NeuroTheology

Brain, Science, Spirituality, Religious Experience

UniversityPress.info

NeuroTheology: Brain, Science, Spirituality, Religious Experience
Rhawn Joseph — Editor.

Includes bibliographical references

ISBN: 0971644586

1. God 2. Evolution 3. Darwin. 4. Origin of Life.
5. Theology 6. Religion 7. Brain 8. Creation Science
9. Neuroscience. 10. DNA. 11. Spirituality

Cover Design by Rhawn Joseph

Acknowledgements: The Neuropsychology of Aesthetic, Spiritual & Mystical States, by Eugene G. d’Aquili & Andrew B. Newberg, was first published in the jouitual lnirst published ipet5(1): 39-52, Sp( ]TJ01 Tw 0 -2.4 TD esi

THE DEATH OF DARWINISM

Purpose, Progress, Silent Genes, & Multi-Regional Human Metamorphosis

by Rhawn Joseph, Ph.D

"Progress is a noxious, culturally embedded, untestable, nonoperational, intractable idea that we must replace if we wish to understand the patterns of history." -Harvard Paleontologist S. J. Gould (1988, p. 319)

Charles Darwin was not the first to profess a belief in evolution for similar theories were espoused by many others, including Anaximander, a Greek Philosopher, some twenty six hundred years ago. Anaximander argued that humans descended from fish.

Over the centuries various scientists have come to similar conclusions and have written page after page that not only parallels the later work of Darwin but which Darwin copied and incorporated into his book (often without citation), including the works and lectures of Edward Blyth, William Wells, James Pritchard, Williams Lawrence, Charles Naudin, A. R. Wallace, and G.L.L. Buffon. When it was pointed out he had copied, almost verbatim, parts of Buffon's 18th century treatise "Natural History," Darwin (1888) was forced to agree that "whole pages are laughably like mine."

Over the last 100 years Darwin has almost been deified by modern Western science and the Western media. Yet, because of the still smoldering controversy regarding the true authorship of his theory, some of his acolytes have also become his apologists, explaining away the obvious similarities between his writings and the theories and observations of his contemporaries and those great men who came before him. Thus Darwin is sometimes described as a "great synthesizer of existing information." The "existing information" that Darwin synthesized, or rather, borrowed, includes, in fact, the crux of the theory of evolution; i.e. natural selection—a theory first formally proposed and distributed, not by Darwin, but by A. R. Wallace.

Although glossed over by Darwin and his acolytes, Darwin had in fact abandoned the field of "evolution" early in his career. Prior to receiving Wallace's land mark paper, Darwin's had spent 15 years studying and writing about barnacles, not evolution. However, upon reading Wallace's brilliant paper, Darwin proclaimed that he had been studying evolution all along, and had been writing an identical paper, and then spent the next 8 months rewriting, and in some places, repeating the works of others without citation, including the brilliant and revolutionary work of Wallace.

Although we can only speculate, Darwin may well have felt he had but no choice but to borrow liberally from the work and ideas of others. Although great things had been expected of him by his wealthy and well known father, and although his father's friends, including a number of well known scientists had also expected that he would some day make a name for himself, Darwin had repeatedly failed to accomplish anything of significance. After repeated failures he had become miserably depressed. Darwin had been forced to drop out of medical school when it became apparent that he did not have the aptitude to become a medical doctor, and then he also failed at his next pursuit, which was theology. And then he failed yet again in his attempts to establish himself as a "naturalist" and scientist, his writings and observations being dismissed as insignificant and mere repetitions of what was already well known—including his observations while voyaging on the Beagle.

Worse, after he was appointed "secretary" of the Geological Society, he subsequently claimed to have made a "significant" discovery and proclaimed that some "mysterious rock formations" at Glenroy Scotland were the remnants of "ancient marine beaches" which had been part of the mainland but had sunk into the sea. Darwin was quickly proved wrong. They had been carved by glaciers.

As fame repeatedly escaped him, Darwin became increasingly withdrawn and depressed. He dabbled in this area and that, and then spent 15 years devoted to the study of barnacles, about which he wrote four short papers.

And then, on June 8, 1858, Darwin received a letter from Alfred Russel Wallace, accompanied by a 12 page summary of Wallace's ideas on evolution, i.e. natural selection. Wallace was a renowned naturalist and had published a number of papers on evolution which Darwin had read and expressed interest in. From an island near Borneo Wallace had forwarded his monograph to Darwin. The paper was utterly brilliant!

Darwin then claimed to have recently arrived at identical conclusions, and thus claimed Wallace's theory as his own. Darwin immediately abandoned the study of barnacles and began feverishly working on a book, a synthesis of the words of Blyth, Wells, Pritchard, Lawrence, Naudin, and Buffon: On the Origin of Species by Means of Natural Selection which he published in November of 1859, almost 18 months after receiving the paper by Wallace. Indeed, the crown jewel was in fact the paper by Wallace, "Natural Selection." As Darwin well knew, this "synthesis" and the theory of "natural selection" would garner him world fame.

Darwin, his well connected friends in the scientific community, and his acolytes have gone to extraordinary lengths to rewrite history and to spin myths regarding Darwin's' utterly insignificant observations when as a youth he sailed on the "Beagle"—observations which were little different from numerous naturalists writing and publishing at the time. Nevertheless, the facts of the matter are that up until receiving the paper by Wallace, Darwin had written absolutely nothing of significance on evolution, and had spent the previous 15 years studying and writing about "barnacles." Not evolution. Barnacles!

Although Darwin claims otherwise, it could also be argued that Darwin's claim to fame, and the crux of his thesis, the theory of "natural section," was devised, originated and first penned and distributed by Wallace and Wallace alone, which is why knowledgeable sources grudgingly credit Wallace as the "cofounder" of the theory of evolution.

Why did Wallace receive only second billing? Why did so many 19th century scientists find it acceptable to attribute the work of Wallace to Darwin? First, perhaps it is true, as Darwin claims, that he had been writing an identical paper on "natural selection" where he made the same exact arguments and came to the same exact conclusions as Wallace, and was thus shocked and dismayed to discover that Wallace had come to the "same" conclusions and had written them down. An amazing coincidence! Thus Darwin rightly deserves credit as being the codiscoverer. However, if that does not seem plausible, the reader might consider the following: Darwin, the former secretary of the Geological Society, was the son of a rich and well known man and part of a circle of exceedingly influential scientists. Wallace was an outsider. And, Wallace believed in God. Darwin did not.

In contrast to Darwin, Wallace was repeatedly struck by the fact that various faculties and anatomical structures had "evolved" and existed prior to the conditions that would make them necessary or useful—especially as pertaining to the "evolution" of woman and man. Evolution, as pointed out by Wallace (1895), is often characterized by the survival of certain animals who already possessed a trait, or physical characteristic, which enabled them to survive in response to changing environmental conditions. That is, these capacities existed apriori, well before they were naturally selected or useful, and to Wallace that suggested intelligent design, progress and anticipation of changing conditions. Moreover, Wallace argued that because this was particularly true of "man" his theory of "natural selection" should not be applied to human evolution.

To Wallace and at least a few of his contemporaries, such as pioneering paleontologist Robert Broom, the obvious evidence of progress, design, and the presence of advanced characteristics prior to their selection, particularly in regard to the evolution of humanity, seemed to imply purposeful anticipation or planning, as if the instructions had already existed apriori; as if human evolution were predetermined.

According to Wallace (1895) the emergence of humanity could not have occurred secondary to random variations or mutations. Evolutionary progress and adaptations made in advance of their utilization and thus before they were maximally adaptive and which have culminated in the emergence of humanity, suggested to Wallace, the presence of a "guiding hand," a "divine intelligence" which designed these features in advance and in anticipation of their later utilization. Wallace came to the conclusion that this "guiding hand" belonged to none other than God, and to combat "Darwinism" announced his belief to the world.

Darwin was furious with Wallace, and immediately fired off a letter announcing his displeasure: "I hope you have not murdered too completely your own child and mine" (Darwin, 1888).

It is because of Wallace's insistence on progress, design, and this guiding hand in the evolution of humanity—and in particular and especially his belief in God— that subsequent evolutionary and genetic theorists have ridiculed and virtually ignored his work as well as the obvious implications of his observations; i.e. adaptive changes and modifications in structure prior to their usefulness suggests that their future employment was predesigned and predetermined. Humans did not evolve their humaness or their human genes. Rather, human genes were inherited from non-human species, often as silent genes and gene-within-genes.

GENE EXPRESSION AND EVOLUTION ARE NOT DUE TO RANDOM MUTATIONS

A major tenant of Darwinian and neo-Darwinian evolutionary theory is that evolution is due to "random mutations" ("variations") and that there is absolutely no evidence of design. "Design is an illusion" we are told. Moreover, according to the more extreme elements of the neo-Darwinian school, the obvious progression from single cell, to Ediacaran fauna, to the Cambrian Explosion, to cartilaginous fish, to vertebrates, amphibian, reptile, repto-mammal, therapsid, mammal, primate, woman and man, is not progress, but "patterns without plans."

Nor have species become more complex and more intelligent. As neatly summed up by Harvard paleontologist S. J. Gould (1988, p. 319) "Progress is a noxious, culturally embedded, untestable, nonoperational, intractable idea that we must replace if we wish to understand the patterns of history." To bolster these arguments, some neo-Darwinians, point to the fact that much of the Earth's biomass consists of microbes and bacteria. Although, certainly, various strains of bacteria and species of plant, insect, and mammal, have remained relatively primitive or simple, so too have the cells of the skin vs the cells of the brain.

That relatively simple creatures have not disappeared and are abundant is not an argument against increasing complexity, design, growth, or progress. Complex species, like complex body parts, are often comprised of, or depend on, relatively simple elements or relatively simple creatures, such as bacteria, in order to survive. We would not be able to adequately digest our food without the assistance of various intestine-dwelling bacteria. Conversely, these bacteria would not be able to thrive outside our stomachs.

Complex creatures and simple plants, insects, and animals are mutually dependent and maintain interrelated lives. For increasingly complex species to have emerged on Earth required that other species undergo relatively little change other than in the form of diversification; otherwise the environment and atmosphere which sustains us could not be maintained.

To point to the existence of bacteria or simple plants and primitive insects, and then arrogantly state that the existence of these simple creatures somehow balances out and thus negates the obvious evidence of evolutionary progress, is philosophically naive and completely disingenuous. It is an argument which is not to be taken seriously. In fact, there is obvious evidence of progress not only among vertebrates but even among insects and plants (Joseph, 2001).

PROGRESS

Be it plant, insect, or animals, life on this planet has been characterized by a progressive metamorphosis where increasingly complex and intelligent species have emerged in a logical, step-wise, sequential pattern. There is nothing random about the evolution of plants, insects or animals, as demanded by Darwinian theory.9veye thatvae-0.1(rcatiots, orm)17.3mu(atiote are randoa. erntaisly)28.1s, th(ei)viden
th(no- Darwinia vi e322.3(w of e)2292(v)20(olutios. anded,e it is th(u(ttedpireiec-s)]TJ T* -0.167 Tw [(bi liyw of e)6292(v

Ne

genetic engines of evolution, introns, i.e. transposons and regulatory and "silent" genes. As compared to all other genomes so far sequenced, human introns have become larger and longer as compared, for example, to fly or worm, i.e., about 50 kb versus 5 kb (Birney et al., 2001). "Worm and fly have a reasonably tight intron distribution, with most introns near the preferred minimum intron length (47 bp for worm, 59 bp for fly) and an extended tail (overall average length of 267 bp for worm and 487 bp for fly). There is a greater size distribution among human introns, with a peak at 87 bp but a very long tail resulting in a mean of more than 3,300 bp" (Birney et al., 2001).

The protein-encoding exons, on the other hand, are roughly the same size. Exons are also conserved, showing up in previous species, often in the same exact location.

Thus there has been an increase in the intron to exon ratio in the human genome which in turn is representative of the extreme importance of introns in human evolution and evolutionary change.

Human genes also differ from the genes of other species as they perform more complex and multi-tasking operations. The average human gene can make three to five primary protein products vs the genes of other species which can create one or two proteins (Aravind et al., 2001; Birney et al., 2001). This is progress.

Human proteins are more complex than the proteins in other organisms. Human proteins are capable of more interactions and do more things and perform more complex operations including alternative splicing tasks which enable them to generate a larger number of protein products. Humans, therefore, produce more proteins that are classified as falling into more than one functional category (426 in human versus 80 in worm and 57 in fly). This is progress.

There has also been an expansion of protein families. Protein families are more numerous in the human than in any other organism (Aravind et al., 2001). Again, contrary to Gould, this is evidence of progress.

In consequence, "the human genome contains greater numbers of genes, domain and protein families, paralogues, multi-domain proteins with multiple functions, and domain architectures. According to these measures, the relatively greater complexity of the human proteome is a consequence not simply of its larger size, but also of large-scale protein innovation" (Aravind et al., 2001).

Although the mantra "random variations" is the basis for Darwinian theology, the evolution of not just these genes but the vertebrate-specific protein domains and motifs have been created according to specific regulatory constraints, and have been built by rearranging preexisting components into a richer collection of domain architectures (IHGSC, 2001); the genetic foundation for their creation and the instructions for their creation, existed apriori. They were inherited. They did not randomly evolve.

SILENT GENES

Introns are "silent" genes, and contain "genes within genes" and can give birth to additional sequence segments, as well as additional genes and even gene clusters which are located deep within the intron; i.e. genes within genes (Henikoff et al. 1986; reviewed in Strachan & Read, 1996; Watson et al. 1992). If one were to twist apart the double helix of an intron, they may well discover "baby genes" and thus genes within genes, and, therefore, species within species locked within. Indeed, introns, and intronic gene clusters are considered a "hot spot" for homologous recombination (Wahls et al. 1990), which, over the course of "evolutionary metamorphosis" may have made possible not only the production of new genes and new nucleotide sequences, but the emergence of increasingly complex and intelligent creatures, such as woman and man.

Consider, for example, the metamorphosis of modern humans versus chimpanzees, both of which apparently descended, on Earth, from a common ancestor 5 million or more years ago (Sibley & Alhquist, 1984; Takahata et al., 1995). Chimpanzees and humans display a 99% homologous sequence identity in nucleotide base pair sequence organization, and 98.4% of activated/coded human and chimpanzee DNA is identical (Goodman, Tagle, & Fitch 1990). There are very few genes in the chimp genome whose counterparts cannot be found often in the same exact location in the human genome, though it is also apparent that chromosomes 4, 9, and 12 are configured somewhat differently.

Those few genes that have been inverted include AF4, which sits on chromosome 4 and which codes for a transcription factor related to leukemia in humans (reviewed in Gibbons, 1998). By contrast, those "chimpanzee" introns which have disappeared from the human genome include a few silent "satellite" introns which, in the chimp genome, are adjacent to the telomere (Royle et al. 1994), a structure which caps the chromosome and regulates gene expression and cell and DNA-based divisions. These chimpanzee introns appear to have shifted to a new position within the human chromosome (a common behavior of episomes, transposons, and plasmids), becoming exons and thus activated, and in so doing possibly promoting the transition from hominoid to hominid and thereby giving rise to the first humans in the process.

Introns are responsible for producing duplicate genes as well as new genes and clusters of genes, including numerous copies of highly repetitive sequences of nucleotide base pairs (Finnegan, 1989; Henikoff et al. 1986; Petes & Fink, 1982). The result is the creation of numerous sequence families (or gene families), some of which are dispersed throughout the genome (Jelinek et al. 1980).

colleagues demonstrated that when they deactivated the sepallata (SEP) genes, flowers that normally consist of sepals, petals, stamens and carpells, were reduced to consisting only of sepals. Thus, the SEP gene is necessary for petals, stamens and carpells formation. Yanofsky et al., report that although the SEP genes are active in flowering plants, and silent in leaves and nonflowering plants, that they were able to activate these silent SEP genes, and in result, leaves were converted into petals.

Silent genes, therefore, can be activated to produce traits, including evolutionary advanced traits, that exist prior to their expression. They are inherited. They do not randomly evolve.

Much of the genome consists of silent intronic genes and nucleotide sequences. Silent genes and silent nucleotide sequences have the capacity to make copies of themselves, and to shift position within the genome (i.e. “jumping genes”): referred to as transposons. Transposable nucleotides show a tendency to leap to the more active GC regions. Once they are incorporated, they thus increase gene density and nucleotide content. These silent genes and silent nucleotides also come to be expressed, and/or they exert regulatory, inhibitory, or activating influences on other genes once they leap to the GC regions. However, these gene activity is not random. It is highly regulated. In other words (and contrary to Darwinism), genes (and the traits they code for) that exist apriori may change position in the genome and become active; and they leap from the non-coding to the coding regions of the genome in a purposeful, controlled, regulated, and predictable fashion.

As transposons are often copies of genes and silent nucleotide sequences, and often copies of copies, the GC regions also consist of more duplicate and repeat sequences of nucleotides than the AT regions. By contrast, more non-repeats are found in the AT regions. However, as pointed out by the International Human Genome Sequencing Consortium, (IHGSC, 2001) “Much of the ‘non-repeat’ DNA in AT-rich regions probably consists of ancient repeats that are not detectable by current methods.”

In other words, many of the transposable elements which have shifted from AT regions to GC regions, where they are then expressed, are themselves exceedingly ancient and likely have pedigrees which extend interminably backwards in time. The findings reported by the International Human Genome Sequencing Consortium, are thus entirely consistent with the theories of evolutionary metamorphosis and intelligent design which posit that “silent” ancestral genes are passed down to subsequent generations and subsequent species, where they may later come to be activated thereby expressing silent traits that had been precoded into the genomes of our ancient ancestors. Genes and traits do not randomly evolve, they are precoded and exist apriori, and are inherited and passed on from species to species in silent form, waiting for a signal to be expressed —findings which are completely contrary to Darwinism.

Genes may be silent (introns) or expressed (exons). Each active gene also consists of active and silent nucleotide sequences. The silent sequences (introns) act as boundaries which define and frame the active zones (exons). The active zones, therefore, have also been referred to as “frames” that consist of exonic nucleotides bordered by introns which may be acting not only to “frame” but to regulate gene expression. If the frame is extended or shortened by a single nucleotide, a “frame shift” results, and the genetic code is altered: just as 3456, becomes a different product if we add or delete a number (63456). Frame shifts are also important contributors to evolutionary metamorphosis, and are largely due to the movement or activity of intronic transposons (as well as the shuffling of exons).

Intronic genes often contain genes-within genes. Intronic genes also make duplicates of themselves. How many genes are duplicates is unknown. However, gene duplication, that is whole gene duplication (WGD) has played a significant role in evolutionary metamorphosis. “In principle, WGD provides the raw material for great bursts of evolutionary change by allowing the duplication and divergence of entire pathways. WGD has played a key role in evolution” (IHGSC, 2001).

For example, there is evidence to suggest that two WGD events triggered the transition from invertebrates to vertebrates, and is thus partly responsible for vertebrate evolution; giving rise, perhaps to the first jawless fish around 500 million years ago.

Additional WGB events may have also contributed to the evolution of primates and then humans. For example, numerous human genes are duplicates and occur in sets of four homologues (e.g., the four HOX genes) which are clustered together on chromosomes 2, 7, 12 and 17; and these appear to have been duplicated at about the time when primates diverged from (non-primate) mammals, and when hominids diverged from hominoids (IHGSC, 2001). For example, a WGB event occurred around 30 million years ago when old world monkeys and apes diverged, and this was followed by a second duplication event between 5 to10 million years ago when hominoids and various species of Australopithecus diverged. This later duplication resulted in the creation of two genes on each side of the chromosome 5 centromere (Courseaux & Nahon 2001).

Transposons (intronic "jumping genes" and nucleotides) have also played a significant role in evolutionary metamorphosis. DNA transposons can produce large-scale chromosome rearrangements, and at least 47 human genes and almost half the human genome have been derived from transposons (IHGSC, 2001). Transposons do not provide any selective advantage for any individual host, but for progeny and thus subsequent generations and subsequent species. This is accomplish in part, by contributing regulatory elements and new genes to the genome which gives rise to new traits and thus new species —all of which have been programmed into the genetic code, the expression of which is under tight regulatory constraints.

This process of creating new genes and duplicate genes is not random, nor is it due to mutation, but is under genetic control and functions in accordance with precise genetic instructions (Berkner, 1988; Moss et al. 1990; Wigler, et al. 1979).

FRAME SHIFTS

The evolution of species, variations among and between species, and the evolution of seemingly "new" adaptive characteristics are a function of a variety of genetic and environmental factors. These include exon shuffling, nucleotide duplications and recombinations, the dispersal of nucleotide sequences to new genomic sites, and in particular, the intronic birth of additional genes.

As noted, genes have the capacity to express a variety of products. Sometimes all it takes are exceedingly minuscule and often minor changes in the location and coding of genes and the coding of different lengths of nucleotide sequence segments to produce wholly different products and appendages (e.g., Drake, 1991; John & Miklos, 1988; Moran et al., 1999; Symmonds, 1991).

For example, there is a specific human gene and nucleotide sequence for human dystrophin. Yet, this same gene can be differentially activated to produce muscle cells if its nucleotide sequence is extended by just a few base pairs. Moreover, this same gene can produce motor neurons and induce Purkinjee, brain cell development; that is, if the same sequence "start point" is located and activated 100 kb upstream (reviewed in Watson et al., 1992). Different traits and different products can be generated by simply extending, or reducing the number of nucleotides in a given sequence. This is referred to as a "frame shift." However, again, these genes and sequences, exist prior to their activation. They did not "evolve," they were inherited.

As is well known, sequences of nucleotides are divided into coding (exons) and non-coding (introns) segments. Introns instruct RNA as to how much of each segment is to be copied. If different "starter" or "stop" introns are activated this results in different segments or sequence lengths becoming expressed, thereby producing a different product; products which are genetically precoded.

Therefore, variation and diversity can be differentially induced if different "starter" exons or promoter introns are activated and an almost unlimited variety of products, structures, and even species can be produced by just minute shifts in nucleotide sequence organization and activation.

Consider, for example, HIV. In a 1996 nationwide AIDS study conducted by the National Cancer Institute, it was discovered that some men who fall prey to the disease, develop the infection very slowly, live significantly longer, whereas others never become infected even after years of engaging in indiscriminate homosexual activity with infected partners. It was determined that these "non-progressors" fail to become seriously ill or infected apparently because they inherited a protective gene (CKR-5) from both of their parents (Centers for Disease Control, 1996). This gene produces proteins (chemokines) which aids in resisting HIV invasion of the immune system (and which protects CD-4 membrane receptors).

Nevertheless, this protective gene is not the result of a genetic mutation, but is secondary to a slight "frame shift" in the activation of the nucleotide sequences in that particular gene. That is, a shorter segment of nucleotide base pairs has been coded and expressed in these individuals and their progeny. Moreover, this particular gene existed prior to the development of the AIDS epidemic, for again, it was inherited and found to exist in the parents of those exposed, and in their parent's parents as well as in other humans. This gene is not a mutant but existed apriori. The gene was inherited. By contrast, mutation is always a pathological process.

Rather, because of a slight frame shift in the coding of a specific sequence of nucleotides, a slightly different product was produced in these "nonprogressors and their parents. Moreover, the potential to produce this product also exists in the genomes of other humans, and their parents, and their parents... such that this gene probably has an ancestry that extends interminably into the long ago.

Again, if different "starter" or "stop" introns are activated this results in different segments or sequence lengths becoming expressed, thereby producing a different protein product. Hence, an almost unlimited variety of products, structures, and even species can be produced by just minute shifts in nucleotide sequence organization and activation, including, for example, the slight frame shift in sequence activation which resulted in the expression of the CRK-5 gene.

Likewise, consider the DNA for producing lymphocytes. As originally proposed by Macfarlane Burnet, and which has since been confirmed, the genetic instructions for producing every possible lymphocyte exists apriori; that is without prior exposure to the antigens which require their production. They exist prior to the diseases which make them necessary.

Hence, once a cell (and its DNA) comes into contact with a specific foreign antigen (including representatives of presumably new diseases), the genetic instructions for creating killer, anti-body making cells are activated and can thus fight and attack diseases that it has never before been exposed to; that is, never been exposed to on Earth. Even when exposed to a supposedly “new” pathogen, the genes already preexist for producing cells which are specifically designed so as to seek out, recognize, and attack this alien, foreign, invader including those representing diseases supposedly never before encountered.

These lymphocytes are not “mutations” but are preprogrammed into the genome and exist as intronic genetic memories which require only the appropriate stimulus in order to be expressed. When activated, these apriori lymphocytes are cloned in great numbers, a process referred to as “clonal selection.”

Again, these genes and these traits did not “evolve.” They were inherited--findings which refute and negate Darwinism.

GENETIC COMMONALTIES

Because genes and traits exist apriori, and as they may be stored as genes within genes (species within species), silent genes and the instructions for creating additional genes, can be passed on to subsequent generations and species. Because the instructions for the creation of additional and specific genes are also precoded, these instructions, but not the actual gene itself, may be passed on; albeit, in some instances as a gene within a gene. As such, two species that diverge from a common ancestor may later generate the same exact gene which the common ancestor (and its direct descendants) does not appear to possess.

Hence, myriad life forms contain the same exact nucleotide sequence segments and “master regulatory genes” which code for the development of the heart, lungs, eyes and brains (D’Souza et al. 1995; Garcia-Fernandex & Holland, 1994; Ruddle, et al. 1994; Strachan & Read, 1996; Watson et al. 1992) —DNA that was independently inherited from common ancestors that had neither heart, lungs, eyes, or brains. Hearts, lungs, etc., were genetically preprogrammed.

These functional, structural, and genetic commonalties include “genes such as Pax6/eyeless which are responsible for the development of eyes in diverse phyla...” and “the expression of distal-less homologues in insect and vertebrate legs, as well as other body growths” (Tautz, 1998). The vertebrate Pax-6 gene cluster is organized and expressed in almost an identical fashion in insects, worms, and mollusks, differing by only 3-6% (Quiring, et al. 1994; Zucker, 1994).

Obviously, identical structures and almost identical genes could not have randomly and independently evolved in three or five different phyla. Rather, they are either a function of gene and plasmid exchange, or they must have been passed on from a common ancestor as silent intronic genes, and genes within genes; genes which were expressed, coded and activated only in response to similar environmental conditions. These traits were preprogrammed to emerge like a chrysalis from a cocoon.

Other inexplicable commonalties include the “independent” evolution in both birds and mammals, of a “double pump” heart and the formation of a interventricular septum which induces a total separation of deoxygenated and oxygenated blood, and endothermy, i.e. the capacity to increase the production of endogenous metabolic energy. Both birds and mammals are endotherms, whereas reptiles and amphibians, the descendants of the common ancestors to birds and mammals, are exotherms who lack a double pump heart or an interventricular septum. And, the common ancestor to birds and mammals died out over 300 million years ago (Kumar & Hedges, 1998).

Likewise, although the common ancestors for birds and bats diverged from a common ancestor who could not fly, both evolved winglike characteristics from forelimbs that originally were not adapted for flight.

Hence, this common ancestor passed on genes which were genetically preprogrammed to give rise to these common features; genes that became activated once environmental conditions and other factors were altered sufficiently: the environment acts on gene selection, and the environment is genetically modified. The only other reasonable explanation is that copies of these genes were released into the environment as plasmids and were subsequently incorporated into the genomes of different highly evolved species (Joseph, 1997, 2000).

Even more remarkable: the human genome and the genome of the higher plants, share homologous DNA-promoters and binding domains (e.g. da and AS-C) including a similar "helix-loop-helix" motif which is involved in cellular division and neuron generation in vertebrates, as well as the production of ovaries and seeds in plants via CHS-A and -J promoters (Joseph, 1998c). These shared plant/flavone human/neural transcription factors, promoters, and genes act to regulate genetic transcription and thus the activation of other genes including those specifying neural vs cellular differentiation and development. However, the common ancestor for mammals and plants diverged anywhere from 1-2 billion years ago; 1 billion years before the evolution, on Earth, of neurons, seeds, or sex organs.

Hence, these traits and these genes were inherited and preprogrammed to emerge in response to changing environmental conditions, and/or were acquired through gene exchange. However, even if due to gene exchange, it can still be concluded that the genes responsible for creating ovaries, neurons, hearts, lungs and so on—or at least the genetic instructions for creating these genes—existed over a billion years ago. Ovaries, neurons, hearts, eyes and lungs did not randomly evolve, they were genetically preprogrammed.

Similarly, plants, fungi, amphibians, non-human mammals, and humans share two of the four HOX clusters of homeobox genes which play a significant role in determining the posterior-anterior axis during embryonic development (D'Souza, et al. 1995; Garcia-Fernandex & Holland, 1994; Harvey, 1996; John & Miklos, 1988; Ruddle, et al. 1994). And yet, the common ancestors for these different species diverged over 2 billion years ago. Indeed, Homeobox genes are exceedingly ancient (John & Miklos, 1988; Radetsky, 1992).

As argued in detail elsewhere (Joseph, 2001), over the course of evolution, innumerable species "evolved" identical characteristics and many of the same identical genes because they inherited from common ancestral stem species, the necessary DNA and the genetic instructions for the creation of these genes and these traits —traits and genes which could not be expressed until the emergence and creation of specific environmental, climatic, and atmospheric conditions (e.g., de Jong & Scharloo, 1976; Dykhuizen & Hart, 1980; Gibson & Hogness, 1996; Polaczyk et al., 1998; Rutherford & Lindquist, 1998; Wade et al., 1997)—conditions which were in fact biologically and genetically engineered. The genetically engineered changing environment promotes gene generation and acts on gene selection—genes which exist prior to their selection, and genes, once activated, that begin to act on the environment, which acts on gene selection, and so on.

Consider, again, the "language gene" which is found, in non-activated form, in non-human mammals. Since only DNA can produce DNA, and as the genetic instructions for creating new genes is contained in DNA, it would appear that these silent genetic instructions and thus the capability for producing all manner of products and species must have existed as intronic genetic potential in the DNA of our ancestors (e.g. Belfort, 1991; Finnegan, 1989; Kuhsel et al. 1990). This would include, of course, the DNA of those creatures who may well have been fashioned by "god" or flung upon the face of our planet billions of years ago; genetic traits that were perhaps coded as silent intronic genetic potential into the double helix of maybe even the very first single celled Adam and Eve.

It is due to the inheritance of dormant, silent intronic genes, and/or their donation and exchange between different organisms (e.g. Mikkelsen et al., 1996; Watson et al., 1992), and their subsequent activation and reorganization, which accounts for the seemingly independent evolution of identical body parts in diverse species (Joseph, 1996, 1997, 2000).

It is because humans and other species have so many of the same exact genes (D'Souza et al. 1995; Garcia-Fernandex & Holland, 1994; Ruddle, et al. 1994; Strachan & Read, 1996; Watson et al. 1992), that they have been able to "evolve" almost identical brains and complex body parts (eyes, wings, fingers and hands), and similar modes of communicating, speaking, behaving, competing or having sex (e.g. Chomsky, 1957, 1972; Ekman, 1993; Eible-EIbesfeldt, 1993; Joseph, 1993, 1996, 2000; Waal, 1989; Wickler, 1973); although they inherited these genes and these behaviors from common ancestors which did not display these traits.

Again, one need only examine the heart, the brain, the skeletal system, and so on, in order to observe what often amounts to little more than slight structural variations between distantly related species whose common ancestors were devoid of similar traits in order to conclude that these traits and the expression of these genes and behaviors were genetically preprogrammed. In other words, evolution is not due to the natural selection of "random mutations," or the coincidence of nature arriving at the same exact solution by chance, but is genetically preprogrammed, and unfolds in accordance with the DNA-instructions inherited from creatures that first emerged on Earth--creatures which were either fashioned by intelligent design, or which came from other planets, or both.

Just as a caterpillar is genetically programmed to undergo metamorphosis and emerge as a moth or butterfly, so too were humans and all manner of creatures (or variations thereof) genetically programmed to emerge, equipped with similar genes and similar traits that were inherited from those life forms which were among the first to take root on this planet.

INTELLIGENT DESIGN

The structure of DNA is such that it contains the genetic instructions, or at least, the genetic capability, for creating all manner of life; some of this information being stored within introns. DNA also contains the instructions for genetically engineering the environment in order to promote DNA dispersal and development. Although Darwin and current neo-Darwinian evolutionary biologists such as Gould insist that variation is random, or that there is absolutely no evidence of "design" (Dawkins, 1987), this view is completely at odds with the facts and with what is known about DNA.

Certainly, natural selection is not "random." Contrary to Darwin's and neoDarwinian theory, there is also nothing random about the organization or expression of DNA (Calladine & Drew, 1992; Strachan & Read, 1996; Watson et al., 1992) which is the source of all variation. There is nothing randomly variable about DNA or its expression of variability, except, perhaps in regard to those "mutations" that result in disease and death. In fact, almost all species maintain vast genetic libraries that have been conserved for hundreds of millions of years (D'Souza et al. 1995; Garcia-Fernandex & Holland, 1994; Miklos & Rubin, 1996; Ruddle, et al. 1994; Strachan & Read, 1996; Tautz, 1998; Watson et al., 1992).

According to Courseaux & Nahon (2001) of the Human Genome Project, "the many processes in genome evolution have shown that de novo generation of building blocks—single genes or gene segments coding for protein domains—seems to be rare." That is, new genes are not produced randomly or by chance. "Instead, genome novelty was mainly built by modification, duplication, and functional changes of the available blocks by processes of gene duplication, exon shuffling, or retrotransposition of genes." The creation of new genes has been under precise regulatory control (Courseaux & Nahon, 2001).

Likewise, Caron et al., (2001) of the Human Genome Project, have concluded that "highly expressed genes" and clusters of interacting genes, "cannot be explained by random variation." These analyses show that regions of highly expressed genes most likely represent a higher order structure in the genome (Caron et al. 2001). In fact, the chromosomes themselves "reveal a higher order organization of the genome" (Caron et al. 2001).

Dr. Gene Myers, chief computer scientist at the Maryland headquarters of Celera Genomics, who was responsible for creating the map of the human genome has stated that the architecture of DNA is so incredibly complex, "It's like it was designed."

That "design" includes the clock-like functioning of those genes which have given rise to "new" species, albeit in a clock-like, highly predictable fashion. For example, as is evident based on ribosomal RNA, over the course of the last 3 billion and more years, genetically programmed species and preprogrammed traits, have come to be expressed in a step-wise fashion, as if programmed by a preset "genetic clock."

All species contain similar types of ribosomal RNA (rRNA). However, there are obvious differences between species in base pair rRNA organization. There is nothing random about these differences, as they in fact differ in a predictable step-wise fashion as we ascend the ancestral tree. For example, those species which have an almost identical nucleotide base pair rRNA organization presumably diverged only recently or have diverged only minimally, e.g., bacteria.

When comparing humans to bacteria, there are significant and predictable differences in the sequences of DNA and RNA nucleotide bases, and it is these same predictable differences which have enabled various investigators to make accurate and verifiable predictions about divergence or the emergence of various species.

Data from a "molecule clock" based on the analysis of eight different genes in seven different classes of invertebrates (e.g. starfish, snails, eels, spiders), for example, predicted the existence of invertebrates which diverged over 1 billion years ago (Wray et al., 1996)—a prediction since verified by Seilacher et al., (1998) who found evidence of complex multi-cellular organisms in sediments over 1 billion years old.

And, it was data derived from a “molecule clock” which predicted that complex fully modern microbes had become established over 3 billion years ago (Woese, 1989, Woese et al., 1990)—a prediction that has now been repeatedly verified (Hoffman et al., 1999; Mojzsis, et al., 1996; Schopf, 1993, 1999).

Likewise, genetic data from a “molecular clock,” that is, from the genes of more than 200 modern animal species, also corresponds with fossil findings indicating that the ancestors to birds and mammals diverged over 310 million years ago, and that the ancestors of modern mammals, including elephants, horses and cows, emerged 20 million to 45 million years before the demise of the dinosaurs (Kumar & Hedges, 1998).

In fact, this same step-wise sequential progression is evident from an examination of the approximately 100 amino acids that comprise an exceedingly important protein which participates in oxygen utilization: cytochrome c. Cytochrome c. is found in all animals, and consists of amino acids. However, cytochrome c. becomes increasingly different, albeit in a step-wise, clock-like fashion, as we descend the ancestral tree. Of the approximately 100 amino acids that comprise human cytochrome c 99 are identical to those of other primates, such as the rhesus monkey, 89 are shared with other mammals, 86 with reptiles, 82 with amphibians, 79 with fish, 69 with the silkworm, 57 with wheat, and 55 are identical to those of yeast (Denton, 1986; de Duve, 1995).

This progression is evident not only based on DNA, but the fossil record. Complex life has evolved in an organized and purposeful, step-wise manner, leading from simple cell to all manner of creatures, including modern woman and man.

THE TICKING OF THE GENETIC CLOCK

The progressive metamorphosis of increasingly intelligent and complex life on this planet, culminating in the emergence of modern woman and man, appears to have unfolded in a genetically predetermined, “molecular clockwise” fashion. That “evolution” is regulated in accordance with the “ticking” of a genetic “clock” is evident from an examination and comparison of various genes and ribosomal RNA belonging to diverse species (e.g., Denton, 1998; Kumar & Hedges, 1998; Lewin, 1988; Wray et al., 1996; Woese et al., 1990). Because this genetic “clock” appears to have been “ticking” at the same rate, simultaneously, among all branches of the tree of life (Denton, 1998), and as this “clock” on Earth, began to “tick” almost 4 billion years ago, it thus appears that the continued “ticking” of this same “genetic clock” has determined the successive emergence of increasingly intelligent and complex species (e.g., Kumar & Hedges, 1998), culminating in woman and man.

Just as the genome of the caterpillar is programmed to produce a butterfly, or the DNA of a fertilized ovum gives rise to an embryo then a fetus... neonate... child... juvenile... adult, the metamorphosis and progression which characterizes life on this planet appears to have been preprogrammed into the DNA of some of the first Earthlings. It is this genetic predetermination which also explains why although the Earth has been struck five times by life-destroying meteors, that certain species immediately recovered, and why no new phyla have emerged since the Cambrian Explosion.

As summed up by Denton (1998) “the rate of change in many genes is regulated by a clock which seems to tick simultaneously in all branches of the tree of life.” Indeed, this was evident over a decade ago, for according to Lewin (1988), “the notion of and evidence for a molecular clock... has become... pervasive.”

The expression of this genetic clock requires that the climate, atmosphere, oceans, and the environment, be genetically engineered so as to prepare the planet for those yet to be born. Thus, the environment is also modified in a genetically preprogrammed clock-wise fashion (Joseph, 1997, 2000). Indeed, the environment acts on gene selection (de Jong & Scharloo, 1976; Dykhuizen & Hart, 1980; Gibson & Hogness, 1996; Polaczyk et al., 1998; Rutherford & Lindquist, 1998; Wade et al., 1997), which acts on the environment, which acts on gene selection, thereby creating a complex feedback mechanism which gives rise to diverse products and species. And these genetically engineered environmental changes have acted on the DNA of each successive generation of species, our ancestors, whose DNA gave birth to our own.

There are in fact, genes (e.g., tim, mTim, hTIM) and proteins which perform specific “clock-like” timing functions and which interact to form regulatory feedback loops (Clayton et al., 2001). Moreover, these “genetic clocks” have been shown to be directly in tune with changing environmental and climatic conditions.

Specifically, the clock-like regulatory genes and proteins so far identified are composed of interacting positive and negative transcriptional translational feedback loops, the core components of which include two basic helix-loop-helix (bHLH)/PAS-containing transcription factors, CLOCK and BMAL1 which interact and pair up via their PAS (protein) domains (PER, ARNT and SIM. These transcription factors perform clock-like circadian operations in fungi, insects and mammals.

CLOCK and BMAL1 drive the rhythmic transcription of three Period genes (mPer1-mPer3) and two Cryptochrome genes (mCry1 and mCry2) which interact to inhibit transcription, forming a negative feedback loop. According to Clayton et al., (2001) “at the same time, mPER2 contributes to the transcription of Bmal1, which is rhythmically expressed with a peak phase opposite to that of mPer/mCry, forming a positive feedback loop. The push-pull action of the positive and negative feedback loops perpetuates the self-sustaining nature of the circadian clock” which in turn is sensitive to seasonal and climatic fluctuations.

These canonical clock genes and their homologues have been identified in Drosophila (tim) mice (mTim) and humans (hTIM), as well as in the worm, Caenorhabditis elegans (tim-1). According to Clayton et al., (2001) these findings suggest that the “closely related worm tim-1, mouse/human Tim and fly tim-2 genes are descendants of an ancestral timeless gene that duplicated in the arthropod lineage after the split with nematodes and vertebrates.”

However, these genes exist prior to their selection and are expressed in a highly regulated, predictable fashion, which refutes darwinsim. Evidence based on DNA, genetics, and the fossil record refute Darwinism. The ticking of the genetic clock refutes Darwinism.

Genes and the traits they code for, exist prior to their expression, and many genes have been expressed in a predictable, clock-like fashion, thus giving rise, in a step-wise sequence, to increasingly complex and intelligent species.

Because the emergence of H. sapiens sapiens, and all manner of species appears to have been genetically preprogrammed to emerge in a predictable, step-wise fashion, this phenomenon has been referred to as “evolutionary metamorphosis” (Joseph, 1996, 1997, 2000a). However, rather than a 9-month gestation period, or the single seasonal metamorphosis which characterizes the transition from caterpillar to butterfly, humans are an end product, or perhaps a midway product of a process which takes several billion years to unfold; albeit in accordance and in parallel with suitable changes in the genetically engineered environment.

Thus, metamorphosis is not a one-step progression (caterpillar-butterfly) but a leaping, branching, multistep progression involving numerous successive species, many of which are genetically preprogrammed to give rise to the next in a “molecular clock-like” fashion. The ticking of this genetic clock, however, also requires that the environment be genetically engineered in preparation for the generation of subsequent species.

DNA-SUPRA ORGANISMS

All forms of life consist of packages of DNA which have manufactured an organism in order to interact with the environment. A fat hairy spider crawling along the ceiling is the product of DNA engineering, and each and every spider-cell contains a packet of DNA which created the cell and which contributed to the creation of the spider. The “spider” is merely a vehicle through which the DNA navigates its way around the world. The same is true of fish, frogs, reptiles, and so on. These are manifestations of DNA activity and every organism functions in accordance with specific DNA-instructions.

DNA strives for expression and dispersal. According to the theory of evolutionary metamorphosis, the DNA of diverse species are also interactional and together may be viewed as constituting a supra-DNA-organism which acts on the environment in order to promote DNA activation and dispersal. That is, DNA acts to genetically engineer the environment which in turn acts on gene selection which acts on the environment which leads to the expression and dispersal of additional DNA. Thus, just as DNA contains the instructions for creating and nourishing an embryo in parallel with the genetic alteration of the womb, DNA also contains the instructions for altering itself and the external environment so as to promote not just diversity, but the emergence of increasingly complex and intelligence animals, including the likes of woman and man.

Recognizing the role played by diverse species-and thus their DNA in the biological construction of the atmosphere, climate, and even the contents of the oceans, is integral to understanding evolutionary metamorphosis, including extinction, and the failure of some species to “evolve.” Just as body parts or dead cells may be sloughed off or absorbed during embryonic, fetal, and neonatal development, over the course of "evolution" some species have been sloughed off and became extinct once they were no longer needed. Just as some body parts remain relatively simple, e.g. the cells of the skin versus the nerve cells of the brain, over the course of "evolution" some species have remained relatively simple and others have become more complex—all are integral to the survival of the supra-DNA-organism.

Again, the DNA or diverse species can be seen as an interactional supra-DNA organism which acts on the environment. Once certain organisms have accomplished their genetic mission, they become extinct, whereas other cells, including simple organisms continue to thrive as their output is essential to maintaining and promoting life—that is, the life of the supra-DNA-organism. Coupled with unforeseen environmental catastrophes, the need to modify the environment in order to promote DNA dispersal and development, and the fact that the environment acts on gene selection and activation (e.g., de Jong & Scharloo, 1976; Dykhuizen & Hart, 1980; Gibson & Hogness, 1996; Polaczyk et al., 1998; Rutherford & Lindquist, 1998; Wade et al., 1997) explains the periodic lack of progress in complexity over eons of time, and then the sudden surges in progress and complexity, during different epochs of the Earth's history.

THE ENVIRONMENT REQUIRES SOME CREATURES TO REMAIN SIMPLE IN ORGANIZATION

It is necessary that some species remain relatively simple and basically identical to their ancestors from billions of years ago. There is a genetic need to maintain certain environmental, climatic and atmospheric conditions (such as oxygen levels). In consequence, certain species never progress. In fact, there are specific repressor proteins and a variety of genetic mechanisms which act to prevent genetic change, even in response to changing environmental conditions. For example, regulator proteins referred to as "chaperones have been found in all organisms studied and protect against" genetic change or activation such as in response to changing environmental and climatic conditions and other stresses, such as alterations in oxygen levels (Cossins, 1998).

For example, a genetically manufactured protein, "Hsp90 is one of the more abundant chaperones. At normal temperatures it binds to a specific set of proteins, most of which regulate cellular proliferation and embryonic development. These signaling proteins form complex webs of molecular switches that allows signals both within and between cells to be transduced into responses... and act against genetic variation" and prevent the expression of silent characteristics (Cossins, 1998, pp. 309-310). For example, these proteins may prevent DNA expression by acting as a buffer between these silent genes and nucleotides and the environment, so that they are not expressed except in accordance with specific genetic instructions.

Again, consider Hsp90. Hsp90 targets multiple signal transducers which control and act as "molecular switches" which in turn control gene expression. Hsp90 "normally suppresses the expression of genetic variation affecting many developmental pathways" (Rutherford & Lindquist, 1998). However, Hsp90, also reacts to environmental stress including diet and fluctuations in temperature (Rutherford & Lindquist, 1998). As demonstrated by Rutherford and Lindquist (1998, p. 341) Hsp90 acts as an "explicit molecular mechanism that assists the process of evolutionary change in response to the environment" and it accomplishes this through the "conditional release of stores of hidden morphological variation.... perhaps allowing for the rapid morphological radiations that are found in the fossil record."

However, in order for these repressor proteins and other regulating genetic mechanisms to be switched off or on, requires contact and exposure to specific environmental agents.

Initially, the new Earth was devoid and lacking these environmental agents, such as free oxygen, calcium, and so on. Hence, in order for certain genes and gene sequences to be activated, required that these products be liberated and/or manufactured. Hence, some species immediately began secreting oxygen as a waste product, which in turn acted on gene selection.

It is because of the genetic need to create a precursor product in massive amounts (such as calcium), which explains why some species emerge, thrive, alter the environment, and then become extinct. Some species emerge simply to produce a specific product and are then jettisoned. Just as the placenta is a nurturing biological construction that is jettisoned with the birth of the baby, there have been periods when much of the Earth's biomass served only to produce and secrete products that were fundamental for the metamorphosis of future, more complex species, such as calcium to build bones. Once their genetic mission was accomplished, many of these creatures were jettisoned and became extinct. Consider, again, the calcium carbonate secreting Ediacaran fauna.

As oxygen levels increased in the atmosphere and in the sea, and as the planet again began to warm, oxygen breathing multicellular eukaryotes emerged (e.g. Brocks et al., 1999). By 2.3 billion years ago the Earth's land masses were covered with thick bacterial mats and other organisms. Many of these organisms secreted a variety of organic acids which formed laterites (iron rich deposits) by leaching iron from the upper layers of rock and soil. However, as pointed out by Dr. Ohmoto, "in order for laterites to form, there must be organic material and atmospheric oxygen;" substances secreted by and the residue of even earlier life forms.

By 1.6 billion years B.P., the Earth's climate and environment had been dramatically altered and animals began evolving into different species (e.g., Hedges & Kumar, 1999) who in turn began to prepare the world for subsequent generations. Then around 600 million years ago the calcium carbonate secreting Ediacaran emerged in every ocean and sea, releasing materials into the environment which enabled shellfish and bony complex oxygen-breathing creatures to "evolve" and undergo metamorphosis.

However, the Ediacaran fauna and subsequent generations would not have been able to thrive if not for the thick layers of bacteria which had been building up for over 2 billion years —much of which then served to nourish the Ediacaran fauna and those who emerged during the early phases of the Cambrian Explosion—just as thick mats of blood cells sustain the ovum within the womb. One species served as the nutrients for a later appearing species who prepared the world for the next generation of increasingly complex organisms.

Figure 39. *Ediacaran fossils from the late pre-Cambrian period. A Tribachidium (above), sea pen (right) annelid worm (left).*

THE CAMBRIAN EXPLOSION

THE METAMORPHOSIS OF THE EDIACARAN FAUNA

Ediacaran fossils have been discovered throughout the world, and date from 580 billion to 560 billion years B.P. (though some authors have assigned them a date of 600 million years B.P.) These were soft bodied, leaf- and disk-shaped, plant-like creatures, consisting of only 11 or fewer cell types (compared with over 200 cell types for mammals). They ranged in size from over 3.5 feet to less than 1/2 inch (Glaessner, et al. 1988). They also rather suddenly became extinct.

The emergence of Ediacaran fauna was not just a genetic experiment gone awry, as some scientists have speculated, for these creatures and their waste products altered the planet so as to make the next stage of metamorphosis possible. Because they secreted calcium carbonate, from which shells and bones are constructed, the Ediacaran fauna made possible the metamorphosis of shell fish and the skeletal system. Once their genetic mission was accomplished, the Ediacarans disappeared from the scene and there followed an explosion of shelly and bony life in every ocean, lake, river and stream—aptly referred to as the Cambrian Explosion as it took place during the Cambrian era.

THE CAMBRIAN EXPLOSION

"If it could be demonstrated that any complex organ existed which could not possibly have been formed by numerous successive, slight modifications, my theory would absolutely break down." -Darwin, 1857.

With no history of derivative ancestral forms, all manner of complex life suddenly emerged with gills, intestines, joints, brains, and modern eyes equipped with retinas and fully modern optic lenses. These included organisms with a hard tubelike outer-skeleton consisting of calcium carbonate, and all manner of "small shelly fish" (Anabrites, Protohertzina), as well as sponges, jelly fish, mollusks, brachiopods, and the first arthropods (e.g. trilobites) which immediately sprouted legs and primitive brains. In fact, every phylum in existence today emerged during the Cambrian Explosion, including some phyla which emerged then became extinct.

The survivors included the phylum Chordata; i.e. tunicates and the first jawless fish who possessed a notochord and simplified brain that consisted of a brainstem and limbic forebrain.

Hence, during the Cambrian epoch there was also a cerebral and thus a cognitive explosion as the first true brains were established; brains which would continue to “grow” and continue to unthe evolution of all Earthly life trace their ancestry to those creatures who were among the first to emerge on this planet. However, Darwin and neo-Darwinians champion the "organic soup" and believe that life and its DNA emerged from non-life following the random mixing of organic molecules. And yet, there was little or no free oxygen, which is necessary for the construction of DNA. The basic elements for DNA construction did not exist on Earth.

However, let us pretend that life did emerge from an organic soup. If that is the case, then, given the lack of Earthly ingredients, that soup must have first been stirred on another planet.

Cosmic collisions are commonplace, not only between stars, but entire galaxies. And, if life first arose on another planet, it can be assumed that some of those creatures were cast into space, encapsulated in debris, and not only survived their long journeys, but fell upon innumerable planets, only to begin genetically engineering their new worlds if at all possible. Hence, although life may ultimately trace its roots to a single cell that emerged from an organic soup, the theory of evolutionary metamorphosis views life as having arisen, on Earth, from numerous "seeds" which, in turn, may ultimately trace their origin to a single astrobiological source.

If there was a "single seed" from which all life has descended, this "seed" first appeared tens of billions if not hundreds of billions of years ago, on another planet thus giving rise to identical seeds; that

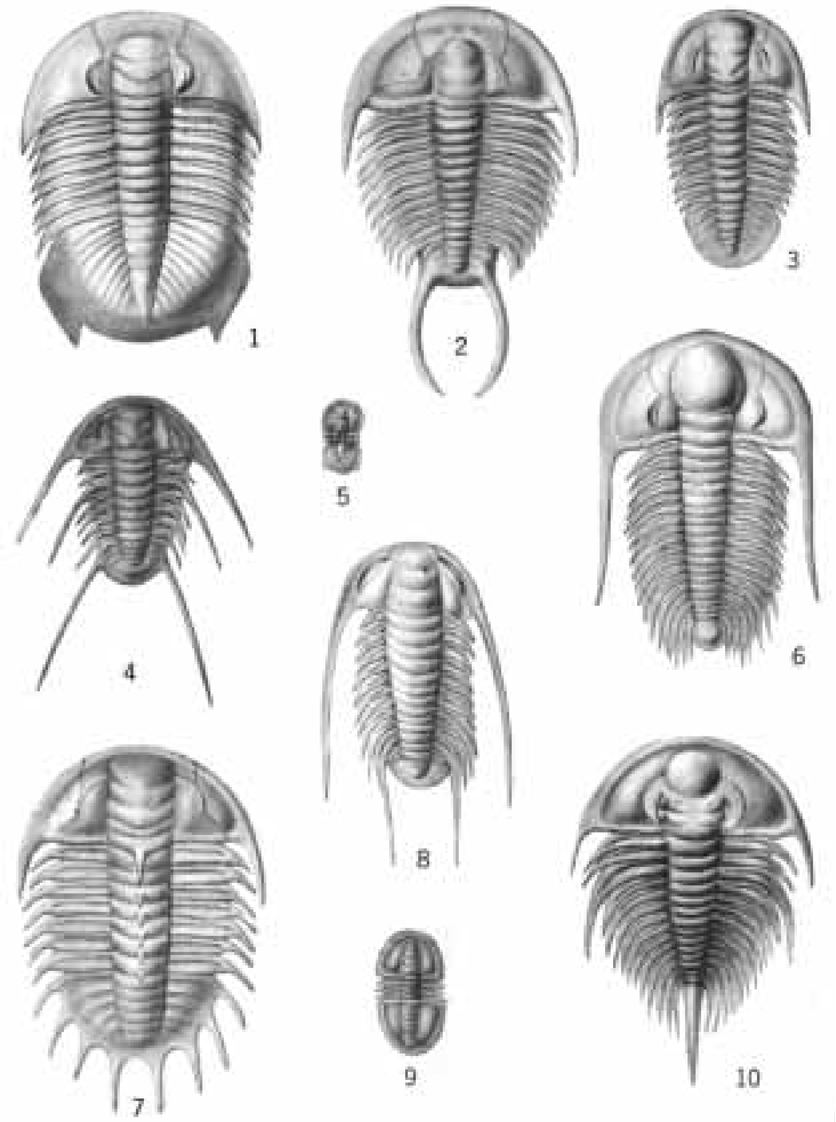


Figure 40. *Cambrian Trilobites. Drawn by L.S. Douglas. Reprinted from Dunbar, 1960. Historical Geology, Wiley, New York.*

is creatures with identical or similar DNA and DNA-based genetic instructions.

Because of this genetic commonalty, rather than a single seed and a single Earthly-trunk with innumerable branches, the theory of evolutionary metamorphosis posits a forest of trees with innumerable branches, each of which has the genetic potential to bear identical fruit. Only the theory of evolutionary metamorphosis and this forest of basically identical "genetic trees" can explain why different species of humanity, such as Homo erectus, Neanderthals, and Cro-Magnons shared the planet during overlapping time periods, and why over half a dozen species of Australopithecus and a variety of Homo Habilis appeared almost simultaneously in different parts of the world.

Since the genetic instructions for creating all manner of life is also DNA based, then it would appear that these genetic instructions and the genetic potential to create all manner of life, are also astrobiological in origin and/or a product of intelligent design. It is these ancestral astrobiological origins, the antiquity of life, and the genetic memories and instructions which they have passed down, which explains the progressive emergence of increasingly complex and intelligent life on Earth—an unfolding which has occurred according to specific DNA-based instructions and genetic memories—just as the fertilized single cell that gives rise to an embryo is genetically predetermined to create a fetus, then a neonate, child...adult.

Just as an embryo is not a random construction, all subsequent species to emerge on Earth have been genetically preprogrammed, the expression and coding of which are associated with intronic genes and intronic gene sequence activation, exon shuffling, "frame shifts," intron and plasmid insertion and exchange, and a host of other genetic variables which are yet to be identified.

Only the purposeful, controlled, and highly regulated expression of genetically pre-coded instructions can account for the obvious evidence of a step-wise, sometimes leaping progression in increasing intelligence and complexity which has characterized the metamorphosis of a rather narrow range of life on this planet. Indeed, only precise genetic instructions can account for the fact that basically similar species have emerged multi-regionally across distant lands, from distinct pockets of ancestral species which also emerged multi-regionally, and this includes the multi-regional metamorphosis of a wide variety of wide ranging species of Australopithecus, H. habilis, H. erectus, and Neanderthals. The planet was genetically seeded to grow all manner of species, including humans and all manner of variations thereof.

PROGRESS AND MULTI-REGIONAL METAMORPHOSIS

Every phylum in existence today emerged during the Cambrian Explosion, including the phylum Chordata. The first members of the phylum chordata possessed a simplified brain that consisted of a brainstem—which controls rhythmic and reflexive motor behaviors— and a limbic forebrain which mediates all aspects of emotional and motivational functioning including memory.

The evolution of the brain began with the metamorphosis of the first nerve cells; i.e. specialized sensory-motor cells capable of inducing movement in reaction to sensation such as light vs shadow. These cells were loosely organized along the outer membrane/skin and most probably did not intercommunicate except indirectly following the release of various chemical transmitters.

As the climate and environment began to change, and as the environment acts on gene selection, over the course of evolution a collection of like-minded cells began to directly interact, forming a nerve net, and then to congregate in the anterior head region, giving rise to a primitive ganglion brain. During the Cambrian Explosion, the ganglionic brain became a primitive brain, which in some species including cartilaginous fish (e.g. sharks) and later, in "bony fish" (Osteichthyes), consisted of a brainstem (concerned with reflexive sensory motor functions, visual and "auditory" perception, the sleep cycle) and an olfactory bulb-equipped forebrain which analyzed environmental chemical input and also induced gross motor behavior in response to motivationally significant stimuli.

Tunicates were among the first chordates (subphylum Urochordata) to emerge beneath the sea, some 500 million years ago, and were soon followed by the first jawless fish (e.g. Astraspis, Arandaspis), who in turn gave rise to cartilaginous (Cyclostomes) "bony" fish. Over the ensuing 100 million years, and within the vast oceans and seas, various species of "fish," e.g. "bony fishes," "ray fins," developed additional brain matter, and some species of "bony fish" later developed lungs and limbs; i.e. lobed finned fish.

Armored and jawless fish, sharks, and lobed finned fish were all in possession of the prototypical brain, the basic framework of which would be inherited by all subsequent species, including amphibians, reptiles, and even woman and man (Nieuwenhuys & Meek, 1990b; Stephan, 1983).

The brains and bodies of these animals, however, did not become just more variable—as demanded by Darwinian theory—but increasingly complex and hierarchically organized and sophisticated. For example, unlike other fish which are externally fertilized and which lay eggs in the open water (eggs which are then greedily gobbled by yet other denizens of the sea), the lobe finned fish were fertilized inside the body and could bear the young alive.

By 370 million years B.P., a wide range of lobed finned fish began to appear in almost every ocean and sea. These included Dipnoans, Sarcopterygia, and Coelacanths, who began to venture forth upon the Earth where they then began to breed.

Numerous species of lobed-fins lived mainly in rivers and freshwater seas and could venture forth and live on land as they had evolved internal air sacs which were embedded within their fins. Likewise, some of the first land-based plants also evolved air sacs. These air sacs could pass oxygen directly into the blood stream. This “breathing” ability enabled the lobed fins not only to venture forth, but to hole up in caked mud during the dry seasons. As the environment acts on gene selection, it is the lobed finned fish who presumably gave rise to the next stage of complex animal life.

Lobe finned fish were (and are) in many respects a transitional prototype for all land based creatures, as their “fleshy-lobed” fins were supported by an internal skeleton consisting of a humerus, femur, radius, ulna, tibia and fibula (Caroll, 1988; Jerison, 1973; Nieuwenhuys & Meek, 1990b; Romer, 1970). The lobe finned Coelacanths, in fact possessed jointed bones shaped somewhat like arms and legs. It is from these lobed fins that legs would eventually “evolve,” and it is these lobed fins coupled with the air sacks (primitive lungs), that enabled these creatures to periodically leave the water so as to venture along river banks, oceans fronts, and onto dry soil, some 400 to 350 million years ago (Caroll, 1988; Colbert, 1980; Jarvik, 1980; Jerison, 1973; Romer, 1970).

Presumably it is from one or any number of the various species of lung/air sack equipped lobe

Figure 41. *Stages in the evolution of the nerve net in three flatworms (Acoela, Polycladida, Rhabdoceoela). A. Epidermal nervous system and nerve cells. B. Nerve net with bilobed ganglia. C. Cephalization of brain with loss of nerve net. (redrawn from Hyman, 1951). (Below) the brain of an armored fish, which became extinct 325 millions years ago.*

Figure 42. *Rhythmic swimming motions of (A) three fish, and (B) three salamanders which utilize the same movement patterns which are in sequence with the trunkal muscle activity. The limbs are extensions of the axial muscles.*

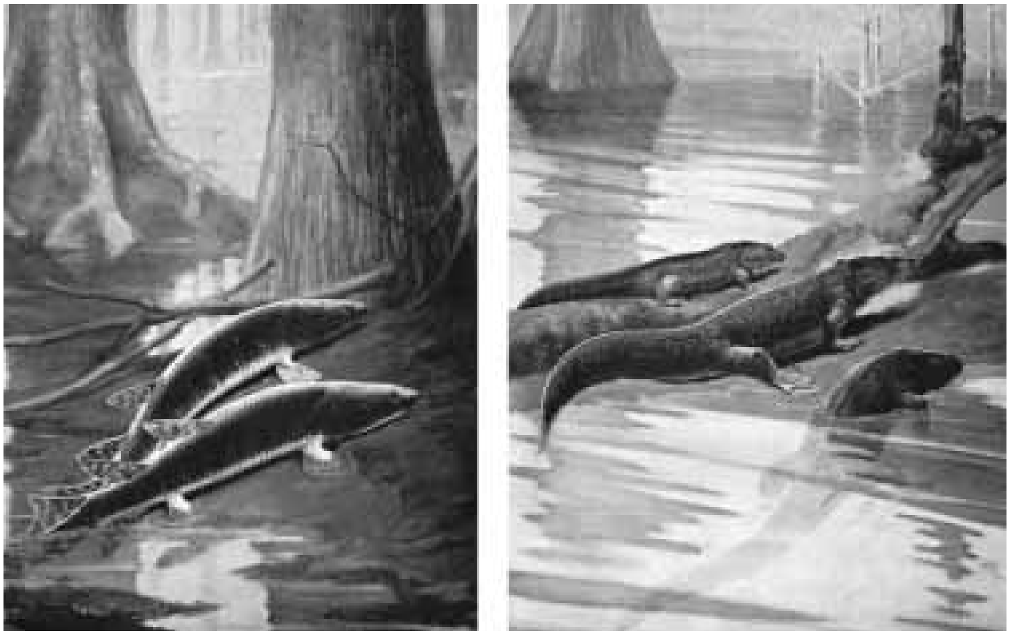


Figure 43. *Stages in the transition from lung fish into Labyrhinthodants. American Museum of Natural History.*

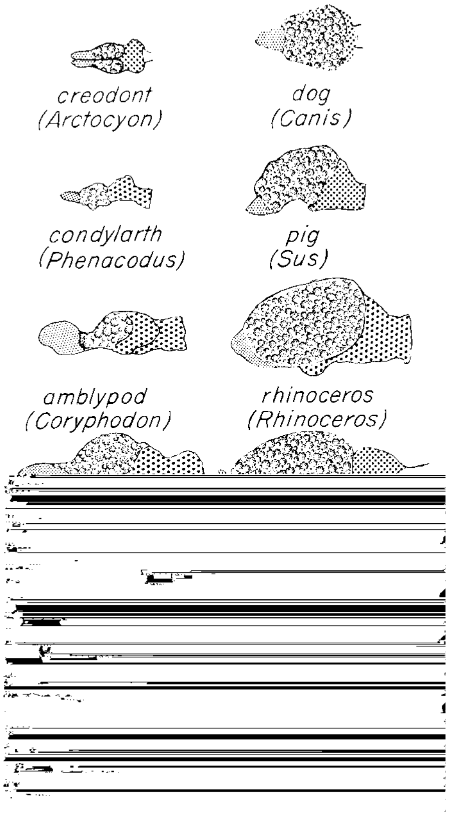


Figure 44. *Skeletal and cranial evolution leading from 1) lobed finned fish, 2) early amphibian, 3) primitive reptile, 4) repto-mammal, 5) therapsid, 6) placental mammal. Reprinted from Howells, 1997. Getting Here. Compass Press,*

Figure 45*. The brains of repto-mammals/ therapsids (left) paired with the brains of modern mammals of similar size. Reprinted from Dunbar, 1960. Historical Geology, Wiley, New York.*

finned fish, that all terrestrial vertebrates evolved (Romer, 1970), beginning, perhaps with primitive oxygen breathing amphibians, such as the seven fingered Ichthyostega whose forelimbs were hitched to the skull. This odd physical organization, however, enabled these and like-minded animals not only to walk but to perceive and hear vibration transmitted through their feet.

By 360 million years ago a variety of five-toed amphibians, some up to 15 feet long were swarming over the planet. And, for a brief time amphibians “ruled” the world as they were more social, and more intelligent than the more solitary insects who, along with plants, had dominated the planet. Insects rapidly diminished in size.

It was not the lobed finned lung fish, however, but their descendants that gave rise to amphibians. These amphibian-like creatures looked something like a cross between a fish and a big salamander, with flat heads and long tails, and short stocky feet like a turtle. These include the eusthenopterons, as well as the Ichthyostegas which used four feet in order to move about (Colbert, 1980; Jarvik, 1980; Jerison, 1973; Romer, 1970).

Hence, by 350 million years ago the lobe finned fish presumably evolved into a fish with legs, the eusthenopteron and ichthyostegas, which in turn evolved into amphibians, some of which grew up to 15 feet length and who sported an enlarged olfactory lobe which dominated the forebrain.

REPTILIAN METAMORPHOSIS

Amphibian dominion was sooner overturned by reptiles who were superiorly endowed physi-

Figure 46. *The brain of a fish, frog, and bird.*

Figure 47. *Comparison of neocortical evolution and the evolution of the lobes of the brain, across five species. Abbreviations: OB-olfactory bulb, A-primary auditory cortex, F-frontal neocortex, P-parietal neocortex, Pir-piriform lobe, TO-tuberculum olfactorium,V-visual cortex. From Gloor, 1997, The Temporal Lobe and Limbic System. Oxford University Press. New York. Contrary to Darwinism, the brain has not become more variable, but more complex.*

cally and neurologically as their forebrain consisted of a greatly expanded limbic system and included distinctive limbic system structures such as the amygdala, hippocampus, and striatum which conferred tremendous intellectual powers and social-emotional signaling and associational capabilities upon these animals. Amphibians, therefore, did not just become more variable, they gave rise to a unique and superior species.

Unlike their amphibious cousins, the reptiles were better engineered for living on dry land, having evolved scaly waterproofed skins, hip and shoulder girdles, as well as a "new" method of giving birth. In contrast to amphibians who must return to the water to breed and produce young (tadpoles which undergo metamorphosis in order to become an adult), the reptiles could breed and lay amniote/cleidoic (shell covered) eggs on land from which emerged miniature adults.

The brain also increased in size and became more complex. With the evolution of reptiles the limbic forebrain mushroomed in size and gained hierarchical control over the motor functions of the brainstem (Herrick, 1948; Nieuwenhuys, 1967). The limbic forebrain could now feel emotions and directly control all aspects of body movement. In part, the increase in the size of the forebrain was induced by the increased emotional and motor demands of living on dry land, such that the motor aspects of the forebrain began to increasingly differentiate and to evolve in response to and in order to meet these new motoric needs; made possible by the limbic-striatum.

Yet another factor in the encephalization of the brain was that animals were now living in a perfumed world of smell, and these odors provided an incredible wealth of information that the limbic forebrain became specialized to analyze. As the environment acts on gene selection, olfactory input to the limbic system forced this structure to also evolve and differentiate and to become increasingly capable of analyzing a wide range of motivational stimuli. The brain did not become more variable, as demanded by Darwin's theory, but was growing larger and increasingly complex.

THERAPSID & REPTO-MAMMAL METAMORPHOSIS

Over the ensuing 25 million years, the descendants of reptiles diverged, one branch of which giving rise to the intellectually, neurologically, and physically advanced repto-mammals, around 250 million years B.P., who in turn gave rise to therapsids who emerged multi-regionally (Bakke, 1971; Brink, 1956; Crompton & Jenkins, 1973; Crompton, et al. 1979; Duvall, 1990; Maglio, 1978; Romer, 1966; Quiroga, 1979). Yet another branch gave rise to dinosaurs, around 225 million years B.P., who also emerged multi-regionally and appeared worldwide—presumably descending multi-regionally from ancestors who also emerged multi-regionally from multiple ancestral species.

Hence, primordial reptiles split into three lineages, the anapsids which gave rise to modern turtles, synapsids which gave rise to repto-mammals and then therapsids, and diapsids which gave rise to dinosaurs, and birds, and present day reptiles (Caroll, 1988).

Repto-mammals emerged some 250 million years ago, and these creatures briefly ruled the Earth. Although the initial repto-mammals were sprawlers, over time they became physically more refined, and eventually gave rise to therapsids, 200 million years B.P..

Therapsids were exceedingly technologically advanced, physically and neurologically. For example, in contrast to reptiles and amphibians, the elbows were now directed backward and the knees forward which greatly improved their ability to run and manipulate their limbs. In addition, the legs were now located beneath rather than alongside the body which enabled them to run long distances without compressing the chest and lung which allowed them to simultaneously breath while chasing prey. Reptiles must stop in order to breath since their legs, situated alongside their body and chest cavity, constrict the expansion of the lungs as they run.

The therapsids also developed a secondary bony palate which enabled them to chew food and to simultaneously breathe without danger of choking to death. Reptiles must cease to breathe in order to swallow large chunks of their food.

Another advantage occurred in regard to thermoregulation. Therapsids became warm blooded. Reptiles must sun themselves or run around and rely on behavioral thermoregulation. For example, if a reptile fails to move from a cold to a warm location (or vice versa) their body temperature soon approaches that of the external environment. They must move about in order to gain heat by sunning themselves, or cool off by sitting in the shade.

By contrast, the limbic system of the repto-mammals and then the therapsids evolved a means of regulating body temperature internally. Whereas lizards, frogs, fish, etc., have only scales, the therapsids also evolved a coat of fur, as well as sweat glands that release excessive internal heat. Moreover, with the metamorphosis of the repto-mammal therapsids, the ear underwent important modifications and the limbic forebrain began to expand with new tissues emerging and growing additional layers. Because the inner ear and additional brain tissue had emerged, vocalized communication assumed a new importance.

The increased importance of vocalization was made possible by the expanded development of the 4-5 layered cingulate gyrus; a structure that caps the 3-layered allocortical limbic system, and which is implicated in maternal offspring behavior and vocal communication (Joseph, 1999b, 2000a).

With the development of the cingulate gyrus, the therapsid's ability to communicate expanded beyond simple gestures, posturing, or olfactory-pheromonal signaling, and now included the capacity to produce a variety of complex meaningful sounds, such as between mother and infant, including, perhaps the separation cry. The five-layered cingulate gyrus provided the brain power to engage in prolonged maternal care, which in turn promoted the development of language, love, and the family (Joseph, 1993; MacLean, 1990).

Nevertheless, although exceedingly advanced, the repto-mammals were struck down and nearly became extinct following a great cataclysm when the Earth was twice struck by massive meteorites, around 250 million and 225 million years B.P. (Rampino & Haggerty, 1994). These catastrophes were followed by a "giant volcanic eruption"—all of which acted to split apart the already fracture land masses and to blot out the sun with dust, thus dropping temperatures and killing off over 50% of all marine life and all larger size terrestrial animals. These catastrophes killed off most but not all of the larger sized repto-mammals, and gave the much smaller dinosaurs a competitive advantage. The remaining repto-mammals were displaced by these "terrible lizards" who then began to evolve multi-regionally on every continent.

Those dinosaurs who may have evolved multi-regionally included the 36 foot-long Suchomimus tenernsis, who had teeth shaped like steak knives, and whose fossil remains have been discovered in Egypt, Brazil, England, and central Niger in Africa. Likewise, although Tyrannosaurus rex, the most fearsome meat eater in history, is associated with the Americas, similar species, including almost all the dinosaurs discovered in Utah, also emerged in Asia (Cifelli et al., 1997). Although they may have migrated, and despite being (for the most part) cold blooded and swam the oceans from Asia or crossed over the frozen tundra of the Arctic in order to appear in the Americas it could also be argued that these cold blooded raptors evolved multi-regionally (that is from multiple ancestral "seeds").

Following every mass extinction, although the majority of species are typically wiped out, others manage to recover. As the environment acts on gene selection, and as the remaining repto-mammals were relegated to a nighttime environment, their brain was forced to further evolve and to grow. They adapted to lurking about at night and hiding beneath deep foliage during the day—a life style which induced further expansions in the olfactory dominated forebrain which became increasingly adapted to process olfactory and auditory cues.

THE ENVIRONMENT AND THERAPSID MULTI-REGIONAL METAMORPHOSIS

By 200 to 150 million years B.P., the repto-mammals had become therapsids (Caroll, 1988). In addition to the other changes already mentioned, the therapsid brain (the dorsal pallium) was now capped with a five layered (mesocortical) cingulate gyrus—the evolution of which ushered in a revolution in vocal-emotional communication and infant-maternal behavior (Joseph, 1993; MacLean, 1990).

By 150 to 85 million years ago, various suborders of therapsids had given rise to the intellectually and neurologically superior mammals, who in addition to a five layered cingulate gyrus, had evolved a six layered neocortex. Yet, because the environment acts on gene selection, those therapsids living in sheltered pockets of primeval swamp and jungle, remained therapsids—just as in some pockets of the world, Homo erectus remained Homo erectus, and Neanderthals remained Neanderthals, although Cro-Magnon were beginning to swarm over the planet.

Because the environment acts on gene selection, different environmental and climatic conditions can produce not only diverse subspecies, but enhance or slow the rate of species metamorphosis depending on where they dwell. Metamorphosis occurs at different rates under different geological and climatic conditions, and thus at different times periods for the same species, and often not at all. An unvarying environment, coupled with related genetic factors hinders the development of the next stage of metamorphosis.

Hence, in a few isolated swamps and jungles of the world which have undergone little change over the course of the last several hundred million years, huge insects, amphibians and reptiles abound and jungle dwelling mammals still lay eggs -much like repto-mammals.

Egg laying "mammals" (monotremes), tend to be found only in a few isolated regions of the world such as in the primeval swamps and jungles of New Zealand. These egg layers include the anteaters and the even more primitive duck billed platypus. Monotremes are in fact quite primitive, and appear in the fossil record as far back as the earliest periods of the Pleistocene.

By contrast, throughout much of the rest of the world, species of amphibians and reptiles have diminished in number and diversity, and monotremes have disappeared, whereas mammals have climbed the next step of the evolutionary ladder. The egg and the embryo are now nourished inside the womb (placentals).

Egg laying mammals, the monotremes, therefore, are more like therapsids and repto-mammals than true mammals (placentals). Like repto-mammals, monotremes not only lay eggs, but are without breasts. Instead, they suckle their young via modified sweat glands which secrete milk. Over the course of evolutionary metamorphosis these sweat glands eventually became the mammillary glands of the more advanced mammals (Duvall, 1988).

The monotremes, therefore, are a type of very advanced repto-mammal, a therapsid which has yet to reach the next stage of metamorphosis. In other lands and environments, however, the monotremes have disappeared as they evolved into or were replaced or killed off by more advanced mammals who emerged almost simultaneously and multi-regionally throughout Africa, Eurasia, and North America.

These advanced mammals, however, did not simply crawl out of the earth, or emerge from stone or clay. Advanced mammals are the multi-regional descendants of therapsids who are the multi-regional descendants of repto-mammals, who in turn, once laid eggs.

Given that repto-mammals, therapsids, and mammals (including primates) have emerged on every continent, it could be argued that the genetic seeds to produce mammals have matured at different rates, albeit in different environments (Joseph, 1997). Environmental factors coupled with multiple trees of life, explains why modern human mammals still share the planet with primitive egg layers who are little different from their repto-mammal grandparents who strutted their stuff 200 million years ago.

Since the environment acts on gene selection it can influence the rate and speed of evolutionary metamorphosis and the activation and exchange of genetic material. Hence, it not surprising that primitive and modern versions of the same species may coexist, albeit in different environments, e.g. an isolated, steaming swamp and jungle, vs the fruited plains and happy hunting grounds of Eurasia, Africa, and North America. Those who appear to be more primitive and who have lagged behind, live in an environment which has not promoted the next stage of genetic metamorphosis. Those "genetic seeds" have yet to mature. In fact, this same unequal relationship where primitive and more advanced species coexist, albeit in different environments, is characteristic of all manner of Earthly life, including bacteria, plants, insects, reptiles, mammals, primates, and even the genus Homo.

MAMMALIAN METAMORPHOSIS

As noted, with the development of the cingulate gyrus, the therapsid's ability to communicate expanded beyond simple gestures, posturing, or olfactory-pheromonal signaling, and now included the capacity to produce a variety of complex meaningful sounds, such as between mother and infant, including, perhaps the separation cry. The five-layered cingulate gyrus provided the brain power to engage in prolonged maternal care, which in turn promoted the development of language, love, and the family (Joseph, 1993; MacLean, 1990).

As therapsids (e.g., Probainognathus from the Triassic followed by Periptychus from the Paleocene), continued to evolve and the brain continued to grow the mesocortical five-layered cingulate began to sprout a small nub of neocortex (Quiroga, 1980); i.e. the six layered new cortex. In later appearing therapsids, e.g. Phenocodus, the now, enlarged brain, began to resemble that of primitive mammals, e.g., opossum or hedgehog.

When the first mammals began to scurry about 85-130 million years ago (e.g. Kumar & Hedges, 1998), the gray mantle of the outer surface of the brain, the six layered neocortex ("new cortex") had begun to encapsulate the old brain, forming the frontal, parietal, temporal, and occipital lobes in the process.

It was the development of this new brain and the neocortex which provided mammals and primates with an enormous competitive intellectual edge that enabled them to take advantage of the cosmic catastrophe which presumably wiped out most of the large, cold blood, land based dinosaurs when a massive meteor struck the Yucatan peninsula, some 65 million years ago (Alvarez, 1986; Alvarez & Asaro, 1990; Rampino & Haggerty, 1994; Raup, 1991).

The enormous energy released from this meteor strike destroyed much of life in the Americas. Moreover, due to the dust thrown into the air sunlight was blocked out for months. Temperatures dropped, thus killing off all remaining large sized cold blood animals; events which were then followed by an acid rain and a greenhouse type warming.

Any remaining dinosaurs were quickly eradicated by surviving mammals, and in consequence, mammals gained dominion over the day as well as the night. As the environment acts on gene selection, the mammalian brain quickly adapted to processing visual as well as auditory stimuli, and expanded yet again. With the ensuing evolution of primates, monkeys and apes in particular, the entire forebrain became adapted for engaging in prolonged and detailed analysis of visual and auditory stimuli (Gloor, 1997; Stephan, 1983) and climbing in trees.

Over the course of later mammalian and primate evolution and as these creatures gained complete dominion over much of the planet, the neocortex began to expand at a rapid rate (Stephan & Andy, 1977). In fact, when comparing the brains of “living fossils” such as insectivores with that of humans, it appears that the six to seven layered neocortex expanded by a factor of 156 (even when taking into account differences in body size), whereas the 3-layered limbic system allocortex and five-layered mesocortex (cingulate gyrus) and all associated olfactory-limbic structures developed at a much reduced rate.

For example, limbic system structures such as hippocampus and septum are only 4 times larger and the amygdala is 6 times larger when comparing humans to insectivores. By contrast, the olfactory

Figure 48. *Skeletal structure of (A) a primitive reptile, and (B) three repto-mammals. Note placement of legs has shifted from alongside the body, to beneath the body. From Maclean, 1990. Courtesy of Plenum Publishing. Note: Contrary to Darwinism, the skeletal system has not become more variable, but more complex.*

Figure 43. *The brain of a lizard.*

Figure 49. *The limbic system across four species.*

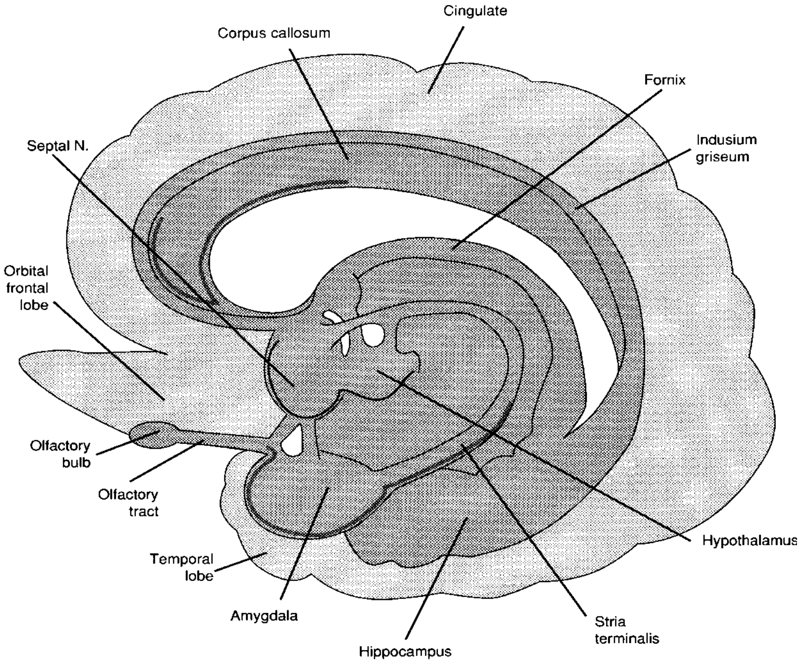
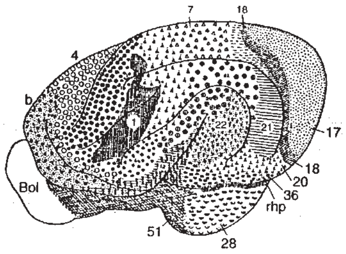


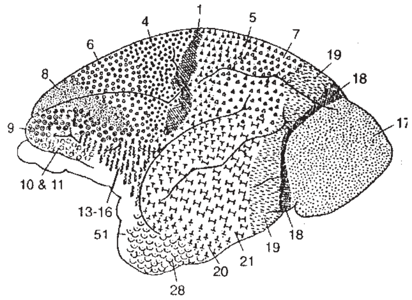
Figure 50. *The human limbic system.*

Cat

Kinkajou



Lemur



Human

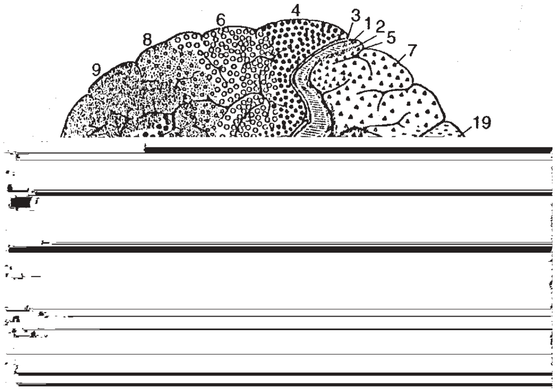


Figure 51. *The expansion and growth of the forebrain and the reduction in the olfactory regions. Contrary to Darwinism, the brain has not become more "variable" but increasingly complex.*

bulb is 40 times smaller (Stephan & Andy, 1969; Stephan, 1983), which is due to the reduced importance of smell and olfaction in human behavior.

Hence, contrary to Darwin's theory, the brain did not become more variable, but "evolved" new structures and tissues which mushroomed in size.

MULTI-REGIONAL PRIMATE METAMORPHOSIS

It is only with the demise of the dinosaurs that primates were able to emerge from the underbrush and the darkness of night. By 55 million years ago, during the early Eocene, at least some orders of primates (e.g. Tetonius) evolved a large occipital lobe (visual cortex), as well as an emerging temporal (auditory) lobe and frontal lobe (Radinksy, 1967, 1970). Thus, by 55 million years ago, ancestral primates had evolved a brain which resembled that of modern day prosimian primates.

Over the ensuing years, and as primates adapted to living in the trees, which in turn required major adaptations in the eyes and hands, the basic pattern for the primate neocortex became established and the frontal and temporal lobes and the "hand" area of the frontal-parietal lobes continued to expand.

The first prosimian primates to scurry about this planet may have diverged from several different mammalian lines some 70-100 million years ago. Primates, like earlier mammals, reptiles, and amphibians, came to live on every continent. Although modern day neo-Darwinian theory demands a single line of descent, like the mammals, dinosaurs, reptiles, amphibians, plants and insects before them, primates appear to have emerged multi-regionally and almost simultaneously throughout the world and from multiple branches from multiple trees, rather than from a single seed, trunk, or twig.

Of course, it is possible that many species may have simply migrated from one land to another, for example, from North American to South America. However, migration is less likely as to the emergence of, for example, primates in South America and Africa-Eurasia. The great oceans are too vast a distance to be covered without first dying of thirst and hunger. Of course, as species can be hurtled from planet to planet, migration remains a distinct possibility.

Throughout the world, many species of primate took to living amongst the branches of the trees. In consequence tremendous alterations occurred in the fingers, and hand-eye coordination—as the environment acts on gene selection. For example, claws became grasping fingers whereas the eyes moved to the front of the face thus providing for depth perception and stereoscopic vision. Within the brain there were tremendous expansions of the visual, auditory, tactual-gestural cortex.

It was presumably from these widely dispersed tree loving stocks that gave rise to "old world" monkeys in Africa, India, Asia, and "new world monkeys" in the Americas about 40 million years ago (Leaky, 1976, 1988; Pfeiffer, 1985). The wide ranging stock of "old world" monkey, in turn gave rise to apes (hominoids) about 30 million years B.P., with what would become chimpanzees and gorillas eventually appearing in Africa, and Orangutans appearing in India and Asia. Presumably numerous branches from these varied primate-hominoid trunk lines diverged again, and yet again, and gave rise to the ancestral lines which led to the emergence of the first primitive Adam and Eve.

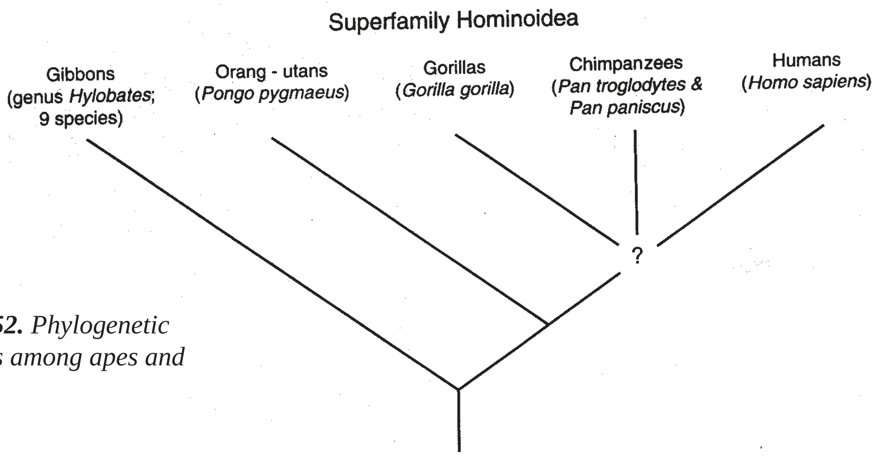


Figure 52. *Phylogenetic relations among apes and humans.*

FROM HOMINOID TO HOMINID

By 30 million years B.P., apes had emerged multi-regionally dwelling in Africa, China, and India, literally from sea to shining sea. And it is from these wide ranging hominoid stocks that a variety of hominoid/pre-hominids began to "evolve," including Dryopithecus, Sivapithecus, Ramapithecus, Ankarapithecus, Ouranopithecus, and Giganotopithecus.

Evolutionary metamorphosis is most likely to occur when an organism is exposed to a multiplicity of changing environments, or where two divergent worlds meet. For the pre-hominid hominoids such as Dryopithecus, Sivapithecus, Ramapithecus, Ankarapithecus, Ouranopithecus, and Giganotopithecus, the netherworld of change was found where the forest ended and began to recede and the savanna and grasslands began to expand. This great change occurred during a period in which parts of the planet were bathed in renewed warmth.

As the changing environment acts on gene selection, the descendants of these pre-hominid hominoids gave rise to a wide variety of pre-human species which began to "evolve" multi-regionally. These included Australopithecus who was later followed and joined by Homo habilis who was joined and then followed by H. erectus who was joined and then followed by Homo sapiens who was joined and then followed by H. sapiens sapiens—the wise man who knows he is wise and who would soon dominate and then threaten a good part of the planet's multiple life forms with death and extinction.

MULTI-REGIONAL HUMAN METAMORPHOSIS

FROM HOMINOID TO HOMINID

As to the ancestors of the first pre-human hominids, there are several candidates, each of which may have given rise to a distinct or similar branch of the emerging human race. These ancestral species include Dryopithecus, Sivapithecus—ape-like hominid/hominoids who emerged in Europe and India, about 16 million years ago. Other candidates include Ramapithecus whose remains have been discovered in Africa, India, and Southwest China (Jurmain, et al. 1990; Munthe et al. 1983). Ramapithecus, in fact, appears closely related to Dryopithecus and Sivapithecus.

Other possible candidates include Ankarapithecus of Turkey, Ouranopithecus of Greece, and Giganotopithecus whose 8 million year old remains have been found in India, China, and Vietnam (reviewed in Howell, 1997). Giganotopithecus may have descended from Ramapithecus and may have

Figure 53. *A map that displays the distribution of some late Tertriary apes. Reprinted from Howells, 1997. Getting Here. Compass Press, Washington D.C.*

later given rise to Homo habilis in Asia.

Nevertheless, these species of hominoid pre-hominid have for the most part been rejected as human ancestors. Conventional wisdom requires an African origin for the proverbial ape-hominid-human ancestor, and these species lived in the "wrong" parts of the world. Indeed, conventional wisdom requires that the facts fit the theory, and those facts and fossil remains which are inconvenient or inconsistent with accepted theory, such as the evidence for multi-regional metamorphosis, are conveniently rejected and dismissed.

MULTI-REGIONAL METAMORPHOSIS OF AUSTRALOPITHECUS & HOMO HABILIS

Around five million years ago and in reaction to yet another major change in environmental and climatic conditions, some species of hominoids began to increasingly live upon the ground. Although they spent much of their time in trees, it is while on the ground, around 5 million years ago, that the descendants of Ramapithecus and/or Giganotopithecus, Ankarapithecus, Ouranopithecus, or some other primate-pre-hominid, underwent further evolutionary metamorphosis and gave rise to a variety of more advanced pre-hominids, such as Ardipithecus ramidus and Australopithecus Afarensis.

Again, however, contrary to conventional wisdom, but consistent with the theory of evolutionary metamorphosis, a wide range of species collectively referred to as Australopithecus (A. aethopicus, A. africanus, A. robustus, A. boisei), emerged multi-regionally, throughout Africa (see Grine, 1988; Leakey & Walker, 1988; Skelton & McHenry 1992) as well as in China and Java, e.g. A. robustus (reviewed in Barnes, 1993).

Around 2-3 million years ago Australopithecus was joined by other possible human ancestors: Homo habilis (the handy man). Again, contrary to conventional wisdom, but consistent with the theory of evolutionary metamorphosis, several varieties of H. habilis (e.g. H. rudolfensis, H ergaster) appeared in Africa, as well as in China (Dragon Hill) and Indonesia (reviewed in Barnes, 1993, and Howells, 1997).

In fact, as reported in the July 5, 2002, issue of the journal Science, a 1.75-million-year-old homo habilis skull was found in Eruo-Asia, near the medieval town Dmanisi, 50 miles southwest of Tbilisi, the Georgian capital. The skull was found along with more than 1,000 crudely chipped cobbles, which are the tools commonly associated with Homo habilis. The skull has the canine teeth and face of Homo habilis and the cranial capacity of the new skull is also 600 cubic centimeters, which is "near the mean" for H. habilis.

The discovery of this skull is completely at odds with the out-of-Africa theory of human origins. In fact, as pointed out by Dr. Ian Tattersall, a specialist in human evolution at the natural history museum in New York City, the skull closely resembles a 1.9-million-year-old Homo habilis skull from Kenya.

As summed up by Dr. David Lordkipanidze who made the discovery: "We have a new puzzle."

Figure 54. *One of the many interpretations of the various phylogenetic relations among different species of hominids. Reprinted from Zigmund et al., 1999 Fundamental Neuroscience, Academic Press, San Diego.*

What we have is evidence of multi-regional human evolution.

Indeed, like their purported ancestors, these species collectively referred to as Australopithecus and H. habilis "evolved" multi-regionally. However, unlike their predecessors they evolved the capacity to stand upright and to make and use tools.

MULTI-REGIONAL METAMORPHOSIS OF H. ERECTUS

Like their ancestors, the fossil evidence indicates that Australopithecus and Homo habilis continued to evolve multi-regionally and to undergo metamorphosis in various parts of the world, thus giving rise to a wide variety and wide ranging species collectively referred to as Homo erectus (Binford, 1981; Brown, et al. 1985; Jia, 1980; Johanson & Shreeve, 1989; Leaky, 1976, 1982; Pfeiffer, 1985; Rightmire, 1990; Swisher et al., 1996; Stanley 1979, 1981).

With the metamorphosis of Homo erectus, who first appeared around 1.9 million years ago, the brain gradually doubled in size, approaching within 15% of a modern human by 500,000 years B.P.

The Homo erectus were the first individuals to have harnessed fire and the first who developed crude shelters and home bases. They also utilized various earth pigments (ochre) for perhaps cosmetic or artistic purposes. In this regard, these peoples were beginning to experiment with individual creative and artistic expression.

Figure 55. *Homo erectus from Africa, dated to 1.6 million years. Reprinted from Howells, 1997. Getting Here. Compass Press, Washington D.C.*

Figure 56. *(Above) Homo erectus from Asia. Java man (top), Solo man (middle) and Peking man (right). Reprinted from Howells, 1997. Getting Here. Compass Press, Washington D.C.*

However, contrary to conventional wisdom which requires an African origin, the earliest fossil evidence indicates that like H. Habilis, H. erectus emerged multi-regionally, beginning in Euro-Asia, i.e., the Caucasus (Georgian Republic) around 1.9 million years (reviewed in Howells, 1997).

H. erectus emerged multi-regionally in Asia, Africa and Europe. The skeletal remains of H. erectus (and associated stone tools) have been discovered in Ceprano Italy (dated to 800,000 B.P.), and in Java, Indonesia, (Pithecanthropus erectus) and near the Solo River (e.g. Solo Man, Java Man)—sites dated from 1.8 million to 700,000 B.P (respectively). Likewise, H. erectus (H. erectus pekinesis) have been discovered in Northern China (e.g. Peking Man) and in Zhoukoudian, Yuanmou and Xihouda China—sites dated from 500,000 to 750,000 to 800,000 to 1.5 million years B.P. (Jia, 1975, 1980; Jurmain et al. 1990; Stanley, 1979, 1981; Wu & Wang, 1985).

Although conventional wisdom and neo-Darwinian theory requires it, it is not likely that “Georregionally, the fossil evidence suggests the same for archaic H. sapiens, whose remains have been discovered in Africa, Asia, Europe, the Middle East, and India. And, contrary to the single seed, out-of-Africa scenario, the remains of evolutionarily advanced archaics ("early moderns") appear in China (Dingcun, Maba, Dali, Jinniushan) 10,000 years before similar species appear in East Africa; i.e., from sites dated to 130,000 B.P. and 120,000 B.P. respectively (Barnes, 1993; Butzer, 1982; Grun et al. 1990; Howells, 1997; Rightmire, 1984).

Archaic H. sapiens in fact died out before the more primitive H. erectus, i.e. 29,000 B.P., (Neanderthals) vs 27,000 B.P. (H. erectus), whereas another species of incredibly advanced humans, Homo sapiens sapiens, had already emerged 75,000 years B.P. And, the first H. sapiens sapiens did not first appear in Africa, but in Australia (75,000, B.P.) followed by China (67,000 B.P.), Israel, Romania, and Bulgaria (43,000 B.P.), Iraq and Siberia (40,000 B.P.), Spain and France (35,000 B.P.), and Brazil, Peru, Chile and North America (30,000 to 50,000 B.P.). By contrast, during these same time periods, sub-Sahara Africa was still populated with archaic Homo sapiens; African Neanderthals.

Indeed, rather than originating in Africa where archaic H. sapiens roamed until 30,000 B.P., "modern" H. sapiens sapiens had already established numerous settlements in Australia and were fashioning complex tools as early as 60,000 B. P., including grooved "waisted blades" which could be bound to a handle.

What this means is that four different species of humanity were living in different parts of the world simultaneously, H. erectus, archaic, early modern, and "modern" H. sapiens sapiens—which is evidence of multi-regional evolution occurring at different rates in different branches of humanity, in different geographical regions. Although it could be argued that the descendants of one of these geographical groups merely migrated and killed off all competitors, this view is not supported by the fact that different types of humanity, for example, different types of H. habilis and H. erectus, are found in Africa vs Asia, with those in Asia (e.g. H. erectus) appearing before those in Africa, or those in Australia (e.g. "moderns") appearing before those in Africa or Asia.

Asian H. habilis and H. erectus differed significantly from their African counterparts, and so too did European vs African Neanderthals, with the European branch having a bigger brain. Australian and Asian "moderns" also appeared tens of thousands of years before their counterparts in Africa; which is not consistent with the out-of Africa scenario but instead supports the multi-regional and even the out-of-Asia or out-of-Australia view of evolution. In fact, whereas "modern" appearing H. sapiens sapiens do not emerge in North East Africa until around 35,000 B.P. the remains of Asian moderns have been found in China from sites dated as long ago as 67,000 B.P. (see Howells, 1997).

In fact, not only do "modern" humans appear outside of Africa thousands of years before "moderns" appear in Africa, but evolutionarily advanced humans were living in Northern Siberia as long ago as 250,000 to 300,000 years B.P. (Waters, 1997). Siberia is an exceedingly hostile environment requiring advanced survival skills as temperatures drop to below 70 degrees in winter. In fact, stone tools dated to 250,000 years B.P., were discovered along a river near Irutsk, Siberia—tools similar to those found in North America.

"What this indicates," according to Michael Waters of Texas A. & M., who helped date one of these sites and associated artifacts, "is that these people had the ability to deal with a rigorous environment. They could control fire, they had a survival strategy, they could make and find shelter, clothing, boots, etc." However, these advanced behaviors and capabilities, such as the ability to fashion complex clothing, do not appear in sub-Sahara Africa until near the end of the Upper Paleolithic.

Hence, similar to the step-wise worldwide pattern of multi-regional, multi-phylectic metamorphosis which has characterized the progressive emergence and increased complexity of plants and animals (Joseph, 1997, 2000a), the available evidence suggests that human "evolution" has unfolded multi-regionally in a step wise, progressive fashion, with some groups lagging far behind and others being left behind altogether and becoming extinct.

The Earth (and other planets) were genetically seeded to grow humans, and all manner of variations thereof.

This proposition and the fossil record are also consistent with evidence derived from the Human Genome Project.Much of the genome consists of silent intronic genes and nucleotide sequences. Silent genes and silent nucleotide sequences have the capacity to make copies of themselves, and to shift position within the genome (i.e. "jumping genes"): referred to as transposons. Transposable nucleotides show a tendency to leap to the more active GC regions. Once they are incorporated, they thus increase gene density and nucleotide content. These silent genes and silent nucleotides also come to be expressed, and/or they exert regulatory, inhibitory, or activating influences on other genes once they leap to the GC regions. In other words (and contrary to Darwinism), genes (and the traits they code for) that exist apriori may change position in the genome and become active; and they leap from the non-coding to the coding regions of the genome.

As noted, exons, introns and other transposable elements (e.g. "jumping genes") move about within the genome and insert themselves into new positions thus changing the genetic "code" as well as producing new genes via exon shuffling, retrotransposition, and gene duplication (Courseaux & Nahon 2001). "Dozens of genes... and about half of the human genome have been derived from transposable elements" and widespread DNA transposon activity is involved in speciation events (IHGSC, 2001); that is, the creation of subsequent species. This process including the creation of large-scale chromosome rearrangements via DNA transposon activity, is under genetic control and functions in accordance with precise genetic instructions (Caron et al. 2001; Courseaux & Nahon 2001). However, with each progressive step in the evolutionary metamorphosis of increasingly complex creatures, "there has been a marked decline in the overall activity of transposable elements" with the greatest decline occurring following the emergence of the hominid lineage; i.e. woman and man (IHGSC, 2001). With each step up the evolutionary ladder, families of transposons drop out in an almost clock-like fashion, with the last identifiable transposon extinction occurring following the divergence of humans and chimpanzees. "Only a single LTR retroposon family is known to have transposed since our divergence from the chimpanzee 7 million years ago (IHGSC, 2001).

These and other findings reported by the International Human Genome Sequencing Consortium (IHGSC) are entirely consistent with the theory that DNA strives to fulfill specific genetic goals which include the replication of life forms that long ago lived on other planets, including creatures quite similar to woman and man. Indeed, having served their purpose and having achieved their "genetic goals" "DNA transposons appear to have become completely inactive" with the evolution of humans (IHGSC, 2001).

The Earth was genetically seeded to grow humans. The multi-regional evolution of humans is evidence of intelligent design.

THE MYTH OF AFRICAN ORIGINS
THE STORY OF EVE

Conventional wisdom is of a single line of descent, and that modern humans "evolved" in Africa, from earlier species of humanity who also "evolved" in Africa, with each successive species migrating out of Africa, and then killing off and replacing earlier species who had also originated and migrated out of Africa before them.

Although one of the central tenants of Darwin's theory is that of "random variation" it has yet to be explained why that variation can only occur in Africa, and why that variation did not lead just to variable species, but increasingly intelligent and resourceful, and more advanced species. Variation does not equal increased complexity and the fossil record is indicative of a step-wise sometimes leaping progression yielding new structures and increased complexity.

Harvard paleontologist, Gould, solves this problem by denying the obvious and by claiming there is no evidence for progress. Yet others refer to mutations. Random mutations resulted in the production of successive superior species simply by chance, and these mutations repeatedly took place only in Africa.

Thus, according to modern neo-Darwinian theory, mutations were being continually produced in Africa and only in Africa, and each subsequent race of mutants migrated out of Africa only to be later replaced by more advanced mutants who also mutated in Africa.

Not only is the out-of-Africa, single seed, mutation scenario contradicted by the fossil evidence, but by logic and genetics.

For example, a "mutated" gene is generally eliminated before it has a chance to be expressed. It would be eliminated and replaced by a normal duplicate gene.

Moreover, even if the mutant gene were not eliminated, in order to produce a viable breeding pair, requires that two of the same exact mutations appear simultaneously in the same population, in both a man and a woman—and by chance—otherwise, the mutated individual might be unable to breed and pass on his/her superior mutated traits. Nevertheless, even if this mutated individual was not sterile and did breed, the mutation would likely disappear from the gene pool; either that or perhaps only an intermediate individual would be produced.

Even if we disregard those genetic mechanisms which eliminate "mutations" the fact remains that for evolution to be successful requires that multiple individuals and thus multiple mating partners "step-forward" as a group to the next stage of species evolution in order to produce viable offspring. A scenario such as this, however, is not consistent with neo-Darwinian theory, though it is entirely compatible with the theories of evolutionary metamorphosis and intelligent design.

THE TROUBLE WITH EVE

According to the "Eve" hypothesis, all modern humans descended from female ancestors living in Africa about 250,000 years ago. There are numerous problems with this theory, beginning with the fact that the assumptions upon which it rests have been shown to be invalid; e.g., that mitochondrial DNA (which in humans consists of 37 genes) is only inherited from the mother. In fact, fathers also contribute mitochondrial DNA. In addition, the estimates based on mitochondrial DNA "mutation" rates has been shown to be statistically erroneous (Templeton, 1992; Wolpoff & Thorne, 1991).

Specifically, based on an initial analysis of a small fragment (610 base pairs) of the mitochondrial genome (which consists of about 16500 base pairs), taken from 189 individuals, it was argued that there is greater diversity within Africa than outside Africa—as based on the varying patterns in sequencing (Stoneking & Cann, 1989; Vigilant et al. 1991). From this data it was concluded that all humans must have descended from African ancestors. However, others have found, using the same data, that all humans could have also descended from ancestors who lived in New Guinea (Ruvolo & Swafford, 1993).

As per more recent data provided by Chu et al., (1998), regarding the origins of modern Chinese, it is noteworthy that although these investigators also claim an African origin, that the

Figure 57. *Many anthropologists embrace the "single seed" hypothesis whereas all modern humans have a common ancestor which originated in Africa. As conceptualized by Williams Howells (1997), these different groups can be clustered together to form 28 Cranial Clusters which are all linked together, and 42 genetic clusters which are also linked ("Buriats" are "North Asians, and "Caucasoids" include Egyptians). Nevertheless, the genetic and cranial groups are not equivalent. Hence, Australoids are closer to Africans based on cranial clustering, but are closer to Southeast Asian and Pacific Islanders based on genetics. Reprinted from Howells, 1997. Getting Here. Compass Press,*

East Asian population they studied were genetically more closely related to "Native American" Indians, followed by Australian aborigines, and New Guineans. Hence, this data could also be interpreted to mean that anatomically "modern" humans originated in Australia and then migrated to New Guinea, then to southern Asia, and then the Americas.

A more serious problem with the Eve hypothesis, is genetics. Those advancing the theory of "Eve" are staking their claims by making grossly erroneous assumptions about the maternal role in inheritance and "mutation." As reported by the International Human Genome Sequencing Consortium (2001) genetic material on female "chromosome Y is unusually young, probably owing to a high tolerance for gain of new material by insertion and loss of old material by deletion. Several lines of evidence support this picture." Transposed "elements on chromosome Y are on average much younger than those on autosomes. Similarly, MaLR-family retroposons on chromosome Y are younger than those on autosomes, with the representation of subfamilies showing a strong inverse correlation with the age of the subfamily. Moreover, chromosome Y has a relative over-representation of the younger retroviral class II (ERVK) and a relative under-representation of the primarily older class III (ERVL) compared with other chromosomes. Overall, chromosome Y seems to maintain a youthful appearance by rapid turnover."

By contrast, "the mutation rate in the male germline appears to be fivefold higher than in the female germline." Men pass on mutations to their offspring twice as often as women, such that "most mutation occurs in males." Higher male mutation rates are due to the fact that men make billions of sperm, while women are born with far fewer eggs. These numbers favor mutations being introduced when sperm-producing cells copy DNA on the Y chromosome. Males, therefore contribute more to evolutionary change."

As the Eve theorists have ignored the male contribution and have instead focused on "supposed" mutations in maternal-mitochondria, and have further erroneously assumed that mitochondria are inherited only from the maternal line, it can only be concluded that the Eve hypothesis is completely without any scientific foundation and should not be taken seriously.

And then there is the Neanderthal problem. Neanderthals did not evolve into Cro-Magnon peoples, as they coexisted for at least 20,000 or more years. And, European Neanderthals are genetically unrelated to modern Europeans (Krings et al., 1997; Ovchinnikov et al., 2000). If all species of humanity first evolved and then migrated out of Africa, how is it that two separate samples of DNA from different Neanderthals living in distant lands indicate that although these peoples were closely related, they are unrelated to modern peoples living in Europe? The answer? Because they evolved from an ancestral "tree" that significantly differed from that of the Cro-Magnon.

Although the environment acts on gene selection, and slight changes in the environment can activate different genes and gene sequences, thus producing variant versions of the same species, and although environmental differences can explain why African Neanderthals had an even smaller brain than Neanderthals living in frigid Europe, it cannot explain why two highly dissimilar species of humanity lived side by side for almost 20,000 years--with one group, Neanderthals, failing to evolve into the other. Rather, they "evolved" from different ancestral stocks who in turn "evolved" under different environmental conditions.

The evidence based on Neanderthal DNA, like the fossil record, is consistent with the theory of evolutionary metamorphosis. The Earth (and other planets) were genetically seeded to grow humans, and all manner of variations thereof.

And why didn't the Neanderthals evolve into modern people? First and foremost, they dwelled in Europe during an epoch of extreme Arctic cold—a bleak and frigid environment which limited experiential opportunities. They also failed to evolve because once the weather began to change, the Cro-Magnons moved in, and over the next 20,000 years the Neanderthals were either eradicated by the intellectually and technologically superior Cro-Magnons, and/or they died out due to the diseases that the Cro-Magnons brought with them as they invaded Neanderthal lands.

These later possibilities are also consistent with the theory of multi-regional evolutionary metamorphosis—as is the Sumerian claim that "gods" from other planets genetically altered some of the primitive humans living upon the Earth (e.g., Neanderthals), in order to create an intellectually superior being fashioned in the image of the gods, but who could serve as slave labor, i.e., the Cro-Magnon. According to the Sumerians, the men and women created in the image of the gods were also exceedingly sexually prolific, and their population mushroomed out of control. In contrast, according to the Sumerians, the more primitive species of humanity were sexually exceedingly primitive (suggesting that Neanderthal women had not yet lost their estrus) and once they came into contact with the god-like human creations of the gods, the Neanderthals died out as a species.

EVOLUTIONARY METAMORPHOSIS

Admittedly, it is possible that representatives of various distinct species simply migrated from place to place, thus giving rise to the illusion of multi-regional metamorphosis. Likewise, although the fossil and genetic evidence does not support the out-of-Africa, single line of descent model of pre-hominid human evolution, it remains a strong possibility that various species of pre-human "ape" may well have migrated across distant shores.

Migration becomes less likely given the numerous, and quite strikingly different species of Australopithecus, H. habilis, and H. erectus who emerged multi-regionally. Moreover, migration cannot explain the obvious independent evolution of Neanderthals and Cro-Magnon who apparently "evolved" from different branches of the human-genetic forest.

Nevertheless, even if we reject the multi-regional model as applying to most species, only the purposeful expression of genetically coded instructions can account for the obvious evidence of a step-wise, sometimes leaping progression in increasing intelligence and complexity which has characterized the metamorphosis of a rather narrow range of life on this planet. Only precise genetic instructions can account for the fact that basically similar species of humanity have emerged multi-regionally across distant lands, from distinct pockets of ancestral species which also emerged multi-regionally, as is evident in the case of Neanderthals and Cro-Magnons.

Because so many different species of humanity have emerged in distant lands, and as this pattern of multi-regionalism was repeated with Australopithecus, H. habilis, H. erectus, and H. sapiens, it thus appears that the planet (and others like it) was genetically seeded to grow humans; and that these genetic instructions were maintained in the genomes of the first creatures to be flung upon the face of this planet billions of years ago.

Over the course of "evolution" and the genetic engineering of the earthly environment, the unlocking and release of these "genetic memories" and silent traits, has resulted in the multi-regional replication of creatures (or variations thereof) who may well have been created by "god" and/or whom lived on other planets, including fish... frogs... reptiles... repto-mammals... mammals... primates... and woman, man....

DARWINIAN TAUTOLOGIES

With the exception of Wallace's theory of "natural selection," Darwinian and neo-Darwinian theories are in fact tautologies which mask what is little more than circular thinking and which can only predict by hindsight and from the present to the past; i.e. Breeders breed. Survivors survive. The fit are fit.

Specifically, according to Darwin's theory 1) Species reproduce themselves. 2) Random reproduction errors and small variations lead to variations in the population. 3). If these copying errors and random variations are adaptive and provide "fitness," they are naturally selected and passed on to offspring, thus leading to the survival of the fit. Hence, we know that a trait or a species is "fit" if those who have this trait survive, breed and produce offspring. However, there is no way to predict who is fit unless they survive and reproduce, which really means: those who reproduce are fit, and that almost all females, regardless of species, are fit, whereas the majority of males are not fit. Indeed, almost regardless of species the majority of males never breed (Bateman, 1948; Cade, 1985; Carpenter, 1942; Clutton-Brock, 1987; Fedigan, 1992; Howard, 1978; Johnson, 1972; Lott, 1979; McCann, 1981; Thornhill, 1981; Trivers, 1976; Zuckerman, 1932).

Of course, if we examine Darwin's proposition from the standpoint of the species as a whole, what his theory then explains is that a species is fit until it ceases to exist at which point it is no longer fit. And those species who survive are fit so long as they survive. Once they cease to survive they are no longer fit. Indeed, what his theory really means is that those who survive survive, those who reproduce reproduce, and those who die die.

Disregarding the obvious circular reasoning of these tautologies and the fact that Darwin is playing word games where survive=fit, and death=unfit, let us consider the male spider who breeds and is then eaten by his mate, and whose progeny fails to breed because they die— a common fate of infant spiders. Is this male spider who is eaten, and whose progeny die, more "fit" than the celibate male spider who grows fat and lives to an old age? Indeed, sometimes those who survive are not necessarily "fit" but only lucky, and ditto for those who breed, for among the animal and insect kingdom, the vast majority of males never breed (Bateman, 1948; Cade, 1985; Carpenter, 1942; Clutton-Brock, 1987; Fedigan, 1992; Howard, 1978; Johnson, 1972; Lott, 1979; McCann, 1981; Thornhill, 1981; Trivers, 1976; Zuckerman, 1932). Non-breeding males are produced in staggering numbers. Is the animal who breeds and is eaten or who is injured and dies protecting his access to a sex partner, but who produces non-breeding progeny somehow more “fit” that those animals who never produce sons and daughters but still live to a ripe old age?

Or, consider Alois and Klara Hitler, father and mother of Adolf Hitler. By Darwin’s definition, because Alois and Klara produced several sons and daughters they were more “fit” than those Germans who failed to breed. Nevertheless, the children of Alois and Klara did not breed, and the actions of their son, Adolf, resulted in the death of up to 40 million people including his relatives and millions of Germans. His birth resulted in the destruction of the German nation!

Of course, the Darwinians may counter that Darwin was referring to species and not individuals. However, this argument is equally illogical, as over 95...% of all species which have appeared on Earth, have become extinct (Rampino & Haggerty, 1994; Raup, 1991). If we apply Darwin’s theory to the rise and fall of species, then species, as a rule, are not “fit.”

It is perhaps true, as is evident within the capitalist business community, that “survival of the fit” is the name of the competition game and the rule of success. However, those who run these businesses do so with certain goals in mind. That is, the behavior of the successful company is characterized by foresight, the development of long and short term goals which are intelligently considered, intelligently designed, purposefully planned and carried out, purposefully modified, etc., and so on. This is not Darwinism! Darwin’s theory emphasizes random variations. If a business owner relied on Darwinism to run his business, he and his business would quickly become extinct.

As neatly summed up by one of the more prolific and vigorous defenders of Darwinism, Richard Dawkins (1987, p. 5) “the blind, unconscious, automatic process which Darwin discovered, and which we now know is the explanation for existence, has no purpose in mind. It has no mind, no mind’s eye. It does not plan for the future. It has no vision, no foresight, no sight at all.”

As applied to business, or even every day life, Darwinism would be a disaster. Behavior is purposeful, goal directed, and so to has been “evolution.”

Human behavior is purposeful and is guided by intelligent (and often not so intelligent) choices. Our actions, and those of most higher animals, are not guided by random factors. Humans have learned to exert control of their environment and to chose the environment in which they dwell. Humans utilize selective breeding, and even the manipulation of genes to create new breeds and to transfer traits from one species to another--which is a form of purposeful and goal-directed evolution by “intelligent design.”

Despite dogmatic claims to the otherwise, Darwin’s tautological theory is contradicted by logic, the obvious, and the nature of DNA. “Evolution” is not due to random mutations. Mutation always results in death or disability. Likewise, those who breed are not more “fit” than those who do not—as is evident among modern humans where those in poverty and who suffer ill health and an early death rate, have the highest birth rates and whose children are poorly fed and suffer from malnutrition, violence

Figure 58. *Estimates of the percentage of all genera to become extinct since 600 million years ago. There have been five major extinctions. Based on Rampino & Haggerty, 1994. Reprinted from Jakosky, 1998.*

and disease, and who die at staggering rates before they are old enough to breed. This is "fit?"

Darwin's theory and neo-Darwinian evolutionary theory, including the inexplicable statements of Gould where he argues against progress, are completely refuted by the patterns of history, the fossil record, and by everything we know about genetics. There is obvious progress in neurological and human evolution, and there is evidence of obvious progress and increasing intelligence and structural technological capability across different phyla over the last 600 million years. And there is absolutely nothing random about DNA organization or expression.

As per the amazing claim that evolution is based on "random mutations" let us consider the so called "language gene," known as FOXP2. This gene existed prior to the evolution of language, and is found in the genome of other mammals, including mice, rats, dogs, cats, chimpanzees, and so on, but in a non-activated protein-protected form. The gene was identified by Dr. Anthony P. Monaco of the University of Oxford. FOXP2 is believed to switch on other genes during the development of the brain thus giving rise to the neural circuitry which supports human language. However, Dr. Svante Paabo and colleagues at the Max Planck Institute for Evolutionary Anthropology, reported in the August, 2002 issue of Nature, that the same exact gene exists in a non-activated form, in mice, chimpanzees and other primates (Enard, et al. 2002). According to Dr. Paabo, the FOXP2 gene has remained largely unaltered during the evolution of mammals. However, in humans, this formerly

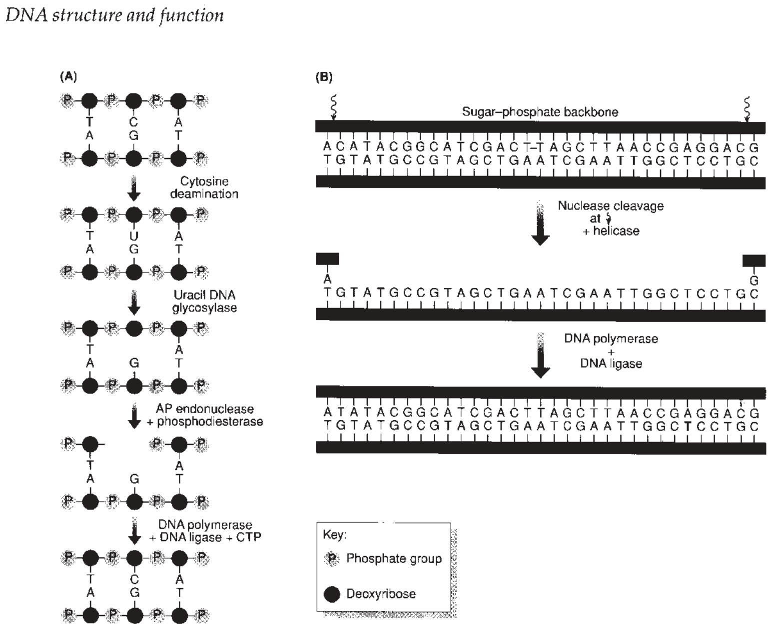


***Figure 59A**. DNA repair pathways involving excision and repair. (A). Base excision repair and replacement. (B) Nucleotide excision and replacement. Reproduced from Strachan & Read*

***Figure 59B.** Schematic depiction of RNA-splicing. RNA-splicing involves removal of non-coding intronic segments and splicing exonic segments back together. Human genome organization, depicting coding and non-coding (intronic) genetic material. Reprinted from Strachan & Read, 1996, Human Molecular Genetics. Wiley, New York.*

silent gene became activated through changes in the shape of its protective protein coat. Protein prevents the activation of genes, and removal or alteration in the shape of this protein overcoat, allows for the gene to be activated.

Thus, the "language gene" did not randomly evolve through random mutations. It existed prior to the evolution of humans and prior to the evolution of language, in a silent, non-activated state.

Regardless of species, DNA displays a high degree of stability in regard to shape, form, organization, enzyme activity, composition, duplication and so on. The genetic code is, for the most part, universal (Strachan & Read, 1996; Watson et al. 1992) and there is no evidence or randomness in its organization or expression—as demanded by Darwin's theory.

Numerous genes and physical traits are shared by diverse phyla whose common ancestors did not posses the traits or the genes that each phyla supposedly randomly and "independently" evolved —a function, we are told by the Darwinians, of "coincidence" and "convergent" and "parallel" evo-

Figure 60. *The Death of Darwin, as recorded by the satirical magazine, Punch. "Punch" got it wrong, for in this depiction there is an obvious progression, and Darwin and his followers do not believe in "progress," some referring to it as a "noxious" concept.*

lution where nature just happens to arrive at the same solution and creates the same exact gene; indeed perhaps the same coincidence which Darwin offers to explain the "laughable" similarity between his work and others, or the same "coincidence" that Darwin relies upon to explain how he just happened to come up with the same exact theory proposed by Wallace.

"Coincidence" is not a scientific explanation.

As per the "evolution" of the same genes and the same traits in different species and phyla, obviously the Darwinian explanation is not logical. Rather, these diverse phyla inherited the genetic instructions to create the same genes so as to create identical or similar body parts. Either that, or these genes were released into the environment and transferred between species (Joseph, 1997, 2000).

Myriad life forms contain the same exact nucleotide sequence segments and "master regulatory genes" which code for the development of the heart, lungs, eyes and brains (D'Souza et al. 1995; Garcia-Fernandex & Holland, 1994; Ruddle, et al. 1994; Strachan & Read, 1996; Watson et al. 1992)—DNA that was independently inherited from common ancestors that had neither heart, lungs, eyes, or brains. In addition, the vertebrate Pax-6 gene cluster is organized and expressed in almost an identical fashion, differing by only 3-6%, in insects, worms, and mollusks (Quiring, et al. 1994).

And, the human genome and that of the higher plants, share homologous DNA-promoters and binding domains (e.g. da and AS-C) including a similar "helix-loop-helix" motif which is involved in cellular division and neuron generation in vertebrates, as well as the production of ovaries and seeds in plants via CHS-A and -J promoters (Joseph, 1998c). However, the common ancestor for mammals and plants diverged well over 1.6 billion years ago; 500 million to one billion years before the evolution, on Earth, of neurons, seeds, or sex organs.

These traits and these genes were preprogrammed to emerge in diverse phyla and did not coincidentally evolve in seperate and different species due to random mutations as is demanded by Darwinian theory. Rather, it appears that these genes and the genetic potential to create these genes and identical body parts, is a function of genetic inheritance and the intronic generation of "genes within genes" and thus species within species.

It is also possible that these genes may have been acquired laterally—that is, through plasmid exchange. Plasmid exchange may well explain why members of a species often "evolve" as a group and thus collectively step forward as they ascend the evolutionary ladder. Plasmid exchange, however, also appears to be under genetic control, occurring according to precise genetic instructions—a view which is an anathema to Darwinian theorists.

If Darwin's theory were correct, the genetic code in no way could be "universal" and the genomes of diverse species from plant to human would not contain a single identical gene, except for those few that would have been passed on, intact and unchanged, from a common ancestor. If Darwin's theory were correct, members of each individual kingdom of life and each separate phyla would have genomes which were radically different from one another which is clearly not the case. If Darwin's theory were correct, and evolution were due to random mutations, it would not be possible to make accurate predictions about ancestral species based on a "molecular clock" derived from rRNA or the genes of different plants or animals.

Although there is nothing random about the genetic code or the emergence of new species, Darwinian and neo-evolutionary theorists insist on randomness in the expression of mutations, and insist on purposelessness, presumably because the alternatives are too discomforting to consider. Many scientists reject the obvious for fear of discovering the "guiding hand of god." Unfortunately, by plucking out their eyes and by demanding that we do likewise, they have blinded themselves to the important implications of what has occurred on this planet over the course of the last billion years. They have blinded themselves to the patterns of history.

In their eagerness to avoid any possibility of a life affirming "god" many have instead embraced a malignant process that typically results in death or severe disability. They preach that all life is random, purposeless, and a product of "adaptive" random mutations. As preached by Darwin's Temple Priests, random mutations, and not "god" are responsible for the miracle of life, evolution, and creation. However, by accepting this gospel they have failed to clearly see the patterns of unplanned traits and cellular modifications and thus the random evolution of new species is thwarted.

Mutations and "unplanned" alterations in chromosomal structure are actively negated by repressor and heat-shock proteins, and a special subclass of oncogenes. Mutations, be they "adaptive" or malignant, like all unusual cellular formations and abnormalities in chromosomal structure, are associated with aberrant oncogene activity. A malignant progression ensues (Kim et al., 1994; Modrich, 1994; Sancar, 1994).

Neo-Darwinian evolutionary theory requires that these mutated errors be allowed free expression, that all corrective mechanisms just happen to fail, that the numerous duplicate copies available be forsaken, and that these mutations miraculously turn out to be adaptive and life promoting.

Moreover, these chance variations (mutations) must occur during the same time period in at least one male and one female who are unrelated and who live in close proximity, so that at least one viable breeding pair is produced, so that they may produce a mutated offspring. In fact, neo-Darwinian theory requires that these mutations randomly and simultaneously appear by chance, at the same time period, in the same location, in at least two unrelated breeding pairs, so that numerous mutated offspring are simultaneously produced who can interbreed thereby leading to the establishment and propagation of new species. And what is the likelihood of a scenario such as this occurring randomly and by chance?

The only way this scenario can work is if the trait was in fact genetically predetermined acting as silent genetic potential. Again, consider the work of Rutherford and Lindquest (1998). According to these authors, these traits can only be dispersed in the population with a high degree of probability, if they were predetermined. “If a population containing ten independent additive determinants affecting” the expression of “the trait, each present at a frequency of 0.1, the probability of an individual having at least six of these determinants, and thus the trait, is 1 in 7,000.

However, if the repressor protein were deactivated or its threshold for release lowered, thus “lowering the trait’s threshold” for expression “by just one or two determinants, the probability of the appearance of the trait increases to 1 in 600 or 1 in 78. Once the frequency of a trait is increased in this manner, given a moderate degree of fitness advantage, selection could increase the frequency of genetic polymorphisms affecting the trait” so that it becomes widely “expressed in the population (Rutherford & Lindquest, 1998, p. 341).

Although the theory of evolutionary metamorphosis is based on the existence of traits which exist prior to their expression—and for which there is abundant scientific support (e.g., de Jong & Scharloo, 1976; Dykhuizen & Hart, 1980; Gibson & Hogness, 1996; Polaczyk et al., 1998; Rutherford & Lindquist, 1998; Wade et al., 1997), Darwinian and neo-Darwinian theory rejects predetermination. According to these theorists, evolution is random and due to chance variations, and traits cannot be genetically precoded and exist apriori, but are due to mutations

Again, for this Darwinian-mutated scenario to be successful requires that an error or abnormality in the genetic code not only go undetected and uncorrected but that the exact same mutation randomly, miraculously and simultaneously appear in numerous males and females who just happen to be living in close proximity, thereby allowing mutated mates to meet and to breed numerous progeny who also miraculously contain and express the mutated error. Darwinian theory, however, also negates this as a likelihood as these variations must occur by chance, and what is the likelihood of numerous identical variations appearing in the same group at the same time, randomly and purely by chance?

If the “mutation” did not simultaneously appear in numerous potential mates and in numerous surviving progeny, this new, mutated individual would die in a single generation and a new mutated species could not emerge; that is, unless this genetic change wasn’t an error but genetically planned and part of the genome and was thus activated in numerous members of the same species.

According to neo-Darwinian orthodoxy, however, the production of new species is not genetically planned and is not encoded within the genome. Rather, the emergence of new species is the consequence of the production of random variations (“mutations”) and thus “errors” in the genome which just happened to be advantageous to the organism, unlike other mutations which kill the host. We are “mutants” -so say the Neo-Darwinians.