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Preliminary Results of a Cognitum Study Investigating the Traditional Tetrapod Classes

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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

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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

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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

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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.