Gene Duplications and Nonrandom Mutations in the Family Cercopithecidae: Evidence for Designed Mechanisms Driving Adaptive Genomic Mutations

Jean K. Lightner*

Abstract

Historically, creationists have explained the diversity in created kinds primarily in terms of initial created variability, Mendelian inheritance, chance deleterious mutations, and natural selection. Baraminology research suggests that some animal kinds represented by a single pair on the ark less than 4500 years ago have diversified significantly and are now represented by entire families. This suggests that other mechanisms are present that generate diversity to allow animals to adapt. Research on the RNASE gene in Old World monkeys suggests that programmed adaptive genetic changes were involved in gene duplication and subsequent nonrandom adaptive mutations.

Introduction

Historically, many creationists have explained the diversity in baramins (created kinds) primarily in terms of initial created variability, Mendelian inheritance, chance deleterious mutations, and natural selection. Baraminology research has found that species believed to belong to a single baramin often consist of families and sometimes several families of organisms (Wood, 2006). The degree of phenotypic diversity present within baramins implies significant genetic diversity and the involvement of additional mechanisms designed to generate variety (Lightner, 2006; Lightner, 2007; see also Wood, 2003; Ashcraft, 2004). One of the most challenging and promising areas of future creationary biological research is in identifying genetic diversity within baramins and researching suitable mechanisms to explain this diversity. This research is crucial for a coherent creationary model that accounts for the present diversity within baramins of land animals and birds after a severe genetic bottleneck less than 4500 years ago at the time of the Flood (Genesis 6–8; Ussher, 2003).

Biblical Starting Point

Since the Bible provides the only account of origins and early history from an eyewitness perspective, examining it first will eliminate many unnecessary rabbit trails. God created animals according to their kinds, with the ability to reproduce and with the intent that they fill the earth and seas (Gen. 1:21–25). Initially, all creation was declared "very good" (Gen. 1:31); but later humans rebelled,

* Jean K. Lightner, D.V.M., 11 Meadowlawn Dr. Unit 9, Mentor, OH 44060, jklightner@gmail.com

Accepted for publication September 17, 2008

and the earth was cursed (Genesis 3; Rom. 8:18–22). Many centuries later human wickedness became so great that the earth was judged with a global flood. After the Flood, land animals and birds preserved on Noah's ark reproduced and filled the earth again (Gen. 8:16–17). God created the earth to be inhabited, and He cares for His creation (Isa. 45:18; Ps. 147:8–9; Matt. 6:25–34). Given this, it seems that animals would be designed with the genetic ability to adapt as they spread throughout the earth.

The fact that humans were created in the image of God (Gen. 1:26–27) has a variety of implications. In the present context, this implies that uniquely human traits, not including sinfulness, reflect the Creator. Some examples include abstract thought, advanced communication ability, creativity, appreciation for beauty, engineering abilities, and computer programming skills. God communicates to us (Heb. 1:1–2; 2 Tim. 3:16) and does so even using abstract concepts such as sin and redemption (Rom. 3:23–24). The beauty and creativity in creation is seen around us in the vast variety of living things in various sizes, shapes, and colors. The amazing adaptations in nature have inspired a whole field of science, biomimetics, in which engineers study and copy designs in God's creation. It follows that, as a programmer, God should be clearly evident somewhere in creation.

Genomes: Sophisticated Computational Information Storage Systems

Evolutionists have historically viewed the genome as the product of random mutations and other chance processes, including fortuitous events and culling by natural selection. The genome contains not only protein-coding genes, but also considerable noncoding regions, often referred to as "junk DNA." Yet the scientific literature contains a tremendous amount of data indicating that various types of repetitive DNA, including transposable (or mobile) genetic elements (TEs), are important for proper genomic function (reviewed in Sternberg and Shapiro, 2005). These TEs have traditionally been viewed as parasitic. So far over 50 human diseases are known to result from movement of TEs, which is estimated to represent approximately 0.3% of all human mutations. Many other TE insertions are considered neutral (Belancio et. al., 2008).

For all the scientific literature on the genome, we appear to have only a preliminary understanding of how it functions. The snapshots of data do not necessarily give us a clear picture of either what happens over time, or information about the causes and potential purpose related to these changes. For example, some mutations cause early death and may not be detected. This means that detrimental mutations may be more common than is now assumed. Many neutral mutations never reach sufficiently high levels in a population to be detected, thereby obscuring the rate and pattern of mutations. Additionally, there may be a significant reporting bias in cases where mutations cause disease because disease investigation is comparatively well funded; this may cause mutations to appear disproportionately deleterious. Furthermore, sequencing is generally done on only one or a few individuals; thus we often do not know how common allelic diversity exists at these loci. All these factors may serve to obscure a comprehensive understanding of genetics. Furthermore, the term "neutral mutation" generally refers to mutations whose effects are subtle or unknown. The large number of "neutral" mutations should make creationists very suspicious that something important may be occurring that has not yet been characterized.

Attempting to account for the molecular data generated since the modern synthesis theory of evolution was conceived, some evolutionists see the need to view the genome differently. Some think of DNA as a data storage medium and have described genomes as "sophisticated computational information storage systems" (Sternberg and Shapiro, 2005, p. 108.) Using this metaphor, protein-coding genes are the data files and TEs serve to format the genome so that the "data files" are in the right place at the right time for organisms to function. Given the Biblical teaching of the Curse, one might expect that such a complex system would occasionally fail, resulting in disease or death, though this remains a small part of the whole picture. Sternberg and Shapiro (2005) conclude:

> As we increasingly apply computational metaphors to cellular function, we expect that a deeper understanding of retroelements and other repeats, the integrative fraction of cellular DNA, will lead to increased understanding of the logical architecture inherent to genome organization. In the era of biocomputing and systems biology, the study of cellular information processing promises to revolutionize not only the life sciences but also the information sciences. We anticipate learning powerful new computational paradigms as we come to understand how cells use myriad molecular components to regulate millions of biochemical events that occur every minute of every cell cycle. Our expectation is that, one day, we will think of what used to be called "junk DNA" as a critical component of truly "expert" cellular control regimes (p. 114).

Some creationists also have argued that TEs play an important role in all living organisms. TEs mediate an increase in genetic diversity: they may activate or inactivate genes, increase the copy numbers of genes, and possibly allow for horizontal gene transfer between eukaryotes (Bergman, 2001; Wood, 2003).

Gene Duplications and Adaptive Mutations in Old World Monkeys (Cercopithecidae)

Shifting back to the general question of accounting for genetic diversity within baramins, a fascinating article by Jianzhi Zhang (2006) may provide insight into mechanisms for generating diversity. Zhang studied the pancreatic ribonuclease (RNase) gene in a number of primate lineages (Zhang et al., 2002) and found the gene (RNASE1) ostensibly duplicated in the douc langer (*Pygathrix nemaeus*), a leaf-eating monkey.

Leaf-eating monkeys (colobines) are a subfamily (Colobinae) of Old World monkeys (Cercopithecidae) (Myers et al., 2008). A previous baraminology study suggested that Cercopithecidae represents a single baramin (cited in Wood, 2006). The colobines differ from others in this family in that their diet is primarily leaves rather than insects and fruit. They have a ruminant-like digestive system with bacteria in the foregut fermenting the leaves, which are high in cellulose. Subsequently, the bacteria are digested to recover the nutrients. These bacteria have a high ratio of RNA nitrogen to total nitrogen compared to other cells. Thus, foregut fermenters require higher levels of RNase to efficiently utilize bacteria as a nutrient source. Furthermore, the pH in the small intestine of colobines (pH 6 to7) is significantly lower than that of humans (pH 7.4 to 8) (Zhang, 2006).

Molecular dating of the duplicated gene in douc langer (designated RNASE1B) suggests that it had arisen after the Asian colobines had diverged from the African clade. To test this, Zhang sequenced RNASE 1 and flanking regions in a guereza (*Colobus guereza*), an African colobine. In addition to RNASE1, the gene was apparently duplicated twice (RNASE1β and RNASE1γ) in the guereza. Phylogenetic analysis indicates that the RNASE1 duplications were independent in the Asian and African colobine lineages.

Nonrandom Changes in the Duplicated Genes

The duplicated genes in both species have undergone considerably more changes at the protein sequence level than the RNASE1 genes. Specifically, DNA sequence comparisons suggest that in the douc langer there have been zero amino acid substitutions in RNASE1 and 10 in RNASE1B since the duplication. In the guereza there have been two substitutions in RNASE1, 10 in RNASE1β, and 13 in RNASE1γ since the first duplication. These rapid nonsynonymous substitutions are largely confined to the coding region. The synonymous and noncoding sites of the duplicated genes have significantly fewer changes.

Zhang (2006) cites evidence that not only are the timing and placement of the substitutions nonrandom, but the specific amino acids substituted are nonrandom as well. In douc langer, seven of the nine amino acid substitutions in the mature peptide involve a charge change, and all seven increase the negative charge of the protein (R1G, R4Q, K6E, R32L, R39W, R98Q, A122D). Similarly, in the guereza, ostensibly between the first and second duplications, seven of the nine amino acid changes affected the mature protein, 4 of these involved charge changes, and all four increase the negative charge of the protein (R4Q, K6E, R39W, N88D).

Functionally Relevant Results of the Nonrandom Changes

Zhang (2006) hypothesized that these proteins had independently undergone similar functional changes. Recombinant proteins were used to measure catalytic activity at various pHs. In the douc langer (Zhang et al., 2002) the optimal pH was 7.4 for RNASE1 and 6.3 for RNASE1B. In the guereza (Zhang 2006), the optimal pH was still 7.4 for RNASE1 and 6.7 for both RNASE1β and RNASE1γ. Little difference was seen in catalytic activity among these enzymes at their optimal pH. Thus the enzymes encoded in these duplicated genes now perform more optimally at the pH present in the small intestine of colobines (i.e. pH 6 to 7).

Furthermore, there were three parallel amino acid substitutions between the douc langer and guereza, two of which are fairly uncommon replacements in most proteins. By reconstructing putative ancestral proteins, Zhang demonstrated that all three of these substitutions were important in changing the optimal pH of the enzyme by removing positive charges. It was also demonstrated that these derived proteins no longer degrade double-stranded (ds) RNA, a function present in RNASE1 of humans, rhesus monkey, and both colobines. While dsRNA is not typically present in the diet, it has been suggested that it may be important for antiviral defense, and it is known that human RNASE1 is expressed in tissues outside the pancreas. This suggests that retention of the RNASE1 gene in colobines may be necessary for the animal's survival.

Evolutionist versus Creationist Interpretations of the Data

Throughout the paper, Zhang (2006) uses statistical methods to demonstrate that these changes in amino acid sequence are nonrandom. Since the data are interpreted in an evolutionary paradigm in which mutations are *assumed* to be random, Zhang *assumes* that natural selection is able to account for these observations. In reality, even if random mechanisms could produce the mutations (which is questionable; see Bergman, 2005), there is no evidence that natural selection can produce the nonrandom pattern observed. Natural selection is a phantom rarely observed; it is primarily a rationalization to justify a purely materialistic origin of life (Bergman, 1992). Patterns existing in nature

invalidate natural selection as a major driving force. For example, individuals with higher fertility should reproduce and have more offspring with higher fertility; thus natural selection should tend to maximize reproduction rates. However, in nature lower reproductive rates are observed, keeping the population in balance rather than maximizing individual "reproductive success" (Ivanov, 2000).

Additionally, natural selection does not have the power to fix beneficial mutations unless there is an enormous disparity in reproduction rates between carriers and noncarriers of mutations (ReMine, 2005; 2006). Zhang (2006) cites fossil evidence that, when interpreted within the evolutionary paradigm, suggests colobine monkeys had shifted their diet and physiology several million years prior to the duplications in the RNASE genes. This is entirely inconsistent with the contention that natural selection can account for the fixation of a series of beneficial mutations in the population since the changes in the enzyme were not necessary to initially exploit the environment.

Evolutionists sometimes cite this type of evidence to demonstrate that gene duplication, random mutation, and natural selection can explain the acquisition of "new information." In fact, my attention was first directed to Zhang's article after an evolutionary scientist made this specific claim. In reality, these data do not help the evolutionary paradigm. The changes not only require the previous existence of a functional gene, but a gene that can be modified to produce functionally relevant results. It also requires gene duplication, which hardly appears to be simply a chance event, as indicated by an investigation of insecticide resistance in blowflies (Lightner, 2008).

For a creationist researcher who understands the critical importance of being able to explain intrabaraminic diversity, this article has significant implications. Zhang's research provides strong circumstantial evidence that the genomes of mammals were designed to be able to undergo adaptive genetic changes. Given that the rhesus monkey (family Cercopithecidae; subfamily Cercopithecinae), which does not carry a duplicated RNASE1 gene, and both colobines with their respective duplicated genes probably descended from two monkeys preserved on Noah's ark less than 4500 years ago, designed mechanisms appear to be operating. This would include mechanisms to cause gene duplications and subsequent changes (in the duplicated gene only) that are incorporated into the germline.

Directed genetic mutations are consistent with the concept of a computational genome linked to environmental stimuli. This would allow migrating animals to exploit novel environments and niches fairly rapidly, perhaps within a few generations. It is unknown at what rate such genetic changes occur; it probably varies, depending on the type of change involved. In the example discussed here, gene duplication appears to have been necessary to allow another function of RNASE1 to remain intact. The gene duplication might initially allow for greater RNase activity while the subsequent changes allowed for improved performance in a small intestine with a lower pH. TEs may have played a role in gene duplication and possibly horizontal gene transfer. Homozygosity may have been increased in these animals through gene conversion. Animals not affected by these genetic changes would likely retain a more varied diet and would be free to migrate elsewhere. Thus, directed mutations combined with the founder effect appear to provide a more rational explanation for these observations than random mutations and intense natural selection.

Conclusion

The research reported by Zhang (2006) provides strong circumstantial evidence that the genome of mammals was designed to allow for programmed adaptive genetic changes. A tremendous need exists for creationists to dig deeper into the available literature and assess the genetic variability within baramins. As we do, we will be better able to understand what types of changes occur and to consider what types of mechanisms may be involved. This is critical to further developing a more coherent creation model that accounts for rapid speciation and adaptation in a way that acknowledges the awesomeness of the Designer.

Acknowledgements

I am thankful that the Zhang (2006) article was brought to my attention on CRSnet (cf. Gen. 50:20; Rom. 8:28).

References

CRSQ: Creation Research Society Quarterly

Ashcraft, C.W. 2004. Genetic variability by design. *Technical Journal* 18:98–104.

Belancio, V.P., D.J. Hedges, and P. Deininger. 2008. Mammalian non-LTR retrotransposons: for better or worse, in sickness and in health. *Genome Research* 18:343–358.

Bergman, J. 1992. Some biological problems with the natural selection theory. *CRSQ* 29:146–158.

Bergman, J. 2001. The molecular biology of genetic transposition. *CRSQ* 38:139–150.

Bergman, J. 2005. The mutation repair systems: a major problem for macroevolution. *CRSQ* 41:265–273.

Ivanov, Y.N. 2000. Laws of fertility, role of natural selection, and destructiveness of mutations. *CRSQ* 37:153–158.

Lightner, J.K. 2006. Identification of species within the sheep-goat kind (Tsoan monobaramin). *Journal of Creation* 20:61–65.

Lightner, J.K. 2007. Identification of species within the cattle monobaramin (kind).

Journal of Creation 21:119–122.

Lightner, J.K. 2008. Patterns of change over time: organophosphorus resistance in the Australian sheep blowfly. *Journal of Creation* 22:81–84.

Myers, P., R. Espinosa, C. S. Parr, T. Jones, G. S. Hammond, and T. A. Dewey. 2008. The Animal Diversity Web. http://animaldiversity.org (as of May 7, 2008).

ReMine, W.J. 2005. Cost theory and the cost of substitution—a clarification. *Technical Journal* 19:113–125.

ReMine, W. 2006. More precise calculations of the cost of substitution. *CRSQ* 43:111–120.

Sternberg, R.V., and J. A. Shapiro. 2005. How repeated retroelements format genome function. *Cytogenetic and Genome Research* 110:108–116.

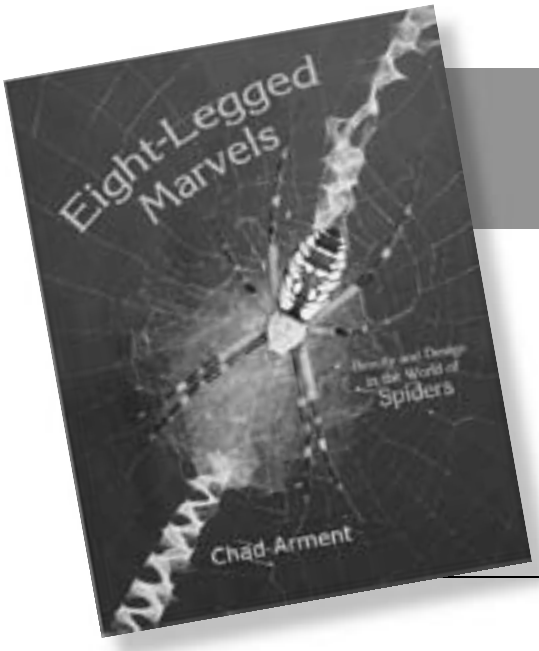
Ussher, J. 2003. *Annals of the World.* Trans. and ed. by L. and M. Pierce. Master Books, Green Forest, AR..

Wood, T.C. 2003. Perspectives on ageing: a young-earth creation diversification model. In Ivey, R.L. (editor), *Proceedings of the Fifth International Conference on Creationism*, pp. 479–489. Creation Science Fellowship, Pittsburgh, PA.

Wood, T.C. 2006. The current status of baraminology. *CRSQ* 43:149–158.

Zhang, J. 2006. Parallel adaptive origins of digestive RNases in Asian and African leaf monkeys. *Nature Genetics* 38:819–823.

Zhang, J., Y.P. Zhang, and H.F. Rosenberg. 2002. Adaptive evolution of a duplicated pancreatic ribonuclease gene in a leaf eating monkey. *Nature Genetics* 30:411–415.



Book Review

Eight-Legged Marvels

by Chad Arment

Coachwhip Publications, Landisville, PA, 2008, 91 pages, $25.00.

Author Arment has written several books on herpetology and cryptozoology. He holds an undergraduate biology degree from Wright State University. This new book offers more than 200 beautiful color photos of spiders. The subtitle reads "Beauty and Design in the World of Spiders." There are about 40,000 known spider species and perhaps five times as many yet unnamed (p. 7). The smallest known spider, *Patu digua* from Colombia, has an adult body size of only 0.37 mm. One of the largest spiders, *Theraphosa blondi*, is a bird-eating tarantula with a twelve-inch leg span. The book offers "a basic biological overview of spiders and their world" (p. 5). There are delightful descriptions of the jumping spider's binocular eyes, mimics, aquatic spiders, and net-casters.

A gracious creation worldview is promoted throughout the book. Well-chosen historical quotes appear by John Bunyan (1686, p. 85), James Brodie (1855, p. 6), A. N. Somers (1902, p. 52), and Robert Frost (1932, p. 85). A truly amazing story appears on page 52: In 1902, naturalist pastor A. N. Somers reported finding an artificial flower constructed by a funnel web spider. The creature had woven together three concentric circles of butterfly wings to attract insects to its web. The outside flower circle was three inches in diameter with the wing petals arranged according to size and color. One can only wish that a current example of such an object could be found and photographed. If the story is credible, it shows impressive intelligence and artistry by the lowly funnel spider. If you do not like spiders, this book could change your mind.

Don B. DeYoung
DBDeYoung@Grace.edu