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# Modeling Holistic Behavior of Biological Systems for Analysis by Systems Theory

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I am engaged in an ongoing study to evaluate squirrel taxonomy from the perspective of young earth baraminology. Data to be considered include interspecific hybridization of sciurids and morphological characters evaluated by baraminic distance and Analysis of Patterns (ANOPA) methods. As in other baraminology studies, the results of these analyses will aid in the re-interpretation of sciurid phylogeny within the young-earth creation framework. Also of significance to the creationist is the biogeography of the squirrels, which is constrained by dispersal from Ararat since the squirrels must have been on the Ark. This paper presents the preliminary results of my work with recommendations for future research and interpretation.

#### **R4. Modeling Holistic Behavior of Biological Systems for Analysis by Systems Theory**

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Due to the complexity of biological systems it is not possible to capture the richness of their interactions by purely studying the individual parts. Only a subset of all possible interactions between individual parts results in functional behavior. This restriction of functional possibilities is sometimes described as an emergent property of the system and emphasizes a holistic approach to the study of biological systems.

By using concepts from systems theory a systemic approach to modeling biological systems is possible. This approach is currently used successfully in such areas as niche theory and organism biology. This presentation looks at a framework for modeling biological systems as Complex Functional Units (CFU's). With this level of abstraction it is possible to model systems from intracellular processes to ecological environments.

Focusing on the number and quality of interactions between CFU's it is possible to determine criteria for the interchangeability of CFU's with similar functionality, but different implementation. Adaptability of CFU's to changing conditions can also be studied to evaluate possible limits to variation.

In order to demonstrate the applicability of CFU's to biology, several examples will be presented. The first is a comparison of  $C_3$  and  $C_4$  photosynthetic processes. Both perform similar functions, but have differences in their implementation. Modeled as CFU's the degree of difference in implementation will be evaluated and applied to  $C_3$ - $C_4$  intermediates. The second example looks at immunology in light of CFU's. This is a preliminary exploration with the goal of evaluating the benefit of a more detailed study in the future.

#### **R5. A Proposal for a Creationist Survey of Viruses**

Jennifer Gruenke<sup>1</sup>, Joseph W. Francis<sup>2</sup>, Todd Charles Wood<sup>3</sup>

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Viruses are ubiquitous and affect biological life at the ecosystem, organismal, cellular, and biochemical/molecular level. The study of viruses and their classification has been influenced largely by the destructive parasitic nature of viruses. According

to most young-earth creationist (YEC) thinkers, the pathogenic nature of viruses arose as a consequence of the Fall (e.g. Bergman 1999). Recently, two YEC theories (Wood 2002; Francis 2003) have proposed possible beneficial functions viruses may have performed before the Fall. Each theory predicts that remnants of these pre-Fall functions may be observable in extant viral lifestyles and that viral pathogenicity will be limited to special circumstances. Based on a preliminary survey of viruses, we find that some viruses can infect multiple host species but may cause pathology in only one or few hosts. We therefore hypothesize that viruses may be providing beneficial functions in hosts and that these functions may be detectable and amenable to study. At the cellular level, viruses interact specifically with a remarkably large number of cell-surface and soluble receptors and can affect many aspects of cell structure and function, including changes at the membrane and organelle level as well as alteration of biochemical pathways and gene expression at the genome level. Thus it appears that viruses not only modulate organisms at the genome level but have the potential to promote non-genetic based phenotype changes. At the tissue level, viruses display an ability to remodel tissues by promoting apoptosis or influencing the manner in which populations of cells interact with one another. We hypothesize that viruses may have been created as "mobile" extraorganismal agents of gene, cell and tissue regulation and/or modification. Viruses also play beneficial roles within ecosystems in multiple ways including participation in mineral cycles and protection of some species from microbial-based pathology. Because viruses appear to have the potential to influence species composition and diversification within ecosystems we hypothesize that viruses may have been created as modulators of such systems. To evaluate these hypotheses further, we propose a systematic literature survey of known viruses to identify all potential beneficial functions and asymptomatic hosts. The survey will serve as the basis for planning future creationist research in virology.

- Bergman J. 1999. Did God make pathogenic viruses? *CENTJ* 13(1):115-125.  
Wood TC. 2002. The AGE-ing process: rapid post-Flood intrabaraminic diversification caused by Altruistic Genetic Elements (AGEs). *Origins (GRI)* 54:5-34.  
Francis JW. 2003. The organosubstrate of life: a creationist perspective of microbes and viruses. In Ivey RL, ed. *Proceedings of the Fifth International Conference on Creationism*. Creation Science Fellowship, Pittsburgh, pp. 434-444.

#### **R6. The HybriDatabase**

Stephanie R. Mace, Kurt P. Wise, Todd Charles Wood  
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Interspecific hybridization has long been regarded as important data in creationist systematics (e.g. Marsh 1941). To facilitate research in hybridization, the Center for Origins Research and Education created a computerized database of hybridization information, the HybriDatabase (HDB). The HDB is implemented in MySQL with perl CGI scripts and is hosted on a linux server running RedHat 8.0. Hybridization records are digitized by student volunteers and are checked by CORE staff before entry into the HDB. Currently, the HDB contains 4437 hybrid records from 36 different published sources. The majority of these records