# Does a "500 million-year-old hormone" disprove Darwin?

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In a paper published by the FASEB Journal in 1999, Danielle Georges and Christian Schwabe described gene sequences from the tunicate *Ciona intestinalis* that were indistinguishable from porcine relaxin (1). Newer data contradict that finding: recently published analyses of the *C. intestinalis* genome do not confirm the presence of relaxin sequences (2). What might seem like a narrow issue of scientific fact has broader implications. To the delight of creationists and fans of intelligent design, the presence of similar relaxin sequences in pigs and sea squirts–species separated by 500 million years–has been used to cast genomic doubt on Darwinian evolution. Indeed, Schwabe has repeatedly cited the tunicate relaxin data, and the nearly identical relaxin sequences he has identified in whales, (3) not only to support his own "Genomic Potential Hypothesis" but also to refute modern evolutionary biology (4).

Schwabe's hypothesis would replace Darwin's theory of common descent with the view of the independent origin of all species, thereby making the origin of life and the origin of species one and the same problem. Moreover, the "Genomic Potential Hypothesis" rejects natural selection of random variations as the mechanism that underlies speciation and adaptation. Thus, albeit Schwabe sees chemistry as the sole force generating genomes and species the independent origin of all species asserted by his "Genomic Potential Hypothesis" coincides with the creationist view of the origin of species.

Since Schwabe therefore is regularly cited by creationists as an "atheistic scientist" who rejects neo-Darwinism, it seems worthwhile to critique his experimental work in the context of his "Genomic Potential Hypothesis." It's an hypothesis that wants to have it both ways. On the one hand, Schwabe argues that the high degree of *diversity* found in the relaxin sequences of different species would date speciation events much earlier than phylogenies based on other data. On the other hand, he argues that the *identity* of tunicate, cetacean, and porcine relaxin sequences cannot be explained by Darwinian selection of random mutants. This concomitant use of sequence *diversity* and sequence *identity* to deny the theory of evolution appears to us at least curious or at worst tautologous.

The 1999 *The FASEB Journal* paper immediately evoked critical responses summarized by an editor's comment (5) that the conclusions rested entirely on PCR and microsequencing data, two methods quite prone to contamination. The authors rejected those concerns and replied that the experiments were carried out in two separate labs and that Georges had never worked with porcine material before (6). Not so: Georges had indeed used polyA+-RNA from pregnant sow ovaries (the organ in which relaxin is produced) in work published well before *The FASEB Journal* paper (7). At any rate, since the genomic sequence was reported to lack introns, the cDNA could have served as a good probe for Southern blot analysis of genomic DNA, a far more robust technique (a description of Southern blot analysis appears in the Methods section of *The FASEB Journal* paper but such data are not presented in the Results section). Indeed, this approach would have enabled the authors to decide whether the sequence variation they observed in one tenth of the PCR products was introduced during amplification, whether it resulted from a polymorphism of the gene or if two different relaxin genes reside within the *Ciona* genome as the authors speculated.

In point of fact, polymorphisms would contradict the "Genomic Potential Hypothesis," because, as rigidly interpreted, the Schwabe hypothesis would predict the independent origins of individuals carrying different alleles (see below). Still, the authors adduce the fact that *Ciona* relaxin is more similar to an infrequent allele of porcine relaxin. They suggest an "occasional exchange" in the respective position of the porcine gene: but that of course implies a mutation. Curiously, Schwabe willingly accepts that "chance mutations" may cause inherited human diseases (8) but denies that mutations can drive evolution. In addition it should be

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noted that Schwabe's hypothesis only relies on the comparison of coding sequences. Therefore he misses other levels of conservation, namely exon/intron structure and gene order. Although it seems unlikely, we cannot completely rule out that the sequence published by Georges and Schwabe is hidden in a part of the *Ciona* genome not represented in genomic libraries or located in clones (itself a Darwinian concept) resistant to sequencing. However, due to the technical problems we have noted, and the flawed arguments advanced in *The FASEB Journal Ciona* paper, we would suggest that the relaxin sequences detailed in the cetacean paper—obtained by the same biochemical techniques—need revisiting.

So much for the shaky sequence data of *Ciona* and cetacean relaxins. On to the more contentious issue: the "Genomic Potential Hypothesis," which claims an independent origin for every single species. We would insist that the Schwabe hypothesis not only contradicts neo-Darwinian theory of evolution, but is in conflict with the fundamental facts of biology based on direct measurements and observations; and these remain *fact*-independent of any particular notion as to the origin of life. Indeed, it is hard to see how genomes of animals with internal gestation or parental care could have originated independently in a primordial soup, independently formed into cellular structures once sufficient complexity had been achieved, independently survived as stem cells that occasionally developed to multicellular organisms, (*e.g.*, human beings) and independently reproduced sexually thereafter, as Schwabe's hypothesis implies. It would be a miracle, indeed.

Be that as it may, physiology and ecology teach us that animals are not candidates for independent origins and survival, because heterotrophy dictates that animal life depends on plants or other heterotrophic organisms. The same is true for fungi. Dependence on other life forms is fact of life: more than half the world's species live inside or on the bodies of other organisms. And developmental biology teaches us that multicellular organisms (all animals and plants) have vectorial constraints that prevent independent origins. For example, in *Drosophila* the products of maternal effect genes initiate the head-to-tail axis while the egg is still in the egg chamber of the mother. But, according to the "Genomic Potential Hypothesis" since each specie originates for the first time, there can be no mothers!

Furthermore, the majority of multicellular animals and plants are diploid. Diploidy originates from the fusion of a male and female gamete. Thus, it is inherently implausible from a genetic point of view that a diploid organism could have originated in a primordial soup, especially if the two haploid genomes carried different alleles. The "Genomic Potential Hypothesis" is therefore in direct contradiction of the facts of cytogenetics: all animals and plants possess chromosomes, which are structures displaying complexities far beyond those of naked DNA. Superimposed on this problem is the origin of sex chromosomes (X and Y in humans). If the genomes of males and females of sexually reproducing species originated independently, then for each species, female and male genomes which differ in additional complicated ways (*e.g.*, epigenetic effects like X-inactivation in females or maternal and paternal imprinting) must have formed independently.

Modern genomic science provides additional reasons to eliminate plants, fungi, and animals from the candidacy of independently arisen species because animals (1,320,000 described species) and fungi have two genomes (nuclear and mitochondrial) and plants have three genomes (nuclear DNA, mitochondrial DNA, and chloroplast DNA). Thus, for each of the described 270,000 plant species three genomes would have had to be assembled independently and to be joined together in a single cell. And, of course, the assembly would have to ensure that compatible components encoded from the different genomes would form proper functional products (*e.g.*, ribulose bisphosphate carboxylase oxygenase) in one of the compartments. That would leave organelle-free eukaryotes and prokaryotes (eubacteria and archea) as potential candidates for independent origins. But there are good reasons to interpret eukaryotes as the result of a merger of two life forms, one of which is a prokaryote. Therefore, almost by definition, eukaryotes cannot be candidates for independent origin.

Are only poor, single-celled haploid prokaryotes left as candidates for independent origin? A subset of these are parasites or symbionts (gut bacteria, for example) which by definition depend on other (usually higher) organism, and so even these creatures fall short. But what about autotrophic prokaryotes and photosynthetic microorganisms? It might point out that photosynthetic prokaryotes are excluded as candidates for direct origin from abiotic materials because photosynthesis requires assembly of highly evolved assemblies of proteins and resonant groups. Finally, autotrophic nonphotosynthetic prokaryotes are the only organisms that could have originated directly from chemical building blocks. If as Virchow insisted in 1855, *omnis cellulae e cellula* (all cells come from a cell), these must be the culprits.

Although it seems reasonable to assume a single origin of life, it is not within the scope of our argument, which is advanced on behalf of common descent and against independent origin.

In summary, common descent is congruent with knowledge independently developed in fields of biology (physiology, ecology, ethology, genetics, cytogenetics, genomics, paleontology, *etc.*) and geology. This is not the case for Schwabe's "Genomic Potential Hypothesis," nor for any other hypothesis that claims the independent origins of species. Schwabe admits that the problem of the origin of life "is complex beyond our present level of understanding" (4). That's for sure. But since the "Genomic Potential Hypothesis" requires that the origin of life and the origin of species are identical, its formulation is an impossible tautology. Four centuries of experimental science have taught us that the biological world is one in which organisms

derive from previous generations of cells, from their own close relatives and from species as far removed as the smallest prokaryote. These biological facts point forcefully to the necessity of a continuous chain of generations. The facts of evolution remain, irrespective of the presence—or absence—of relaxins in one or another species.

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