earthworm coelomocytes using polyclonal anti-TLR-9 antibodies, and positive labeling of *Lumbricus* earthworm coelomocytes with fluorescent LPS.

The results of the experiments suggest that TLR-2, 4, and 9 are not present on EIS. These results are supported by a recently published paper (Engelmann et al. 2005a).

It is very interesting to note that TLRs which are major components of the vertebrate immune system have yet to be found to play the same role in invertebrate immune systems. With respect to invertebrate systems, Toll and its homologues have been found in *Drosophila*, *Anopheles*, *Caenorhabditis elegans*, and *Tachypleus tridentatus* (Horseshoe crab). While these are known to play an indirect role in the host's innate immune response, they have not been found as PAMP-binding surface receptors. However, they are involved in development (O'Neill 2005). Non-disease fighting functions of Toll may be of interest to creationists since this may represent a remnant of Toll's function in the pre-Fall environment.

Our research project now involves two approaches. First, we plan to probe the surface of coelomocytes with all the known antibodies to TLRs and TLR cofactors. Secondly, it is hypothesized that if TLRs do not exist on coelomocytes, as yet uncharacterized PAMP-binding receptors may exist. Hence, we plan to perform experiments using fluorescent ligands of TLRs to investigate this hypothesis.

Engelmann, P., E.L. Cooper, and P. Nemeth. 2005a. Anticipating innate immunity without a Toll. *Molecular Immunology*. 42(8):931-942.

Engelmann, P., L. Palinkas, E.L. Cooper, and P. Nemeth. 2005b. Monoclonal antibodies identify four distinct *Annelid* (invertebrate) leukocyte markers. *Developmental and Comparative Immunology*. 29(7):599-614.

O'Neill, L.A.J. 2005. Immunity's Early Warning System. *Scientific American*. 292(1):24-31.

R3. Genetic Analysis of Stress-directed Adaptive Mutations in Bacteria

K.L. Anderson

Van Andel Creation Research Center

Since the discovery of DNA over fifty years ago, the field of genetics has been dominated by a Darwinian evolutionary paradigm. Within this paradigm is the view that spontaneous mutations arise as random errors. Occasionally results that appeared to contradict this Darwinian paradigm have been noted in studies of bacteria, but typically no significance was attached to these observations. However, as molecular techniques have developed, a more complicated picture of bacterial genetics has emerged that no longer fits within the confines of the Darwinian paradigm of random mutation.

A variety of environmental-stress conditions appear to initiate mutations within various bacteria. These mutations provide an adaptive response for the bacteria to these stress conditions. Commonly referred to as "adaptive mutations" or "directed" mutations, this is a phenomenon apparently unique to bacteria. The mechanism for adaptive mutations is not fully understood

(and probably does not involve a single phenomenon), but it does seem to involve an interaction of environmental conditions that cause specific mutations and specific gene expression. While this appears to be similar to Lamarckism (the idea of acquired characteristics), as asexual organisms, all genomic changes within bacteria are potentially hereditary. In contrast, Lamarck's ideas dealt exclusively with sexually reproducing organisms.

Darwinian evolutionary explanations of "directed" mutations suggest that random mutations generated a means of responding to certain environmental factors by a directed, non-random form of mutation. However, random mutation processes currently lack a sufficient mechanism for the origin of directed mutations. On the other hand, "directed" mutations are consistent with a creation model, where an intelligent creator would impart to biological systems a means of specifically adapting to particular environmental conditions, even adaptation requiring alterations of the organism's genetic characteristics. Glucose-limited bacteria, for example, form mutant strains possessing increased rates of glucose transport. Several lines of evidence suggest such mutations are non-random. Genetic analysis of these mutants also reveals they result from the loss of a regulatory protein, enabling a higher production of specific transport systems. While typically referred to in the literature as acquisitive evolution (in which organisms gain advantageous capability) the loss of a pre-existing system cannot correctly be considered a true acquisition (i.e., the organism lost a function, it did not acquire).

Creation science encompasses various views of mutations and variation, and creationists have typically aligned very closely with Mendelian genetics. Most creationists suggest a limit of both the types of mutations and the level of variation of an organism (i.e., massive genetic changes do not produce Darwinian change). Within this concept of limited change there is considerable divergence of views among creationists as to both the significance of mutations, and the concept of beneficial mutations. However, creationists have given little attention to non-random mutations. These "directed" mutations have only been found in asexual organisms, and probably represent a means the creator used to increase the genetic versatility and adaptability of these organisms. Known examples also appear to be degradative, which fits within creationists' concept of limited genetic change. Since these mutations appear to occur only in asexual organisms, they do not fit strictly within Mendelian principles, and represent another level of genetics within the framework of a creation model.

R4. Preliminary Results of a Cognitum Study Investigating the Traditional Tetrapod Classes

T.R. Brophy

Liberty University

At God's prompting, Adam named all cattle, the birds of the air, and all beasts of the field (Genesis 2:19-20). The ease and accuracy with which Adam accomplished this task suggests that it came natural to him. Sanders and Wise (2003) postulated that "God purposely created organisms in a pattern specifically recognizable to man and created man capable of recognizing that pattern." In addition, Sanders and Wise (2003) defined

the cognitum as “a group of organisms recognized through the human cognitive senses as belonging together and sharing an underlying, unifying gestalt.”

I set out to investigate the cognitum concept as it relates to the traditional tetrapod classes (Amphibia, Reptilia, Aves, and Mammalia). I did this by compiling and randomly shuffling a stack of 57 color photographs representing each of the major groups within the tetrapod classes (3 amphibian orders, 6 reptile orders/suborders, 27 bird orders, and 21 mammal orders). Animals were shown in natural or semi-natural habitats but were not to scale (photographs were approximately 5½” x 8”). Sixty-seven college students, selected on the basis of availability, were asked to sort the stack of photographs and give the criteria they used in determining each group. Students were given very few instructions on how to sort the photographs (other than mechanisms by which to communicate their classification scheme). They were not given pre-designed categories, were not asked to sort photographs into mutually exclusive groups, and were free to create fuzzy boundaries. Preliminary results from this study suggest some interesting patterns.

Students sorted photographs using a variety of criteria including habitat, diet, morphology, behavior, geographic origin, size, rarity, relationship to humans, beauty, and traditional taxonomy. The core group of the bird cognitum corresponds very closely to the traditional Class Aves. Approximately ¾ of the respondents explicitly identified all 27 bird orders as “birds.” The mammal cognitum does not correspond as well with the traditional Class Mammalia. Less than ¼ of the respondents explicitly identified all 21 mammal orders as “mammals.” Many respondents, however, created categories traditionally associated with the Class Mammalia (i.e. rodents, primates, bats) but never explicitly identified them as “mammals.” The pangolin (Order Pholidata) is clearly in the fuzzy boundary of the mammal cognitum. Approximately ¾ of the respondents identified it as a reptile and/or excluded it from the mammal group. A small proportion of the respondents classified the bat and colugo (Order Dermoptera) as “birds.” The amphibian and reptile cognita also differ somewhat from the traditional classes Amphibia and Reptilia. Only a very small proportion of respondents sorted all of the amphibian and reptile photographs in accordance with traditional taxonomy. Several of the common patterns that emerged were as follows: Amphisbaenian and caecilian grouped together as “worms”; lizard included in amphibian group; amphibians and reptiles thoroughly mixed together. Despite the apparent mixing of amphibians and reptiles, approximately ½ of the respondents identified the frog and salamander as “amphibians;” and the snake, turtle, tuatara, and alligator as “reptiles.” Future studies should pay special attention to the effects that particular methodologies (i.e. how organisms are chosen to “represent” a taxonomic group, presentation medium, age/experience of participants, instructions given to participants) have on the resultant classification.

Sanders, R.W. and K.P. Wise. 2003. The Cognitum: A Perception-Dependent Concept Needed in Baraminology. In R.L. Ivey, ed. *Proceedings of the Fifth International Conference on Creationism*. Creation Science Fellowship, Pittsburgh, pp. 445-455.

R5. Diversification by Polyploidy

R.J.A. Buggs

Independent Scholar

Polyploid organisms arise due to aberrant cell division and possess more than two complete sets of chromosomes in their cells. They are commonly classified as auto-polyploids if they arose from a single species and allopolyploids if they arose after a hybridisation event between two species, though it is now recognised that there is a continuum between these two types, according to the extent which the parents had diverged. Many plant genera show a range of ploidy levels, which are often classified as separate species, and polyploidy has undoubtedly contributed to baramin diversification. This raises the question: are polyploids a case of mediated design or of biological imperfection?

Some evidence suggests that polyploidy is a designed mechanism for diversification. Polyploids often differ from their diploid progenitors in cell size, physiology, breeding system and other characters that may affect their habitat tolerances and survival. In the northern hemisphere, polyploid plants tend to be more common in harsher and more northerly environments than diploids. Seventy-one per cent of the world’s agricultural production of food, fodder and fibre comes from polyploid plants. Some successful weeds such as *Spartina anglica* and *Tragopogon mirus* are allopolyploids.

On the other hand, polyploidy can be seen as a case of biological imperfection. The majority of genome-duplication mutations never lead to a viable polyploid lineage, and reduce the reproductive output of the organism in which they occur. Some polyploid lineages have lower fitness than their extant progenitor diploids. The geographical distribution of different ploidy levels within genera can often be explained in terms of historical contingency rather than adaptation to different environments.

The current view among most Darwinist biologists is that polyploidization events are an important mechanism of genome evolution. Could the evidence they use be interpreted by baraminologists as showing that polyploidy is a designed mechanism for diversification? Probably not, as the Darwinist view is influenced by the idea that lineages of most living organisms have undergone ancient genome duplication events, which have played a role in the evolution of new genes. Some evidence is claimed for this in studies of genome sequences, but is not conclusive. There are still a minority of Darwinists who follow G. L. Stebbins in seeing polyploids as evolutionary dead-ends, citing evidence from comparisons within extant plant polyploid complexes. This evidence is likely to be seen as more reliable by baraminologists.

The case of polyploidy shows the difficulties involved in distinguishing imperfection from mediated design. I suggest that polyploidy is a case of biological imperfection, illustrating that imperfection can be an important source of diversification.

R6. An ANOPA Study of Cetacean Sister-Group Relationships

D.P. Cavanaugh & R.v. Sternberg
Independent Scholars

An ANOPA analysis was performed using the morphological data set of Geisler and Uhen (2003), the latter having been augmented by the addition of forty cetacean-specific apomorphies (Sternberg 2005). The character data set used in this study sampled taxa at the ordinal and sub-ordinal levels (Rodentia, Carnivora, Archaic Ungulates, Cetacea, Mesonychidae, Hapalodectidae, Artiodactyla, and Perrissodactyla) involved 235 binary and multistate characters. The 1D ANOPA revealed three major and 3 minor statistical populations. *Andrewsarchus* and *Hapalodectes hetangensis* were selected as outgroups for the 2D and 3D ANOPA analyses: these two taxa occupy the end of the central and major statistical sub-population of the distributions recovered in 1D ANOPA. The 2D ANOPA resulted in three major clusters plus “outliers,” consistent with the 1D ANOPA analysis. Likewise, 3D ANOPA recovered three major taxic “clouds,” shaped roughly as conically stacked, distinctly separated bands. The central band possesses a well-separated outlying cluster of extant whales, porpoises, and dolphins. The taxic distance of recent cetaceans relative to the bulk of the non-cetacean taxa including the “walking whales” is significant, comparable to that of a super-order.

The morphospace of the sampled mammalian taxa was found to have a “thickened” horn-like or flattened conical topology, with taxa parceled into distinct, somewhat band-shaped clouds. The relative scatter, or morphospace variation, significantly increases in the direction (axially) from the basal or stem cloud (Sc1), to the central cloud (Sc2) and finally to the top cloud (Sc3). The morphospace appears to be significantly constrained and shaped by underlying generative rules. Within each cloud/band, taxic disparity shows more of a radial than an axial increase. The Sc1 cloud to Sc2 cloud gap (as measured by the *Hypertragulus/Heptodon* distance) is Pd=0.742. The Sc2 to Sc3 band gap (as measured by the (*P gigantea* → *Ankalagon* distance) is Pd=1.1019. These band gaps exceed maximal taxic (pattern) distances within adjacent clouds, and exceed the benchmark intra-baraminic diversification ranges. The Sc1 band diameter measures a Pd (*Mesohippus* to *Lama*) of 1.135. The Sc2 band diameter measures a Pd (*Balaenoptera* to Leptictid) of 3.544. The Sc3 band diameter measures a Pd (*Hapalodectes hetangensis* to *Protocetus*) of 4.633.

The Sc1 cloud sampled in this data set consists mainly of various artiodactyls including pigs and cameloids, canids, and equids. Most notably, *Rattus* (Sc2) has a significantly closer affinity to modern whales (Pd=02.172 to *Balaenoptera*) than does *Hippopotamus* (Sc1, Pd=2.547 to *Balaenoptera*), widely considered to be the closest modern land mammal to whales. *Basilosaurus* is located in the same sub-class band (Sc2) as the modern whale/dolphin order. The putative basal whale taxa (Geisler and Uhen 2003) are significantly scattered from each other across sub-class bands Sc2 and Sc3. The band assignments and distance to whales (relative to *Balaenoptera*) is as follows: *Ambulocetus* (Sc3, Pd=2.720), *Pakicetus* (Sc2, Pd=1.126),

Artiocetus (Sc3, Pd=3.358), *Rhodocetus* (Sc2, Pd=2.759) and *Protocetus* (Sc3, Pd=4.785). *Pakicetus* is located midway between the main body of the Sc2 cloud and that of the whale/dolphin sub-cloud, separated by approximately twice the largest reference intra-baraminical diversification benchmark.

The mammals sampled are hypothesized to be part of an apobaraminical assemblage, with three subsidiary assemblages consisting in turn of at least 3 subclasses. The modern cetacean cluster is separated from the main body of mammalian taxa at a distance of the magnitude of a super-order. Considering the taxic distribution of putative “walking whales,” their large separation distances from modern whales, and the lack of any coherent diversification trajectory, the Geisler and Uhen (2003) hypothesis of whale origins is not supported by ANOPA analysis.

Sternberg, R.v. 2005. Unpublished assemblage of 40 Cetacean soft body characters.

Geisler, J. H. and M. D. Uhen. 2003. Morphological support for a close relationship between hippos and whales. *Journal of Vertebrate Paleontology* 23(4):992-997.

Cavanaugh, D. P. and R.v. Sternberg. 2004. Analysis of Morphological Groupings Using ANOPA, A Pattern Recognition and Multivariate Statistical Method: A Case Study Involving Centrarchid Fishes. *Journal of Biological Systems* 12(2):137-167.

R7. Theodicy, Theistic Evolution, and the Question of God’s Care for the Animals

D. Fouts
Bryan College

Scripture for the most part attests to the truth that the God of the Universe does indeed care for the creatures in the animal kingdom. This fact should sufficiently answer questions about the justice of God allowing for death and cruel predation among animals only as a consequence of the entrance of sin into the created order by the disobedient sin of Man (i.e., the concept of Theodicy). However, a natural implication of the concept of Theistic Evolution (or if one prefers, Progressive Creationism) is that God allowed perhaps millions of years of death and cruel predation prior to the entrance of sin into the world of Genesis 3.

The issue of Theodicy is very important to the Young Earth position in that the God who is the same from everlasting to everlasting seems to violate his principled justice by allowing cruel predatory animal death to occur for millions of years prior to the creation of Man (and the concomitant introduction of sin into the world) in an old earth model. On the other hand, if death brought about by the Fall applies only to Man rather than to all life, then the justice of God can remain intact, but to those who hold a recent young earth creation, this view violates not only the traditional understandings of Romans 5 and 8, but also the characterization in Scripture that testifies of God’s watchcare of the animals. For instance, man was created at least in part, for the purpose of ruling over/having dominion over the created world. Understanding Gen. 1:26 as a *beth essentiae* leads one to believe that Man was created not in the image of God, but as the image of God, with “image” referring to a representative of the living God to a living world. Too, God offers numerous legal passages and wisdom passages that deal with God’s care for the animal world.

Taken as a whole, the Scripture's testimony of God's care for the animal kingdom seems strongly violated in the model of an old earth interpretation of the fossil record that demands millions of years of cruel animal death under the watchcare of God.

R8. Possible Post-Flood Genetic Changes in Humans that may Contribute to Reduced

Longevity

J. Gruenke

Patrick Henry College

In the pre-flood world, humans routinely lived for about 900 years. After the flood, the human lifespan decreased over a period of hundreds of years. Because the lifespan reduction occurred over many generations, it seems more likely that genetic rather than environmental changes are its primary cause. This research focuses on identifying genetic changes that may account for the difference in human lifespan before and after the flood. In the post-fall world, all organisms experience decay that ultimately leads to senescence and death. Two factors seem to be of particular importance in delay of senescence in humans: reduction of oxidative damage and maintenance of telomeres.

In mammals, there is a positive correlation between average body mass of a species and maximum lifespan. Larger mammals have a lower surface-to-volume ratio, and therefore lose less body heat and have a lower metabolic rate than smaller mammals. Since mitochondria are the main source of free radicals that cause oxidative damage, proportionally less oxidative damage generally occurs in larger mammals. This trend is not seen in fish, most of which are exothermic. Furthermore, reducing oxidation by reducing caloric intake (McCay et al., 1935) or upregulating expression of antioxidant proteins (Sun et al., 2004) has been shown to extend lifespan in some organisms. Intriguingly, one mammal, the little brown bat, lives more than 10-fold longer than predicted by its body mass, despite having a metabolic rate that is similar to similarly-sized mammals. The mitochondria of the little brown bat produce much less hydrogen peroxide than those of the mouse or shrew (Brunet-Rossini, 2004). Since mitochondria are inherited maternally, and post-flood genealogies record many instances of sons living much shorter lives than their fathers, it is reasonable to hypothesize that changes in the mitochondria population account for some of the longevity reduction.

It is also possible that metabolic rates of mammals increased as the post-flood world cooled, leading to increased oxidation and shorter lives. Many of the hormonal changes that would increase metabolism within a species, such as changes to the GH/IGF-1 axis, might also lead to an increase in body size, further increasing survival in a colder environment, and potentially explaining the apparent increase in body size of many mammalian species after the flood. These hormonal changes might also partially account for the apparent delay in puberty before the flood.

Telomeres are the ends of eukaryotic chromosomes. They are shortened with each cycle of DNA replication, but may be lengthened somewhat by telomerase, which is active in some populations of human cells, such as hematopoietic stem cells. If telomeres become too short, the cell ceases growth and

may enter apoptosis (Wong & Collins 2003). In some human tissues, telomere length decreases with age, and longer telomeres correlate with longer life in humans (Cawthon et al., 2003). Telomere length of white blood cells is inherited, and may follow an X-linked pattern of inheritance (Nowrot et al., 2004), again potentially explaining part of the observed reduction in post-flood longevity.

In order for a pre-flood human to experience a 10-fold increase in longevity compared with modern humans, it is likely that both the rate of oxidative damage and the maintenance of telomeres must have been changed. However, many other genetic changes are likely to be contributing factors as well.

McCay, C.M., M.F. Crowel, and L.A. Maynard. 1935. The effect of retarded growth upon the length of the life span and upon the ultimate body size. *J. Nutr.* 10:63-79.

Sun, J., et al. 2004. Effects of simultaneous over-expression of Cu/ZnSOD and MnSOD on *Drosophila melanogaster* lifespan. *Mech. Ageing Dev.* 125: 341-349.

Brunet-Rossini, A.K. 2004. Reduced free-radical production and extreme longevity in the little brownbat (*Myotis lucifugus*) versus two non-flying mammals. *Mech. Ageing Dev.* 125:11-20.

Wong, J.M.Y., and K. Collins. 2003. Telomere maintenance and disease. *Lancet* 362:983-988.

Cawthon, R.M., et al. 2003. Association between telomere length in blood and mortality in people aged 60 years or older. *Lancet* 361:393-395.

Nowrot, T.S., et al. 2004. Telomere length and possible link to X chromosome. *The Lancet* 363:507-510.

R9. An Initial Investigation into the Baraminology of Snakes: Order Squamata, Suborder Serpentes

T. Hennigan

Independent Scholar

It has been estimated that there are about 2300 species of snakes in the world. The species concept has been coming under fire for many years. Evolutionary taxonomists proclaim that the species taxon is the currency of biology, while at the same time realizing that the term has over twenty meanings and each is vigorously debated among biologists. It is my contention that much of the difficulty arises from the presuppositions of a materialistic metaphysic. Viewing through the spectacles of a theistic worldview, I hypothesize that many snake species, within certain families, are part of the same monobaramin.

A literature search was begun in order to determine the extent and frequency of snake hybridization, one of many factors that can be used as additive evidence in identifying probable monobaramins within the apobaramin.

In this initial investigation, three families were identified for their interspecific and intergeneric hybridization tendencies. The families are Boidae, Colubridae and Viperidae. Probable monobaramins were identified within each family. For Pythonidae they include, (1) *Morelia/Liasis* (2) *Antaresia* and (3) *Python*. Within the Colubrids (1) *Nerodia* (2) *Pantherophis/Lampropeltis/Pituophis* (3) *Diadophis* and (4) *Thamnophis*. The Viper monobaramins were identified as (1) *Crotalus/Sistrurus* (2) *Agkistrodon* and (3) *Bitis*.

Although hybridization is only one piece of important evidence, there were two other instances found where evolutionary researchers grouped snakes, thought to be separate species, into

a single species using characters such as color pattern, meristics, tail length and hemipenes. Based on this additional evidence, I have identified *Chilomensiscus* and *Canopsis/Tolucca* as two other monobaramins within Colubridae.

This initial investigation indicates that many genera, within certain families, are phylogenetically related. Many are capable of hybridizing interspecifically and intergenerically, even when they are geographically isolated by vast distances in the wild and display a vast degree of variation within a species. As more data are gathered, and the Serpentes suborder is analyzed holistically and quantitatively, I predict that a creationary model of snake biosystematics will emerge that will avoid the philosophically ambiguous species concept and have a more robust predictive value than the current evolutionary model.

R10. Statistical Evidence for Five Whale Holobaramins (Mammalia: Cetacea)

S.R. Mace and T.C. Wood
Bryan College

As a prelude to a more extensive examination of the whale fossil record, we have analyzed a published dataset of cetaceans (Messenger and McGuire 1998) using baraminic distance and classical multidimensional scaling (MDS). The dataset consists of 207 characters scored for 72 taxa. The characters are skeletal and soft tissue. The taxa consist of 66 extant cetacean species, one composite taxon of family Basilosauridae (suborder Archaeoceti), and five artiodactyl outgroups. The three cetacean suborders are represented by 60 species from all 33 genera from suborder Odontoceti (toothed whales) and six species from the three families of suborder Mysticeti (baleen whales). The archaeocete taxon is a composite of the Upper Eocene species *Basilosaurus cetoides*, *Zygorhiza kochii*, and *Dorudon osiris*. After filtering the dataset for 95% character relevance, we used 121 characters to calculate baraminic distances. Baraminic distance correlation revealed two groups of taxa whose members are positively correlated but which are negatively correlated with each other. The two groups corresponded to the Odontoceti and the Archaeoceti + Mysticeti + Artiodactyla. We hypothesized that the second group actually comprised multiple apobaramins, and we recalculated baraminic distance correlations for the non-odontocete only. These results revealed significant negative correlation between the Mysticeti and Archaeoceti + Artiodactyla. Baraminic distance correlations for just the Archaeoceti + Artiodactyla revealed significant negative correlation between those two groups. We also calculated baraminic distance correlation for just the odontocete taxa, and found significant negative correlation between the Ziphiidae, Physeteroidea, and the remaining Odontoceti. For all baraminic distance correlation calculations, the Mysticeti, Ziphiidae, Physeteroidea, and remaining odontocetes exhibited within-group significant, positive correlation. We calculated three-dimensional MDS on the baraminic distances as recommended by Wood (2005). Our results showed a stress of 0.165 after MDS calculations. The 3D MDS results confirm our distance correlation results, showing six well-defined groups separated by clear gaps. The groups correspond to the Artiodactyla, Archaeoceti, Mysticeti, Ziphiidae,

Physeteroidea, and the remaining odontocetes. We conclude that the extant cetaceans comprise at minimum four holobaramins, based on positive correlation with ingroup taxa and negative correlation in ingroup/outgroup comparisons. These four holobaramins are the Mysticeti, Ziphiidae, Physeteroidea, and the remaining odontocetes. Most significantly, the Archaeoceti, while occupying a morphologically intermediate position between the extant cetaceans and the artiodactyls, are very much closer to the artiodactyls than to any of the extant whale holobaramins. Based on the limited sample, we also propose that Archaeoceti may be a fifth whale holobaramin. Future research should examine more of the archaeocete species to determine their baraminic relationships in greater detail, especially the pakicetids and ambulocetids. Other studies will be needed to evaluate the putative ancestral status of mesonychids or hippopotamids.

Messenger, S.L. and J.A. McGuire. 1998. Morphology, molecules, and the phylogenetics of Cetaceans. *Systematic Biology* 47(1):90-124.
Wood, T.C. 2005. A creationist review and preliminary analysis of the history, geology, climate, and biology of the Galápagos Islands. *CORE Issues in Creation* 1:1-242.

R11. Protein Interactions in Yeast Influence Protein Sequence Conservation

K. McGary
Independent Scholar

Historically, molecular sequence data have been of limited use to baraminologists primarily because they overemphasize continuity (Wood 2002, Wood et al., 2003). With the growing number of molecular data, habitating them would contribute significantly to future baraminological studies. To do so, baraminologists need to understand the patterns of molecular differences that are consistent with independent creation, but that suggest descent with modification. The architecture of biological networks contributes to the differential conservation of protein sequences, which may falsely lead to the inference of common descent. In particular, the amino acid residues that specify protein-protein interactions have been shown to be preferentially conserved relative to other residues on the protein surface (Fraser et al., 2002). In this study, I utilize the well annotated yeast interaction network to analyze sequence conservation between homologous proteins throughout the ascomycete fungi. My hypothesis is that neighboring proteins in the network, which are involved in related cellular processes, will exhibit similar patterns of sequence conservation.

To find the patterns of protein sequence conservation across the fungi, I identified the 588 proteins that have homologs in all 22 currently sequenced fungal genomes using Blast. Homologs were identified using a reciprocal best hits criteria and an E value cutoff of 10^{-4} . Homologous protein sequences were aligned with ClustalW using the default parameters and pairwise distance matrices were generated. All distance matrices were then compared in a pairwise fashion by calculating their root mean squared deviation or their mutual information. Protein pairs were then ranked by the similarity or shared information content of their matrices and scored as related by both a yeast interaction network (Lee et al., 2004) and Gene Ontology process

(GO) annotations. They scored positively if the proteins were neighbors in the network or if they shared the same annotation. The matrix similarity ranked pairs were binned by groups of 1000 and the number of related pairs were summed for each bin and plotted.

As expected, the ranked bins demonstrated that neighbors in the interaction network are more likely than random to share similar matrices. Surprisingly, however, proteins with very dissimilar matrices were also more likely to be neighbors than would be expected at random. Pairs scored by GO annotation demonstrated a weak correlation ($R^2 = 0.395$) between ranked matrix distance and the likelihood of being similarly annotated.

This initial study has shown that the network of biological interactions has a modest but detectable influence on the conservation of protein sequence. Further investigation into biological networks may allow baraminologists to make more informed use of molecular sequence data, which, thus far, has been of limited value in identifying discontinuities. Furthermore, this approach can be used to re-interpret evolutionary phylogenetic studies that appear to have found consistency between phylogenies estimated from multiple genes that are in similar biological pathways.

Fraser, H.B., A.E. Hirsh, L.M. Steinmetz, C. Scharfe, and M.W. Feldman. 2002. Evolutionary rate in the protein interaction network. *Science*. 296(5568): 750-2.

Lee, I., S.V. Date, A.T. Adai, and E.M. Marcotte. 2004. A probabilistic network of yeast genes. *Science* 306(5701):1555-8.

Wood, T.C. 2002. A baraminology tutorial with examples from the grasses (Poaceae). *TJ* 16:15-25.

Wood, T.C., K.P. Wise, R. Sanders, and N. Doran. A refined baramin concept. *Occasional Papers of the BSG*. 3:1-14.

R12. A New Molecular Tool for Investigation of Inter and Intra Baramin Variation

T.G. Standish

Geoscience Research Institute

Taxa with progressively fewer “homologous” traits are assigned to broader taxonomic levels and assumed to share increasingly ancient common ancestors. When assigning taxa to a baramin based on evidence of actual common ancestry, shared characteristics cannot be ignored, but unique traits may ultimately prove more informative.

Recently published genomes of the cryptic nematode species (Nigon & Dougherty, 1949) *Caenorhabditis elegans* (Consortium, 1998) and *Caenorhabditis briggsae* (Stein et al., 2003) provide an opportunity to address questions about the origin of unique sequences in genomes and their usefulness in classification. Common ancestry appears to be the most reasonable explanation for these genetically distinct cell-for-cell identical organisms which thus may provide insight into what nature can achieve when engineering genomes. In this study, the utility of Random Amplified Polymorphic DNA (RAPD) (Williams et al., 1990) for identification of DNA sequences unique to *C. elegans* was demonstrated.

Genomic DNAs from six *C. elegans* strains (AB1, GM, KR314, N2, GM and TR403), three *C. briggsae* strains (DH1300, AF16, and DR1690 [previously designated BO, G16 and Zuckerman,

respectively]) and inbred *C. vulgaris* and *C. remanei* strains were used as templates in RAPD reactions using 20 10mer primers. Two *C. elegans* specific fragments — designated OPA-10₁₂₁₀ and OPA-16₁₁₆₅ (numeric subscripts indicate fragment length in base pairs) — were cloned and sequenced. Sequenced fragments were compared with Genbank published sequences using NCBI BLASTn (Altschul et al., 1997) default settings (Expect = 10, Word size = 11, Low complexity filter). Altering settings did not impact results.

OPA-10₁₂₁₀ and OPA-16₁₁₆₅ fall within putative *C. elegans* protein coding regions, both having putative *C. briggsae* “orthologs” identified by BLASTP. However, while protein alignments reveal similarities, the *C. briggsae* “orthologs” showed significant DNA sequence divergence from the corresponding *C. elegans* sequence. The ability of RAPD to identify unique DNA sequences in cryptic species may translate to a generalized approach applicable to other cryptic taxa.

One of the following seven scenarios may explain *C. elegans* specific DNA fragments: 1) Common ancestry in which *C. briggsae* lost a given sequence through deletion; 2) genetic drift; 3) the neo-Darwinian mechanism producing new sequences in *C. elegans*; 4) convergent evolution of initially different DNA sequences to produce a similar gene product; 5) horizontal gene transfer from an unidentified species to *C. elegans*; 6) some unidentified inherent mechanism for sequence generation produced these sequences in *C. elegans* but not *C. briggsae*; or 7) each species created as separate kinds. Of all of these, option 2) appears to be the most parsimonious, especially given the similarity in protein sequences, and is consistent with the hypothesis that *C. elegans* and *C. briggsae* may be grouped within a monobaramin.

Nigon, V. and E.C. Dougherty. 1949. Reproductive patterns and attempts at reciprocal crossing of *Rhabditis elegans* Maupas 1900, and *Rhabditis briggsae* Dougherty and Nigon. *J. Exp. Zool.* 112:485-503.

The *C. elegans* Sequencing Consortium. 1998. Genome Sequence of the Nematode *C. elegans*: A Platform for Investigating Biology. *Science* 282: 2012-2018.

Stein, L.D., and 35 others. 2003. The Genome Sequence of *Caenorhabditis briggsae*: A Platform for Comparative Genomics. *PLoS* 1(2):166-192.

Williams J.G.K., A.R. Kubelik, K.J. Livak, J.A. Rafalski and S.V. Tingey. 1990. DNA polymorphisms amplified by arbitrary primers are useful as genetic markers. *Nucleic Acids Research*. 18:6531-6535.

Altschul, S.F., T.L. Madden, A.A. Schäffer, J. Zhang, Z. Zhang, W. Miller, and D.J. Lipman. 1997. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. *Nucleic Acids Research*. 25:3389-3402.

R13. The Nature of God as a Curricular Theme in Biology

K.P. Wise

Bryan College

God created everything in part to reveal His nature to man (Ro. 1:20). The structure of the biological is a consequence of and an illustration of the Nature of God. Since complex information is easier to present and understand when united by a simple unifying theme, any study of the physical world (e.g. biology) should be facilitated by organizing it according to the centralizing theme of God’s nature. This should be effective because 1) it corresponds to the actual structure of the biological creation; 2) it encourages

development of a Christian perspective for all biology; 3) it permits a biology course to function as worship; and 4) it prompts the student from that day forward to utilize biology as a means of better knowing God. This communication reports on a course designed to utilize this theme and encourages the development of similar biology courses and texts.

A semester-long introductory biology course for non-majors using the nature of God as a theme was developed, implemented, and repeated twice again at Bryan College. Given that it was a non-major course in biology, it was free of external requirements which arise from developing a curriculum for placing students into graduate or professional schools. The course included a unit on the philosophy of science (because of the ubiquitous misunderstanding of science in the popular world), a substantial component on origins (because of its foundational importance), a substantial component on bioethics (because everyone in our society is likely to have to deal with biotechnology), a substantial component on the human body (because knowledge of our own design can potentially aid all of us), and was organized from the most familiar (*e.g.* ecology) to the least familiar (*e.g.* biochemistry).

The introduction to each unit in such a course (and chapter in a corresponding text) includes a biblical justification of one aspect of God's nature and how that divine character effected the biological creation. This is followed by a description of the physical consequences of that character. Examples of units (and examples of biological topics that can be included in that unit) include (but are by no means limited to):

- Living God (What is Life?; Law of Biogenesis; Defining Life's Beginning and End)
- God as Spirit (Life as Non-physical; Naturalism's Failure; Reductionism's Failure; Inference of the Unseen)
- God's Image (Man's Centrality; Man as Image)
- God Who Desires to be Known (Science's Theological Foundations; Philosophy of Science; Biology as a Way of Knowing God)
- God as Provider (Anthropic Principle; Provisional Cycles: carbon cycle, *etc.*)
- God's Glory (Biology's Beauty)
- 3-Person Godhead (Life's Disparity; Baramins; Life's Mosaic Structure)
- God is Love (Marriage; Family Planning; Body)
- God is One (Community; Ecology; Symbiosis)
- God's Abundance (Life's Diversity; Overdesign)
- God's Omniscience (Design; Complexity; Integration of Complexity)
- God as Delegator (Dominion Mandate; Taxonomy; Stewardship; Environmental Ethics)
- God as Creator (Origins; Mediated Design)
- Holy God (Fall; Carnivory; Biological Imperfection)

R14. Interspecific Hybrids in the Solanaceae

K.P. Wise
Bryan College

The family Solanaceae displays high diversity (~2400 spp.) and high disparity (*e.g.* potatoes, chili peppers, tobacco,

petunias). *Solanum* is both diverse (~1000 spp.) and disparate (*e.g.* potatoes, tomatoes, eggplants, nightshades, mandrakes). This study probes the prospect of success of baraminology research on the Solanaceae.

Those familiar only with food crop members of the family often struggle to understand what unites such disparate organisms into a single family. However, experts insist that the Solanaceae have a distinctive, recognizable body plan. Yet, since no single character unites all members of the family, the familial placement of a number of taxa (*e.g.* *Duckeodendron*, *Goetzea*, *Nolana*) is controversial. Fuzzy boundaries about a gestalt-defined group is reminiscent of the cognitum of Sanders & Wise (2003).

Intra-family classification of the Solanaceae has been difficult and controversial. Morphological classification (D'Arcy 1991) divides the family into 97 genera among 13 tribes and 2 subfamilies. As Sanders (2004) observed for other angiosperm taxa, DNA studies on the Solanaceae (*e.g.* Hunziker 2001; Olmstead *et al.* 1999) suggest substantial modifications on traditional morphological classification – usually increasing disparity apparent from morphology alone.

Abstracts in the *Plant Breeding Abstracts* (1930-present) mentioning interspecific hybrids among the Solanaceae are estimated to exceed 5,000, suggesting substantial data is available for baraminological studies on the family. A sample of those abstracts was examined to develop a preliminary baraminological hypothesis for the family. In *Solanum*, interspecific hybridization links at least 30 species with the eggplant and at least 50 other species with the tomato, whereas no interspecific cross was discovered linking these two groups. However, hybridization has been documented between the tomato (*Lycopersicon*) and species of 1) three genera universally classified in the same tribe (*Solanum*, *Cyphomandra*, *Physalis*), 2) *Capsicum* (universally classified in the same subfamily, but sometimes in a different tribe), and 3) *Petunia* (always classified in a different subfamily). *Petunia* species, in turn, are known to hybridize in their own subfamily with *Nicotiana*, and *Nicotiana* species, in turn, are known to hybridize with *Hyoscyamus* – in yet another tribe back in *Solanum*'s subfamily. In short, no matter the classification, the two largest subfamilies and several of the largest tribes of the family Solanaceae are united by intergeneric hybrids. Based upon the breadth of intra-familial hybridization and the fluidity of intra-familial classification, the entire family Solanaceae is hypothesized to be one monobaramin.

The Solanaceae would make good baraminological subjects. Several important food crops guarantee an abundance of data will be available, and perhaps even research funding. The disparity shown in the family (herbaceous *vs.* arborescent; staple food *vs.* deadly poison; cultivated *vs.* wild; tuber- *vs.* leaf- *vs.* fruit- crop; spicy *vs.* bland) makes it an excellent subject for studying the cognitum concept and mediated design. The large differences in intra-generic diversity (from monotypic genera to *Solanum*) permit study of the diversity of diversity, and the commonness of polyploidy in the family permits study of polyploidy's role in intra-baraminic diversification.

D'Arcy, W.G. 1991. The Solanaceae since 1976, with a review of its biogeography. In Hawkes, J. G., R. N. Lester, M. Nee, and N. Estrada, eds. *Solanaceae III: Taxonomy, Chemistry, and Evolution*. Royal Botanic Gardens,

- Kew, UK, pp. 75-137.
- Hunziker, A.T. 2001. *Genera Solanacearum: The Genera of Solanaceae Illustrated, Arranged According to a New System*. A. R. G. Ganter, Ruggell.
- Olmstead, R. G., J. A. Sweere, R. E. Spangler, L. Bohs, and J. D. Palmer. 1999. Phylogeny and provisional classification of the Solanaceae based on chloroplast DNA. In Nee, M., D. E. Symon, R. N. Lester, and J. P. Jessop, eds. *Solanaceae IV: Advances in Biology and Utilization*, Royal Botanic Gardens, Kew, UK, pp. 111-137.
- Sanders, R.W. 2004. In search of the silver bullet – or – God’s history lesson for systematics. *OPBSG* 4:8-9.
- Sanders, R.W. and K.P. Wise. 2003. The cognitum: A perception-dependent concept needed in baraminology. Ivey, R.L., Jr., ed. *Proceedings of the Fifth International Conference on Creationism*. Creation Science Fellowship, Pittsburgh, PA, pp. 445-455.

R15. The Emergence and Popularity of Marsh’s Baramin Concept

T.C. Wood
Bryan College

I previously claimed that Frank Lewis Marsh was the originator of the “created kind” concept (Wood and Murray 2003, pp. 15-16), but Numbers (2004) has shown that several creationists advocated accepting limited speciation prior to Marsh. George McCready Price (1917, 1924) initially allowed for considerable speciation, eventually suggesting that evolution within the rank of family was acceptable to the creationist. Dudley Joseph Whitney (1928, 1929) also accepted limited speciation, which drew criticism from Byron C. Nelson (1929). Nelson based his own view of species change on Mendelian genetics and on experimentally demonstrable phenotypic changes (1927). Nelson (1929) objected to Price and Whitney partly because Nelson could see no means of limiting the changes, but Nelson’s own views were vulnerable because of his endorsement of gene immutability. Price maintained his views on speciation up to at least 1938, but he abruptly (and briefly) reverted to a form of species stasis following the publication of Harold W. Clark’s (1940) *Genes and Genesis* (see Price 1941). Clark used hybridization to explain speciation and especially such organisms as *Archaeopteryx* (as a reptile × bird) but put no specific limit on evolution. Clark was partially inspired by an obscure statement of Seventh-day Adventist prophetess Ellen White regarding “amalgamation of man and beast” as a method of producing new species (Shigley 1984). Since Price was already arguing with Clark over geological matters (Numbers 1992, pp. 124-129), it is not surprising to find him disagreeing with Clark’s biological ideas also. In the midst of this diverse array of opinions, Marsh (1941, 1944) proposed his *baramin* concept, which Price (1945) supported. Marsh used two distinct arguments for his *baramin*. First, he believed the Genesis phrase “after its kind” was a biological law of reproduction, and therefore any species that could hybridize must belong to the same *baramin*. Second, he claimed that obvious “discontinuity” exists between different *baramins*. Marsh explained the amalgamation statements by reference to Price’s (1931) interpretation, and he never tied his theories to a specific model of species change. In the 1980s and 1990s, interest in Marsh’s ideas revived primarily because his ideas were well-known. In the latter half of the twentieth century, Marsh promoted his biological ideas in papers (e.g. 1964) and a book (1976). Whitcomb and Morris (1961) also promoted

Marsh’s *baramin* with a citation in *The Genesis Flood*. During the same time period, other early creationists did not promote their ideas to the same extent. Price died in 1963, and Whitney died in 1964. Clark (e.g. 1977) published papers mostly on geology, and Nelson produced a revised version of “*After Its Kind*” in 1967. As a result, the most popular ideas at present about “created kinds” are essentially those of Frank Lewis Marsh.

- Clark, H.W. 1940. *Genes and Genesis*. Pacific Press, Mountain View, CA.
- Clark, H.W. 1977. Fossil zones. *CRSQ* 14(2):88-91.
- Marsh, F.L. 1941. *Fundamental Biology*. Self-published, Lincoln, NE.
- Marsh, F.L. 1944. *Evolution, Creation, and Science*. Review and Herald Publishing, Washington, D.C.
- Marsh, F.L. 1964. Genesis kinds in our modern world. *CRSQ* 1(1):30-38.
- Marsh, F.L. 1976. *Variation and Fixity in Nature*. Pacific Press, Omaha, NE.
- Nelson, B.C. 1927. “*After its Kind*.” Augsburg Publishing House, Minneapolis.
- Nelson, B.C. 1929. More about the origin of species. *The Bible Champion* 35(10):539-540
- Numbers, R.L. 1992. *The Creationists*. University of California Press, Berkeley.
- Numbers, R.L. 2004. Ironic heresy: how young-earth creationists came to embrace rapid microevolution by means of natural selection. In A. Lustig, R.J. Richards, and M. Ruse, eds. *Darwinian Heresies*. Cambridge University Press: Cambridge, pp. 84-100.
- Price, G.M. 1917. *Q.E.D.; or, New Light on the Doctrine of Creation*. Fleming H. Revell, New York.
- Price, G.M. 1924. *The Phantom of Organic Evolution*. Fleming H. Revell, New York.
- Price, G.M. 1931. The problem of hybridization. *The Ministry* 4(4):13-14.
- Price, G.M. 1938. Nature’s two hundred families. *Signs of the Times* 65:11, 14-15.
- Price, G.M. 1941. What is the Christian’s best strategy? *The Ministry* 14(9): 16-18, 47.
- Price, G.M. 1945. Book review: *Evolution, Creation, and Science*. *The Ministry* 18(1):14.
- Shigley, G. 1982. Amalgamation of man and beast: what did Ellen White mean? *Spectrum* 12(4):10-19.
- Whitcomb, J.C. and H.M. Morris. 1961. *The Genesis Flood*. Presbyterian and Reformed, Phillipsburg, NJ.
- Whitney, D.J. Feb. 1928. Errors of fundamentalist science. *The King’s Business* 19:82-83.
- Whitney, D.J. May 1929. The miracles of evolution. *The Bible Champion* 35(5):250-252.
- Wood, T.C. and M.J. Murray. 2003. *Understanding the Pattern of Life*. Broadman & Holman, Nashville.