J. Eukaryot. Microbiol., 57(1), 2010 pp. 1–2

DOI: 10.1111/j.1550-7408.2009.00459.x

Introduction: Protistan Biology, Horizontal Gene Transfer, and Common Descent Uncover Faulty Logic in Intelligent Design[1]

AVELINA ESPINOSA
Department of Biology, Roger Williams University, Bristol, Rhode Island 02809

THE International Society of Protistologists (ISOP) organized a pre-meeting workshop entitled ''Horizontal Gene Transfer and Phylogenetic Evolution Debunk Intelligent Design,'' as part of the 1st North American Section meeting held June 11–13, 2009, at Roger Williams University, Bristol, RI, USA. This workshop focused on the acceptance of Darwinian evolution in the United States and the role of intelligent design (ID) in the ongoing controversy between scientific knowledge and popular belief. Intelligent design, a doctrine born in the 1980s, proposes that a ''Designer'' is responsible for the complexity in biological systems and that Darwinism cannot explain holistically the origin and evolution of the natural world, nor the intricate chemical assemblage of most organic structures (Forrest and Gross 2007; Padian and Matzke 2009). The workshop emphasized how to communicate evolutionary principles to student and public audiences by using examples of protistan evolution.

Dr. Guillermo Paz-y-Miño C., University of Massachusetts-Dartmouth, talked about the essence of science, evolution, and the struggle with belief; Dr. Avelina Espinosa, Roger Williams University, discussed how horizontal gene transfer (HGT) and eukaryote metabolic pathways can be used to challenge ID; Dr. Mark Farmer, University of Georgia, analyzed how protistan cell biology and genetics provide examples to dismiss ID arguments; and Dr. Andrea Habura, Wadsworth Center, highlighted strategies to communicate evolutionary theory to skeptical audiences. In this issue, the four participants summarize their presentations in two papers. In the first article, Using Protistan Examples to Dispel the Myths of Intelligent Design, Farmer and Habura offer a broad analysis of ID. In the second article, Integrating Horizontal Gene Transfer and Common Descent to Depict Evolution and Contrast it with ''Common Design,'' Paz-y-Miño C. and Espinosa discuss a case study of protistan protein evolution.

Farmer and Habura (2009) describe the philosophical roots of ID and link it to creationist beginnings. They examine influential ID literature, including *Darwin's Black Box* (Behe 1996) and *The Edge of Evolution* (Behe 2007), to highlight three ID proposals. (1) *Irreducible complexity*, or the premise that biological systems are too complex to have evolved, via natural selection, from simpler to more complex forms (Forrest and Gross 2007; Padian and Matzke 2009); according to ID, a ''Designer'' must have designed fundamental biological processes based on irreducibly complex building blocks (Behe 1996). (2) *Undocumented biological speciation*, or the assumption that speciation events have never been observed directly by scientists, nor could speciation have occurred purely by means of natural laws (Meyer 2004); the latter is based on the supposition that evolution via natural selection is a ''random'' phenomenon and, therefore, an ''accidental'' outcome. (3) *Impossibility of evolution*, or the lack of geological time for complex evolution to occur (Behe 2007), which also relies on the belief that natural selection operates randomly and that the emergence of biological diversity could not have happened since the formation of planet Earth, simply because fortuitous evolution would have taken longer to generate current biological complexity than the age of the Earth itself (problems with this logic are examined by Paz-y-Miño C. and Espinosa, 2009). Farmer and Habura (2009) challenge these ID premises by dissecting one of ID's ''Trojan Horses'' (see Forrest and Gross 2004), the evolution of chloroquine resistance in the protistan pathogen *Plasmodium falciparum*, which causes malaria. Studies have shown that in *P. falciparum*, two amino acid substitutions in a plasma membrane protein are implicated in the resistance to the antimalarial drug chloroquine (Martin and Kirk 2004). A prominent figure of ID, Dr. Michael Behe (2007), has compared and contrasted the evolution of resistance to chloroquine by *P. falciparum* to the incapacity of humans to have developed resistance to *P. falciparum*. Behe (2007) has arrived at the conclusion that, based on the time required for two interacting mutations to originate at random, ''. . . no mutation that is of the same complexity as chloroquine resistance in malaria arose [has arisen] by Darwinian evolution in the line leading to humans in the past ten million years.'' Behe (2007) asserts that ''. . . on average, for humans to achieve a mutation like this [= analogous to chloroquine resistance by *P. falciparum*] by chance, we would need to wait a hundred million times ten million years. Since that is many times the age of the universe, it's reasonable to conclude the following: No mutation that is of the same complexity as chloroquine resistance in malaria arose by Darwinian evolution in the line leading to humans in the past ten million years [the amount of time attributed to Hominid evolution, the taxonomic human family].'' According to Farmer and Habura (2009) and others (e.g. Miller 2007, see also Paz-y-Miño C. and Espinosa, 2009) there is faulty logic in Behe's (2007) view; he diminishes the editing role of natural selection over mutation rate, a process that expedites molecular evolution, and which is responsible for the origin and emergence of further biological complexity (Paz-y-Miño C. and Espinosa, 2009). Behe (2007) rejects naturalistic causation, or the interaction between mutation rate and natural selection, which is responsible for the evolution of drug resistance in *P. falciparum* (Miller 2007), and he also invokes ''design creationism'' to account for significant molecular change which, in his view, is statistically unlikely to reach high levels of complexity via Darwinian mechanisms. Interestingly, Farmer and Habura (2009) counter the claim of irreducible complexity by referring to evidence from two studies which demonstrate that a single amino acid substitution suffices to confer resistance to chloroquine in *P. falciparum* (Jiang et al. 2008; Lakshmanan et al. 2005), implying that, in the natural world, there is room for ''reducible simplicity'' (= a single mutation can work and provide resistance), the opposite of Behe's conceptualization of nature. Farmer and Habura's article is also illustrative of how the malaria example fits the process of speciation and the possibility of evolution (points 2 and 3 above). Various pathogens cause human malaria, for example, *P. falciparum* and *Plasmodium vivax*, two separate and distinctive species of protists that cause different host responses due to their diverse virulence (Müller et al. 2009). Moreover, the occurrence of specific types of malaria, not only in humans, but in other animals, including mammals and birds, suggests a broad adaptive radiation pattern of *Plasmodium* species, which now parasitize hosts of distant phylogenetic backgrounds, a remarkable example of

[1]Introduction to the workshop: Horizontal Gene Transfer and Phylogenetic Evolution Debunk Intelligent Design, 1st International Society of Protistologists—North American Section Meeting, June 11–13, 2009, Roger Williams University, Bristol, RI, USA.

Corresponding Author: A. Espinosa, Department of Biology, Roger Williams University, One Old Ferry Road, Bristol, Rhode Island 02809—Telephone number: +401 254 3137; FAX number: +401 254 3310; e-mail: aespinosa@rwu.edu

speciation and, therefore, classical Darwinian evolution (Roy and Irimia 2008; Janssen et al. 2002; Ricklefs and Fallon 2002).

Paz-y-Miño C. and Espinosa (2009) take this idea of common descent further in their article on the interaction between HGT and common descent. These authors discuss how continuous lateral exchange of genes, or HGT, in bacteria, Archaea, and Eukarya complicate the identification of a single origin and/or dichotomous branching pattern during the evolution of unicellular life. These authors indicate that phylogenies rarely include in their vertical representations of evolutionary history the significance of the lateral acquisition of genetic material by organisms, a problem widely discussed in the recent literature (Andersson 2009; Bapteste and Boucher 2009; Gogarten, Gogarten, and Olendzenski 2009). Various models have been suggested to account for the contribution of HGT to vertical evolution, including a ''reticulated tree'' or ''net'' (Doolittle 1999), which represents interconnected earliest stages of life's history; the ''ring of life'' (Rivera and Lake 2004), where a ''ring'' connects the origin of eukaryotes to a dual genetic merging, via endosymbiosis, of eubacterial and archaebacterial genomes; the ''symbiogenetic whole-organism model'' (Margulis 2009; Margulis et al. 2006), which posits that entire genomes of ''partner organisms'' became integrated and that a serial symbiotic fusion of ancestral lineages gave rise to eukaryotic cells; and the ''pattern pluralism scheme'' (Bapteste and Boucher 2009; Doolittle and Bapteste 2007), which considers that organisms can overlap in various natural and non-exclusive taxonomic units, making vertical inheritance part of the conceptual understanding of evolution, but not the end. Paz-y-Miño C. and Espinosa (2009) highlight that a bifurcated tree-like representation of evolutionary relations, linked by common ancestry—an idea conceptualized by Charles Darwin in The Origin of the Species of 1859, seems better suited for multicellular organisms, where vertical inheritance of genomes is of larger magnitude than horizontally acquired genetic traits (Andersson 2008; Keeling and Palmer 2008; Lopez and Bapteste 2009). Paz-y-Miño C. and Espinosa (2009) merge the reticulated pattern and tree phylogenies with the ring of life, symbiogenetic whole-organism model, and pattern pluralism schemes to propose an ''integrative model of lateral and vertical evolution,'' where both HGT and common descent are graphically depicted and combined. These authors use *Entamoeba histolytica* alcohol dehydrogenase 2 (EhADH2), a bifunctional enzyme in the glycolytic pathway of amoeba, to illustrate how EhADH2 could be the product of both horizontally acquired features from ancestral prokaryotes (i.e. aldehyde dehydrogenase [ALDH] and alcohol dehydrogenase [ADH]), and subsequent functional integration of these enzymes into EhADH2, which is now inherited by amoeba via common descent. Paz-y-Miño C. and Espinosa (2009) discuss how mutation rate coupled with natural selection and HGT coupled with common descent drove the evolution of EhADH2, and perhaps of most alcohol dehydrogenases (ADHE), and contrast this analysis with proposals invoking ''common design'' (i.e. the independent emergence of major taxa with no common ancestry) to explain the interaction between horizontal and vertical evolution. Paz-y-Miño C. and Espinosa (2009) remark that the case study of lateral and vertical evolution of EhADH2 is didactic in the context of the Darwinian perspective, and that selection has acted continuously and cumulatively on ancestors and intermediates of EhADH2. Therefore, a single or multiple emergence of EhADH2 arising from an ''intelligent design'' followed by adaptive change is improbable.

LITERATURE CITED

Andersson, J. O. 2008. Eukaryotic gene transfer: adaptation and replacements. *In*: Hensel, M. & Schmidt, H. (ed.), Horizontal Gene Transfer in the Evolution of Pathogenesis. Cambridge University Press, Cambridge. p. 293–315.

Andersson, J. O. 2009. Horizontal gene transfer between microbial eukaryotes. *In*: Boekels Gogarten, M., Gogarten, J. P. & Olendzenski, L. (ed.), Horizontal Gene Transfer: Genomes in Flux. Humana Press, New York. p. 473–487.

Bapteste, E. & Boucher, Y. 2009. Epistemological impacts of horizontal gene transfer on classification in microbiology. *In:* Gogarten, M. B., Gogarten, J. P. & Olendzenski, L. (ed.), Horizontal Gene Transfer: Genomes in Flux. Humana Press, New York. p. 55–72.

Behe, M. J. 1996. Darwin's Black Box. Free Press, New York, 307pp.

Behe, M. J. 2007. The Edge of Evolution. Free Press, New York, 336 p.

Doolittle, W. F. 1999. Phylogenetic classification and the universal tree. *Science*, **284**:2124–2128.

Doolittle, W. F. & Bapteste, E. 2007. Pattern pluralism and the tree of life hypothesis. *Proc. Natl. Acad. Sci. USA*, **104**:2043–2049.

Farmer, M. A. & Habura, A. 2009. Using protistan examples to dispel the myths of intelligent design. *J. Eukaryot. Microbiol*., doi:10.1111/j.1550-7408.2009.00460.x.

Forrest, B. & Gross, P. R. 2004. Creationism's Trojan Horse: the wedge of intelligent design. Oxford University Press, New York, 432 p.

Forrest, B. C. & Gross, P. R. 2007. Biochemistry by design. *Trends Biochem. Sci.*, **32**:301–310.

Gogarten, M. B., Gogarten, J. P. & Olendzenski, L. (ed.), 2009. Horizontal Gene Transfer: Genomes in Flux. Humana Press, New York, 500 p.

Janssen, C. S., Barrett, M. P., Turner, C. M. & Phillips, R. S. 2002. A large gene family for putative variant antigens shared by human and rodent malaria parasites. *Proc. Biol. Sci.*, **269**:431–436.

Jiang, H., Patel, J. J., Yi, M., Mu, J., Ding, J., Stephens, R., Coopers, R. A., Ferdig, M. T. & Su, X-Z. 2008. Genome-wide compensatory changes accompany drug-selected mutations in the *Plasmodium falciparum* crt gene. *PLoS ONE*, **3**:e2484, doi:10.1371/journal.pone.0002484.

Keeling, P. J. & Palmer, J. D. 2008. Horizontal gene transfer in eukaryotic evolution. *Nat. Rev. Gen.*, **9**:605–618.

Lakshmanan, V., Bray, P. G., Verdier-Pinard, D., Johnson, D. J., Horrocks, P., Muhle, R. A., Alakpa, G. E., Hughes, R. H., Ward, S. A., Krogstad, D. J., Sidhu, A. B. S. & Fidock, D. A. 2005. A critical role for PfCRT K76T in *Plasmodium falciparum* verapamil-reversible chloroquine resistance. *EMBO J.*, **24**:2294–2305.

Lopez, P. & Bapteste, E. 2009. Molecular phylogeny: reconstructing the forest. *C. R. Biol*., **332**:171–182.

Margulis, L. 2009. Genome acquisition in horizontal gene transfer: symbiogenesis and macromolecular sequence analysis. *In:* Gogarten, M. B., Gogarten, J. P. & Olendzenski, L. (ed.), Horizontal Gene Transfer: Genomes in Flux. Humana Press, New York. p. 181–191.

Margulis, L., Chapman, M., Guerrero, R. & Hall, J. 2006. The last eukaryotic common ancestor (LECA): acquisition of cytoskeletal motility from aerotolerant spirochetes in the proterozoic eon. *Proc. Natl. Acad. Sci. USA*, **103**:13080–13085.

Martin, R. E. & Kirk, K. 2004. The malaria parasite's chloroquine resistance transporter is a member of the drug/metabolite transporter superfamily. *Mol. Biol. Evol.*, **21**:1938–1949.

Meyer, S. C. 2004. The origin of biological information and the higher taxonomic categories. *Proc. Biol. Soc. Washington*, **117**:213–239.

Miller, K. R. 2007. Falling over the edge. *Nature*, **447**:1055–1056.

Müller, I., Genton, B., Rare, L., Kiniboro, B., Kastens, W., Zimmerman, P., Kazura, J., Alpers, M. & Smith, T. A. 2009. Three different *Plasmodium* species show similar patterns of clinical tolerance of malaria infection. *Malar. J.*, **8**:158, doi:10.1186/1475-2875-8-158.

Padian, K. & Matzke, N. 2009. Darwin, Dover, 'Intelligent Design' and textbooks. *Biochem. J.*, **417**:29–42.

Paz-y-Miño C., G. & Espinosa, A. 2009. Integrating horizontal gene transfer and common descent to depict evolution and contrast it with 'common design'. *J. Eukaryot. Microbiol*., doi:10.1111/j.1550-7408.2009.00456.x.

Ricklefs, R. E. & Fallon, S. M. 2002. Diversification and host switching in avian malaria parasites. *Proc. R. Soc. Lond. B.*, **269**:885–892.

Rivera, M. C. & Lake, J. A. 2004. The ring of life provides evidence for a genome fusion origin of eukaryotes. *Nature*, **431**:152–155.

Roy, S. W. & Irimia, M. 2008. Origins of human malaria: rare genomic changes and full mitochondrial genomes confirm the relationship of *Plasmodium falciparum* to other mammalian parasites but complicate the origins of *Plasmodium vivax*. *Mol. Biol. Evol.*, **25**:1192–1198.

Received: 10/16/09; accepted: 10/17/09