

July 29, 2009

Number Thirteen

Occasional Papers of the BSG

GENESIS KINDS: CREATIONISM AND THE ORIGIN OF  
SPECIES

PROCEEDINGS OF THE EIGHTH BSG CONFERENCE

Roger W. Sanders  
Executive Editor

## Occasional Papers of the BSG

**Executive Editor:** Roger Sanders, Center for Origins Research, Bryan College, P.O. Box 7802, Dayton, TN 37321, USA

Email: [editor@creationbiology.org](mailto:editor@creationbiology.org)

**Associate Editors:** Joseph Francis (Master's College), Doug Kennard (Houston Graduate School of Theology), Georgia Purdom (Answers in Genesis), Marcus Ross (Liberty University), Todd Wood (Bryan College)

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

### Journal Policies

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

*OPBSG* seeks original scholarly manuscripts in any field related to creationist biology. Guidelines for manuscript preparation are available at the *OPBSG* website <http://www.creationbiology.org/opbsg>. Papers may be submitted electronically to the Executive Editor at [editor@creationbiology.org](mailto:editor@creationbiology.org).

All papers and abstracts submitted to *OPBSG* are subject to peer review by an editor assigned by the Executive Editor. Editors are forbidden from participating in the editing of their own papers or papers of their coworkers. Papers and abstracts are evaluated by at least one external peer reviewer. Editors then evaluate the peer review(s) and determine the suitability of the paper for publication in *OPBSG*. Editorial decisions may be appealed to the editorial board after reasonable efforts to resolve differences. Decisions of the editorial board are final.

A detailed editorial manual is available at the *OPBSG* website <http://www.creationbiology.org/opbsg>.

This document is copyright ©2009 by the BSG. Permission to copy this document is granted provided the entire copyright statement is included.

# Genesis Kinds: Creationism and the Origin of Species Proceedings of the Eighth BSG Conference

## Contents

Contributed Abstracts .....	2
C1. Brown & Sanders, <i>Pentacyclic Triterpenes of Lantana: Co-occurrence of Liver Toxins and Liver Protectants</i>	
C2. Davis, <i>Theological Reasons for Negative Elements in Pre-Fall Creation? God's Use of Negative Elements in a "Very Good" Creation</i>	
C3. Golian, <i>A Minimum Spanning-Tree Approach to Migration Patterns Using Genetic Distances</i>	
C4. Hennigan, <i>The Current Taxonomic Status of Family Ursidae: The Baraminological Implications</i>	
C5. Lightner, <i>Curious Patterns of Variation within the Anatidae Monobaramin and Implications for Baraminological Research</i>	
C6. Loggans, Mudge, & Liu, <i>Transcription of Human Endogenous Retroviruses during the Menstrual Cycle</i>	
C7. Wise, <i>Creation Biology Suggestions From Evolutionary Genetics</i>	
C8. Wood, <i>Odontochelys as an Intermediate Form</i>	

## Contributed Abstracts

### C1. Pentacyclic Triterpenes of Lantana: Co-occurrence of Liver Toxins and Liver Protectants

R. Brown & R.W. Sanders

Bryan College

Sanders (2008) previously enumerated the features of lantana plants that are examples of natural evil. One of these is the occurrence in the leaves and unripe fruits of triterpenes that are toxic to mammals. Here we review the literature concerning triterpenes in *Lantana* and provide a creationist interpretation. Most studies report extractions from *L. camara*, a name used to refer to a number of cultigens derived from hybrids among six to seven closely related natural species of *Lantana*. Thus, the triterpene composition reported for this “species” is variable. Each variant sampled usually has about four to six major triterpenes sequestered. The major constituent usually is Lantadene A, a pentacyclic triterpene in which the rings are all 6-membered, a double-bonded oxygen occurs at position C3, and there is an ester linkage at C22. The additional compounds are due primarily to variation at C3, C22, and C25. Furthermore, the rings can differ in their conformation (chair vs. boat forms). The compounds designated as lantadenes all have four- or five-carbon branched alkene esters at C22 and a double-bonded oxygen at C3 (Hart et al. 1976; Sharma et al. 2000). Several of the lantadenes are mildly to moderately toxic, the most common conformation of Lantadene A (designated I) is more toxic, and Lantadene AII, a less abundant form, is strongly toxic (Sharma et al. 2000). Toxicity involves liver damage, anorexia, and photosensitization of exposed skin and varies by dosage and species of herbivore. It has been suggested that lantadenes are derived from oleanolic acid (hydroxy at C3, unsubstituted at C22), which occurs in significant amounts in the roots and, surprisingly, is a liver protectant, counteracting the effects of the lantadenes.

The co-occurrence of both liver toxins and a counteractive liver protectant based on the same chemical structure lends itself to the study of the origin of natural evil in these plants. In bacteria both gene loss and gene addition by lateral transfer have been proposed to explain the origin of pathogenicity as a consequence of the Fall and Curse. Since oleanolic acid is common in families related to lantana and lantadenes are restricted to lantana, it would appear that the biosynthetic pathway to oleanolic acid was created in

lantana’s ancestor, which may have sequestered oleanolic acid in the aerial parts of the plant. We hypothesize that the origin of the lantadenes were not part of the “very good creation” but originated after the Flood, when lantana is likely to have diverged from its pre-Flood ancestor, making lantadenes a case of mediated design. Although the biosynthetic pathway, enzymes, and underlying genes are unknown, the increased complexity of the lantadenes compared to oleanolic acid suggests that the origin of the toxicity has involved addition of genetic information. Because of the antiherbivore protection that lantadenes afford the lantanas, we predict that this information will be due to high mutation rates of specific transposable elements at specific locations in the lantana genome (see Wood 2002). That is, instead of the genetic information being added through random mutations, it is the result of specific pre-programming in the created baramin to induce mutations that in the leaves turn on a pathway to convert oleanolic acid into a toxin. Because the molecule that was designed to target mammalian liver physiology was a protectant, specific mutations now generate specific molecules with modifications that reverse the beneficial effect of the original molecule. Future research will attempt to test this hypothesis and prediction.

Editor: JWF

- Hart, N.K., J.A. Lamberton, A.A. Sioumis, and H.Suares. 1976. New triterpenes of *Lantana camara*. A comparative study of the constituents of several taxa. *Aust. J. Chem.* 29: 655-671.
- Sanders, R.W. 2008. Lantana (Verbenaceae) as a model to study the origin of traits exhibiting natural evil [Abstract]. *Occasional Papers of the BSG*: 11: 10.
- Sharma, O.P., A. Singh, and S. Sharma. 2000. Levels of lantadenes, bioactive pentacyclic triterpenoids, in young and mature leaves of *Lantana camara* var. *aculeata*. *Fitoterapia* 71:487-491.
- Wood, T.C. 2002. The AGEing process: Rapid post-Flood intrabaraminic diversification caused by altruistic genetic elements (AGEs). *Origins* 54: 5-34.

## C2. Theological Reasons for Negative Elements in Pre-Fall Creation? God's Use of Negative Elements in a "Very Good" Creation

C.J. Davis  
Bryan College

God pronounces his creation very good (Gen. 1:31) and by those words the text might seem to imply that no negative elements existed in pre-fall creation. However, a careful examination of the text in the light of all Scripture shows that this is not God's intent, for there are several pre-fall elements of creation which find no place in the consummation and have some negative connotations in the immediate context itself.

For example, consider the words "without form" and "void" תהו ובהו *tohu vabohu* (Gen. 1:2). These words are universally negative elements elsewhere in Scripture. Moreover, the first days of creation bring a transformation from the formless void to one of order. Thus, "without form" and "void" are two negative elements which existed in pre-fall creation.

Also consider darkness, חשך *choshek* (Gen. 1:2). This word occurs 93 times in the Hebrew Bible, all of which are bad. Notice carefully too that God separates the light from the darkness, and he calls the light good. Any goodness of darkness he passes over in silence. The LXX translates *choshek* with σκότος *skotos* which in the New Testament also is a theologically bad thing. The related word σκοτία *skotia* is also universally negative in the New Testament. At least two places in the New Testament (John 1:1-5 and 2 Cor. 4:6) interpret Genesis 1 and darkness and give darkness spiritually bad significance. Moreover, darkness is explicitly excluded from the final consummation (Rev. 21:25; 22:5).

Similarly, the "deep" תהום *tehom* usually appears in Scripture as a negative symbol. To be sure, there are places where *tehom* appears in a positive sense, but in Genesis 1, it appears in a negative sense because of the following: 1) God does not call anything on Day Two specifically good. 2) The only other time the world is covered completely with water is during the judgment of the flood. 3) The Septuagint brings out the negative aspect of this word by translating it as ἄβυσσος *Abyss*. And 4) the final consummation explicitly has no seas showing that there is a reason why God is not calling the day he deals with "seas" and their separation, good.

Furthermore, the man and his wife are "naked" ערום *arom* in pre-fall creation. This word can have negative or positive connotations. However, nakedness in Gen. 2:25 is negative because of the following: 1) God recognizes Adam and Eve's nakedness as something problematic since he clothes them before exiling them from Eden (Gen. 3:21). 2) The final consummation explicitly states that those in the restored Garden of Eden, that is, the New Jerusalem, will be clothed with robes of righteousness. 3) Exposing nakedness is a bad thing in the Bible.

The purpose of negative elements in pre-Fall creation is to highlight the goodness of the good in relation to the badness of the bad. I.e., God's purpose in allowing the darkness to exist first, is to show to us the greatness of the light as it conquers the darkness and as darkness fails to overpower it. God does not need evil to be good. Rather, God chooses to use evil to show the

greatness of his perfect goodness. For finite people to understand an infinitely wise unlimited God, God knew he must teach them in a way they could understand.

God's purpose in allowing the waters to initially cover the earth, is to show the goodness of the land as the place for mankind to thrive. Darkness and seas are thus "very good" only in the sense of serving as foil to the truly good light and land.

Consider John's reading of Genesis 1 in John 1 where he understands "light" and "darkness" to be more than just facts of creation. John takes those actual, factual, historic events to include God-intended theological symbolism relating to Christ and salvation. Consider Paul's similar reading of Genesis 1 in 2 Cor. 4:6. Such reading of Genesis 1-3 provides the Christian reader with partial insight as to how to approach this part of Scripture.

Editor: JWF

## C3. A Minimum Spanning-Tree Approach to Migration Patterns Using Genetic Distances

C. Golian  
Independent Researcher

Human diversity is evident when comparing gene frequencies in ethnic populations. Creationists should be able to apply knowledge gained from this analysis to substantiate migration patterns occurring after Babel.

The Jean Dausset Foundation (Centre D'Etude du Polymorphisme Humain, ftp.cephb.fr) has created a repository for lymphoblastoid cell lines (LCLs) from over 50 different world populations. Using the allelic frequency for up to 32,356 markers in each population, a genetic distance is calculated for each population relationship by the Manhattan distance between the frequencies and combined into a distance matrix. From the distances, a minimum spanning tree (MST) is created using Kruskal's algorithm,

$$w(T) = \sum(u,v)^E T w(u,v)$$

which adds a safe edge to the tree by finding the edge with the least weight (Cormen 2002, pp. 568-570). This method does not guarantee the discovery of a root, and may actually result in multiple unrelated trees. This resulting tree does have the Northeastern Bantu as the root, consistent with anthropological findings. From here, the African ethnic groups are derived, as well as a focal point of the Caucasus. From the Caucasus, there are two succeeding focal points: Northern France/Spain, and Xining, China. These four focal points are ethnic groups which have large subtrees. The remaining relationship results are largely consistent with popular population relationships, such as Japanese and American Indians deriving from Mongolian populations. With four focal points of migration, different ethnic groups would expand into some of the same areas, such as the Tuscans and Sardinians from the French Basque focal point in Italy with the Northern Italians directly from Caucasus. Comparing these paths to commonly held migration patterns from anthropology, the origins are quite different (Cavalli-Sforza 1994, pp. 29-35, 73-81, 156). Migrations are expected to progress chronologically from the African origin using constant evolutionary rates. In fact, minimum-path approaches are considered to be poor methods

for constructing migration phylogenies due to “errors” like these which they produce.

The theological view maintains people were dispersed directly from a plain east of the Ararat Mountains, the resting place of Noah’s ark. This conflicts with fossil records depicting African origins. The Tower of Babel was attempted, and [Genesis 11:8] *the LORD scattered them abroad from thence upon the face of all the earth*. The four MST focal points are south, north, east, and west from the settlement in Mesopotamia (possibly present-day Iraq) where the tower was thought to be built: *a plain in Shinar* [Genesis 11:1]. As in Jeremiah 49 when God scattered Elam to *the four winds*, an external force caused these people to appear in these locations. Migrations beginning with the four MST focal points provide a method for the table of nations to originate from the few generations in the Genesis 10 account.

The MST characterizes groups from Northern France/Spain and China stemming from the Caucasus, not directly from the Bantu. In Genesis 9, Noah cursed Canaan, son of Ham, blessed Shem, and also blessed Japheth, who would have extended territory *in the tents of Shem*. With tents normally belonging to male descendants, this could foretell the marriage of female descendants of Japheth with male descendants of Shem. One example is the name Meshech, a son of Aram, son of Shem. It is possible his mother was a daughter of Meshech, the son of Japheth, who named her son after her father. This would explain an extension of Japheth in the tents of Shem. If Shem were the forefather of all Caucasians, the MST focal points from the Caucasus could result from such marriages. Meshech is traditionally thought to be ancestor to the Russians, specifically Moscow. Japheth could be the forefather (by marriage) of Russians, as an extension of Shem. From the limited dataset available, the Biblical table of nations account potentially fits molecular genetics comparisons. A center of distribution for modern humans near the expected resting place of the Ark is revealed.

Editor: TCW

- Cavalli-Sforza, L. 1994. *The History and Geography of Human Genes*. Princeton University Press, Princeton, NJ.  
Cormen, T. 2002. *Introduction to Algorithms*, 2nd ed. MIT Press, Cambridge, MA.

#### C4. The Current Taxonomic Status of Family Ursidae: The Baraminological Implications

T. Hennigan  
*Independent Scholar*

Family Ursidae consists of three subfamilies, three genera, eight species, and numerous subspecies. They are subfamily Ursinae: sun bear (*Ursus malayanus*), sloth (*U. ursinus*), brown (*U. arctos*), polar (*U. maritimus*), American black (*U. americanus*), and Asiatic black (*U. thibetanus*), plus two extinct species; subfamily Tremarctinae: Andean bear (*Tremarctos ornatus*) plus several extinct species; subfamily Ailuropoda: giant panda (*Ailuropoda melanoleuca*), and at least one extinct species.

In creationist literature Ursidae has been classified as monobaraminic (Tyler 1997, Wood 2006) and sub-baraminic, defined as having diversified well after the flood, evidenced by first appearance in the fossil record (Wise 2008). In order to clarify our understanding of bear taxonomy and interpret

their relationships within a baraminological framework, the literature was reviewed to determine the current estimates of genetic relationships and the instances of both captive and wild hybridization. Radiation within *Ursus*, from extinct Eurasian bears, appears to have occurred rapidly from the mid to upper Pleistocene (Krause et al. 2008). The genetic analyses focused on discussions surrounding the relationships of the Andean bear and Giant Panda with the rest of the ursid species. Complete mtDNA sequences for all extant and two extinct species were analyzed and compared using the harbor seal (*Phoca vitulina*) as the outgroup (Krause et al. 2008) and suggests that the giant panda is not a procyonid but an ursid and should be included with the other bear species.

The most current hybridization data demonstrates that six out of eight species (excluding the Andean bear and giant panda) exhibit biologically significant holistic similarity because they can readily hybridize both in the wild and in captivity (Gray 1972, Doupe et al. 2007, Galbreath et al. 2008).

A discontinuity matrix was prepared for extant members based on both morphological data and recent genetic research. Unique characters distinguishing them from representatives of all carnivoran family outgroups include mtDNA sequences, specialized carnassial dentition, bile salt metabolism (except in the giant panda), foot morphology, size ratio of cub to mom at birth, ability to alternate between carnivory and herbivory, and gross morphology (Lindburg and Baragona 2004, pp. 38-46). The matrix suggests that there is discontinuity with all other carnivoran groups and indicates that Ursidae is apobaraminic. Therefore, the data suggests that family Ursidae is a holobaramin because they are both monobaraminic and apobaraminic, and that they experienced rapid intrabaraminic diversification after the flood. If true, this means that there is a Creator who has made creatures to be so genetically flexible that they can rapidly adapt to changing environmental conditions. Even according to evolutionary researchers, “it is as if the genome possesses a built-in capacity to modify chromosome numbers such that an increase is triggered by environments characterized by intense selection.” (Nash et al. 1998). Creationist research should continue searching for environmental mechanisms that trigger designed genomic machinery that may cause rapid adaptability in changing ecosystems, allowing the survival and persistence of God’s creatures.

Editor: GP

- Doupe, J.P., J.H. England, M. Furze, and D. Paetkau. 2007. Most northerly observation of a grizzly bear (*Ursus arctos*) in Canada: photographic and DNA evidence from Melville Island, Northwest Territories. *Arctic* 60(3):271-276.  
Galbreath, J., M. Hunt, T. Clements, and L. Waits. 2008. An apparent hybrid wild bear from Cambodia. *Ursus* 19(1):85-86.  
Gray, A. 1972. *Mammalian Hybrids*, 2nd ed. Commonwealth Agricultural Bureaux, Edinburgh.  
Krause, J., and 17 others. 2008. Mitochondrial genomes reveal an explosive radiation of extinct and extant bears near the Miocene-Pliocene boundary. *BMC Evolutionary Biology* 8:220.  
Lindburg, D and K. Baragona, eds. 2004. *Giant Pandas: Biology and Conservation*. University of California Press, Berkeley, CA.  
Nash, W.G., J. Weinberg, M.A. Ferguson-Smith, C. Menninger, and S.J. O’Brien. 1998. Comparative genomics: tracking chromosome evolution in the family Ursidae using reciprocal chromosome painting. *Cytogenetics and Cell Genetics* 83:182-192.  
Tyler, D.J. 1997. Adaptations within the bear family: A contribution to the debate about the limits of variation. *Creation Matters* 2:1-4.

Wise, K. 2008. Baraminology and the fossil record of mammals. *Occasional Papers of the BSG* 11:10-11.

Wood, T.C. 2006. The current status of baraminology. *CRSQ* 43(3):149-158.

## C5. Curious Patterns of Variation within the Anatidae Monobaramin and Implications for Baraminological Research

J. Lightner

*Independent Scholar*

The order Anseriformes (waterfowl) is comprised of three families: Anatidae (ducks, geese, and swans), Anhimidae (screamers), and Anseranatidae (magpie goose; Myers et al. 2008). Only the family Anatidae has recorded intergeneric hybrids. This family is divided into 49 genera distributed among five subfamilies. Hybrid data connects 27 of the 49 genera and four of the five subfamilies. Several pertinent hybrids include *Anas falcata* (falcated teal; Anatinae) x *Tadorna ferruginea* (ruddy shelduck; Tadorninae), *Dendrocygna viduata* (white-faced whistling-duck; Dendrocyginae) x *Netta peposacea* (rosybill; Anatinae), and *Branta canadensis* (Canada goose; Anserinae) x *Cairina moschata* (muscovy duck; Anatinae; McCarthy 2006). *Stictonetta naevosa* (freckled duck; Stictonettinae) is the only member of its subfamily. This rare Australian duck has characteristics found in several other subfamilies. Previously it was classified with Anatinae (Tribe Anatini: dabbling ducks); then it was suggested to have anserine affinities; later it was considered part of Dendrocygnae until it was finally placed in a separate subfamily (Sibley and Ahlquist 1990). Its characteristics closely associate it with other members of Anatidae (Scherer 1993) so that it can be logically inferred that the entire family is monobaraminic.

Scherer (1993) highlights some curious patterns within Anatidae. First, in addition to *Stictonetta naevosa*, other aberrant types exist which exhibit characteristics found in different groups. Second, some interspecific hybrids show characteristics from a third species. Finally, some sequence data appear potentially useful phylogenetically, although they can give conflicting results and do not always correlate well with phenotypic data; other sequence data are surprisingly unhelpful. This leads to an important question: “which characters provide the best information regarding the taxonomic relationships of living things?”

Amino acid sequence data from ovomucoid third domains have been examined (Apostol et al. 1993). Interestingly, regions of this protease inhibitor contacting the enzyme are hypervariable. Strikingly different inhibitory specificities have been noted in closely related birds. Six different ovomucoid sequences were identified within Anatidae. The most common sequence was found in all Tadorninae surveyed (6 of the 10 genera) and some of the Anatinae (4 of the 31 genera). The sequence identified in stiff-tailed ducks (genus *Oxyura*; Anatinae) is identical to that found in swans (genus *Cygnus*; Anserinae). A third sequence was identified in two genera of Anatinae (*Aythya* and *Netta*), but not outside this subfamily. The sequence of *Anser canigulus* (emperor goose) is identical to that of *Branta canadensis* (Canada goose), which is one residue different (D32G) from the sequence shared by *Anser anser* (graylag goose) and *Anser*

*indicus* (bar-headed goose). The sixth sequence was only found in *Dendrocygna* (Dendrocyginae). These sequence data further support the monobaraminic status of the Anatidae, although they don't clarify phylogenetic relationships.

The Anatidae monobaramin lacks a “neat and tidy” phylogenetic tree. This has implications for understanding intrabaraminic evolution. Scherer (1993) suggests Anatidae ancestors were genetically complex (polyvalent) and that, through the process of speciation, natural selection has removed different characters from different populations. He also suggests that different loss-of-function mutations, likely in regulatory regions, may have accumulated in different species. These might explain the (re)appearance of traits in hybrids that are also in a third species. Scherer rejects the idea of convergence as an explanation for aberrant types because strong, similar selection pressure appears absent. However, the role of directed mutations in intrabaraminic evolution may render selection less critical than previously thought (Lightner 2009). Continued investigation into the factors influencing intrabaraminic evolution is critical to the further development of the creation model.

Editor: RWS

Apostol, I., A. Giletto, T. Komiyama, W. Zhang, and M. Laskowski, Jr. 1993. Amino acid sequences of ovomucoid third domains from 27 additional species of birds. *J. Protein Chem* 12(4):419-433.

Lightner, J.K. 2009. Karyotypic and allelic diversity within the canid baramin (Canidae). *Journal of Creation* 23(1):94-98.

McCarthy, E.M. 2006. *Handbook of Avian Hybrids of the World*. Oxford University Press, New York.

Myers, P., R. Espinosa, C. S. Parr, T. Jones, G. S. Hammond, and T. A. Dewey. 2008. The Animal Diversity Web (online). Accessed September 27, 2008 at <http://animaldiversity.org>.

Scherer, S. 1993. Der Gundtyp der Entenartigen (Anseriformes, Anatidae): Biologische und paläontologische Streiflichter. In: Scherer, S. ed., *Typen des Lebens*. Pascal Verlag, Berlin, pp. 131-158.

Sibley, C.G. and J.E. Ahlquist. 1990. *Phylogeny and Classification of Birds: A Study in Molecular Evolution*. Yale University Press, New Haven, CT.

## C6. Transcription of Human Endogenous Retroviruses during the Menstrual Cycle

L. Loggans, A. Mudge, & Y. Liu

*Maranatha Baptist Bible College*

Similarities between human and primate genomes have posed a significant challenge to creationism (Wood 2006). Scattered among human and animal genomes are a class of repetitive genetic elements called endogenous retroviruses (ERVs), which are generally considered remnants of ancient exogenous retroviral infections. Because humans and chimpanzees share orthologous ERVs, evolutionists use these elements as another argument for common ancestry. In light of the abundance of ERVs in vertebrate genomes—occupying a much larger proportion of the genome than protein-coding genes, unraveling the functions of ERVs from a creationist perspective may hold a key to solving the puzzle of genomic similarities.

ERVs may have been created in the cell to perform cellular activities, such as synchronized regulation of interspersed genetic elements by multiple ERV copies. Since the long terminal repeats (LTRs) of some human endogenous retroviruses (HERVs) contain putative steroid hormone response elements, it is probable that expression of HERVs is controlled by sex hormones.

Consequently, expression of HERVs in the female may follow a pattern during the menstrual cycle. Although there is a report that expression of HERV-K in a breast cancer cell line responded to treatment with sex hormones (Ono et al. 1987), there is yet no *in vivo* study in humans regarding the influence of steroid hormones on the activity of HERVs.

Quantification of HERV transcripts by real time reverse transcription polymerase chain reaction (RT-PCR) has been recently developed (Forsman et al. 2005; Muradrasoli et al. 2006). We quantified the transcription dynamics of several HERV groups in peripheral blood leukocytes using SYBR Green-based RT-PCR. First, GeNorm and NormFinder programs were used to select the best reference gene that is stably expressed during the menstrual cycle. Transcription level of the reference gene was subsequently used to measure the relative expression of HERVs. Transcripts from entire classes of HERVs were amplified using degenerate *pol*-based primers, while transcripts from an HERV group (HERV-K10) and a specific locus (syncytin-1) were amplified using non-degenerate *env*-based primers. Temporal expression patterns of HERVs in a reproductive-age woman and a man of similar age were compared.

Of the four housekeeping genes tested (S18 rRNA, glucose-6-phosphate dehydrogenase, a component of RNA polymerase II, and tyrosine 3-monooxygenase), tyrosine-3-monohydroxylase (YWHAZ) was the most stable during the menstrual cycle. GeNorm and NormFinder algorithms yielded similar results. Consequently, YWHAZ was used as the internal reference. Preliminary quantification of HERV transcripts showed that expression of HERVs demonstrated a temporal pattern in the female that was absent in the male. Transcription of all HERV elements that were successfully amplified peaked around ovulation and declined to a minimum around the beginning of menstruation. The pattern was in contrast to the expression of the aromatase gene, which encodes a unique enzyme in the synthesis of estrogens. Transcription of the aromatase gene peaked at the end of the luteal phase and was low during the follicular phase, which is consistent with the normal pattern of estrogen synthesis. All results of quantitative RT-PCR were repeated using different batches of cDNA and different batches of total cell RNA. The patterns were robust.

The experiment will be expanded to include more subjects. Afterwards, selected primers will be used to study the transcription dynamics of HERVs during pregnancy. In addition to clarifying the function of ERVs, studying HERV involvement in human reproduction may shed light on our understanding of certain pathological conditions such as dysmenorrhea and recurrent spontaneous abortions.

Editor: RWS

- Forsman, A., Z. Yun, L. Hu, D. Uzhamckis, P. Jern, and J. Blomberg. 2005. Development of broadly targeted human endogenous gammaretroviral *pol*-based real time PCRs quantitation of RNA expression in human tissues. *Journal of Virological Methods* 129:16-30.
- Muradrasoli, S., A. Forsman, L. Hu, V. Blikstad, and J. Blomberg. 2006. Development of real-time PCRs for detection and quantitation of human MMTV-like sequences (HML) expression in human tissues. *Journal of Virological Methods* 136:83-92.
- Ono, M., M. Kawakami, and H. Ushikubo. 1987. Stimulation of expression of the human endogenous retrovirus genome by female steroid hormones in human breast cancer cell line T47D. *Journal of Virology* 61:2059-2062.

Wood, T.C. 2006. The chimpanzee genome and the problem of biological similarity. *Occasional Papers of the BSG* 7:1-18.

## C7. Creation Biology Suggestions From Evolutionary Genetics

K. Wise

*Truett-McConnell College*

The neodarwinists of the 1940's united mathematical population genetics and Darwin's evolutionary theory to create the field of evolutionary genetics. Some six decades of theory generation and data collection in evolutionary genetics have yielded information about the biological world which should prove useful to creation biologists. Following are some observations (O) of the biological world and related suggestions (S) for creation biology:

O1: Since the function of most DNA is unknown, the deleterious versus beneficial effects of most mutations are also unknown. Where the DNA is understood, most mutations are deleterious, most of the remainder seem to be neutral, and only a minority are slightly beneficial. Truly beneficial mutations are extremely rare. S1a: If deleterious mutational effects were absent in pre-Fall time, mutation processes were different and/or DNA correction mechanisms were more effective before the Fall. S1b: The commonness of non-deleterious mutations leaves open the possibility that some mutational processes could have been operating in the pre-Fall world. S1c: Known mutation processes are woefully inadequate to explain organismal change (even in evolutionary time), so diversification is possible through mutation only if it is by a mutation process as yet unknown to us.

O2: The general health of organisms suggests mutational load is low and thus that mutations are not in equilibrium. S2: This suggests that deleterious mutations are a recent introduction into the history of life, consistent with being post-Fall phenomena.

O3: Expectations of natural selection (NS) theory are at odds with the following observations: a) the low frequency of NS examples; b) the statistics of proposed examples of NS; c) common eukaryotic linkage equilibrium; d) common crossing over; e) high heritable variation; f) high DNA heterozygosity; g) high rates of morphological evolution (even in evolutionary time), h) high biological diversity; and i) ubiquitous biological beauty. S3a: This suggests that NS is not an important factor in either the development or sustenance of modern biology, so should not play a major role in creation biology theory. S3b: If most populations are out of Hardy-Weinberg Equilibrium (HWE), as is assumed in modern biology, then non-selection assumptions of HWE may be more important in biology than generally assumed.

O4: Minimization of deleterious traits is the only demonstrably favorable effect of NS. S4: This suggests that biological overproduction and death (collectively resulting in NS) may have been introduced by God into the animal and human world at the Fall in order to minimize the affects of natural biological evil which entered the world at the Fall.

O5: Whereas variability and heritability should in theory decrease very rapidly in small populations due to genetic drift, both are very high in the biological world. S5: This suggests that small populations probably substantially affected earth's biology only during and immediately after the Flood.

O6: Differences among human races seem to be both superficial and selectively neutral. S6: This suggests that genetic drift (and potentially founder effect) in human populations dispersing from Babel may provide the best explanation for human races.

O7: Eukaryotic organisms commonly display linkage equilibrium. S7: This suggests that biological complexity is not due to DNA linkage.

O8a: NS fails to explain observed cycles of growth and decline in both epidemic pathologies and so-called industrial melanism. O8b: Constant and high DNA heterozygosity is best modeled by genetic drift on rapidly-appearing, near-neutral mutations in large populations. S8: These observations suggest the existence of built-in mechanisms which regularly and/or cyclically reveal latent biological information.

O9: Even when morphological and DNA similarity data produce similar branching sequences in branching programs, morphological and DNA divergence of lineages is commonly unlinked. S9: This suggests that even if changes in DNA accompany intrabaraminic diversification, those changes are not directly responsible for the morphological evolution – e.g. by constantly changing independently of morphology, or by changing in response to the morphological changes, or by triggering what *is* responsible for the morphology changes.

Editor: TCW

## C8. *Odontochelys* as an Intermediate Form

T.C. Wood  
Bryan College

Wise (1995) defined a morphological intermediate as an organism with intermediate features between one group and another or an organism with non-intermediate features found in two different groups. *Odontochelys semitestacea*, as a potential morphological intermediate between turtles and other tetrapods, would seem to fulfill both of these requirements (Li et al. 2008). Whereas all previously-known turtles possess a bony shell, composed of a dorsal carapace and ventral plastron, *Odontochelys* has only a partial carapace but a well-developed plastron. *Odontochelys* also has teeth, which are absent in other turtles but present in many tetrapods. Qualitatively, *Odontochelys* would seem to be an excellent morphological intermediate. To evaluate this hypothesis, I calculated baraminic distances and 3D multidimensional scaling on two datasets that included *Odontochelys*, both of which were evaluated phylogenetically by Li et al. (2008). The first dataset originated from Joyce (2007) and included 136 osteological characters scored for 67 taxa (68 including *Odontochelys*). No non-turtle outgroup taxa were included in this dataset. Four taxa with taxic relevance <0.3 were eliminated from the dataset. Baraminic distances were calculated using BDISTMDS from 65 characters with character relevance >90%. The 3D MDS results show a tight cluster of turtles with a line of Triassic fossils extending from it, ending in *Proganochelys*. *Odontochelys* is not part of this line of Triassic fossils but instead appears adjacent to it. The second dataset originated from Rieppel and Reisz (1999) and included 169 morphological characters scored for 35 taxa (36 including *Odontochelys*). Turtles were represented by a single composite taxon with other tetrapod and candidate turtle ancestors. This

dataset was previously analyzed using 3D MDS on baraminic distances by Wood (2005), who concluded that the turtles were separated from other tetrapods and not obviously close to any of their proposed ancestors. Baraminic distances were calculated for all taxa and 98 characters with character relevance >90%. The 3D MDS results indicate that *Odontochelys* is closely adjacent to the Eosauropterygia but is not intermediate between the turtles and any of their proposed ancestors. Thus, in both 3D MDS analyses, *Odontochelys* occupied odd positions that would not be expected of a morphological intermediate. This is likely due to the lack of known character states for *Odontochelys*. For the Joyce (2007) dataset, 74.3% of the *Odontochelys* character states were unknown, and for the Rieppel and Reisz (1999) dataset, 62.1% of the character states were unknown. While *Odontochelys* does appear to be an excellent morphological intermediate between turtles and non-turtles, its precise relation to the turtles remains ambiguous due to lack of data.

Editor: JWF

- Joyce, W.G. 2007. Phylogenetic relationships of Mesozoic turtles. *Bulletin of the Peabody Museum of Natural History* 48(1):3-102.
- Li, C., X.-C. Wu, O. Rieppel, L.-T. Wang, and L.-J. Zhao. 2008. An ancestral turtle from the Late Triassic of southwestern China. *Nature* 456:497-501.
- Rieppel, O. and R.R. Reisz. 1999. The origin and early evolution of turtles. *Annual Review of Ecology and Systematics* 30:1-22.
- Wise, K.P. 1995. Towards a creationist understanding of 'transitional forms.' *CEN Tech. J.* 9(2):216-222.
- 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* 1:1-241.