STASIS CONSIDERED

by Michael Thomas

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Continuity and Discontinuity

The debate between evolutionists and creationists takes many forms. Unfortunately, it usually centers around issues which are peripheral to the main point of contention, namely, the existence of two opposing perceptions of nature. For the evolutionist, the living world is continuous and the lineages of all existing species can be traced back ultimately to a single common ancestor. Inherent in this theory of continuity is the claim that *transformations* from one type to another are possible. Organisms must therefore possess a sufficient amount of plasticity, which, over time, will make it possible for them to realize such changes.

The creationist perceives the living world from an opposing perspective. Instead of a continuous biological tree linking all creatures, the creationist perceives a series of discrete groups or types. Each type supposedly had an independent origin, and the biochemical, morphological, and behavioral gaps which exist between these types cannot be bridged by the processes proposed by evolutionists. Creationists do not deny change; time, chance, and natural forces are thought to be involved in the fluctuating characteristics of organisms. These factors, however, are insufficient to transform one type into another. Although the exact borders which separate the types of organisms may at times be unclear, sufficient evidence exists to support the idea of discontinuity between types (Denton, 1985).

Inherent in the theory of discontinuity is the notion of *stasis*. Put simply, stasis implies that certain mechanisms exist which prevent an organism of a particular type from transforming to the extent that it no longer belongs to its original type.

Preconceptions in Biology

Evolutionists have proposed a myriad of possible mechanisms thought to generate the variation necessary for transformation (Endler and McLellan, 1988). Such mechanisms include mutation, random genetic drift, gene duplication, exon shuffling, and transposable elements. Creationists, on the other hand, have offered few possible mechanisms for stasis. Until such mechanisms are proposed, experimental research guided by theories of discontinuity will suffer greatly.

The general absence of theoretical analyses or experimental data supporting mechanisms of stasis does not, however, mean that such mechanisms do not exist. Rather, for a long time the majority of the biological community has worked under the

preconception of continuity: most biologists have been looking for, and attempting to demonstrate, change in species. Writing about bacterial evolution about ten years ago, Bennett and Richmond (1978: 54) candidly admitted their preconceptions:

> Of course, our outlook is biased since we are interested, in general, in our ability to produce change; intuitively we are less excited by mechanisms of maintaining the status quo.

Such preconceptions are best explained in Kuhnian terms (Kuhn, 1970). According to the historian of science Thomas Kuhn, science does not proceed as an objective progression toward the truth. Instead, it proceeds as a discontinuous series of unrelated paradigms. Paradigms work to determine what facts are important, how the facts should relate to theory, and aid in the articulation of a theory (Kuhn, 1970: 34). Put simply, paradigms define what is important in a science at any time. And without a doubt, for over a century the principle of continuity has served as the dominant paradigm in the biological sciences. Thus, we see the preoccupation with demonstrating change and integrating it into theories spawned by the paradigm of continuity.

The preconception of continuity goes a long way toward explaining our general ignorance about mechanisms of stasis. At present the proponents of discontinuity may have difficulty outlining mechanisms of stasis, but this should not be surprising: no one has been looking for such mechanisms!

In fact, the common preconception of continuity ought to spur creationists on. For in spite of many decades of intensive world-wide research into the mechanisms of transformation, it is apparent that the payoff has been meager, especially when the origin of higher taxa--i.e., macroevolution--is considered. Macroevolution has never been experimentally demonstrated, nor has a satisfactory mechanism for such transformations been established. Indeed, evolutionist C.R. Woese (1987: 177) recently admitted:

> [T]he term `macroevolution' serves more to hide our ignorance than symbolize our understanding.

If macroevolution (which is predicted by continuity, but denied by discontinuity) cannot be empirically demonstrated--in spite of the fact that for decades the biological community has sought just such a demonstration--perhaps it is time to consider discontinuity and stasis as viable alternatives.

Evidence of Stasis

It is not merely the lack of evidence for macroevolutionary transformations which suggests stasis; very good paleontological and molecular data demonstrate the phenomenon.

The fossil record provides many examples. It is now recognized that once a species appears in the fossil record, it remains for a long time relatively unchanged. Stanley (1981: xv) writes:

> The record now reveals that species typically survive for a hundred thousand generations, or even a million or more, without evolving very much.

A million generations and no change--this is an observable fact, not an interpretation depending on a particular world view. This stasis becomes even more apparent if living species are compared to their fossil counterparts. Pierre Grasse (1977: 76-79) offers a small sample from a rather large list of such species. One example is the opposum (*Didelphis*). A comparison of living opposums with their fossilized counterparts of 70 million years ago demonstrates little change. Grasse (1977: 78) comments:

> Yet the opposums, which live in such widely different environments as damp forests, savannas, subdesert areas, and the edges of town, are subjected to conditions theoretically favorable to evolution. Some of their species...are widely distributed and mutate extensively. They are quite healthy relics, but they refuse to evolve.

When one realizes that the opposum is not a specialized animal, it is surprising from the perspective of continuity that no significant change has occurred in 70 million years.

Another example is the cockroach. When living cockroaches are compared to fossilized cockroaches approximately 280 million years old, little change is observed (Grasse, 1977: 87). In spite of 280 million years of mutations and changing environments, the body plan of the cockroach has not changed. Furthermore, the phenomenal reproductive rate of these organisms translates into a very large gene pool. Surely many advantageous mutations should have been selected for--yet the body plan has remained static.

Examples like these (see Eldredge and Stanely, 1984, for extensive documentation) could be multiplied many times over and the theme would remain the same. Species that have undergone millions of years of mutations, situated in varying environments which ought to be favorable to evolution, exhibit little or no change. Taken at face value, the fossil record clearly demonstrates stasis: we do not have to speculate about the reality of the phenomenon.

Molecular Data

The molecular evidence in support of stasis is equally convincing. In 1983, Martin Kreitman looked at eleven copies of the gene for alcohol dehydrogenase in *Drosophila melanogaster* (Kreitman, 1983). He found that 1.617% of the 2,659 nucleotides which

make up the gene are polymorphic. Of these polymorphic sites, only 14 were in coding regions (the remainder were in introns and flanking regions), and of those 14, only *one* resulted in an amino acid substitution. Using mathematical models, Kreitman determined that an immense bias exists towards silent substitutions (i.e., nucleotide changes which do not effect the amino acid specified).

Why is it that most of the differences in nucleotide sequence are found in noncoding regions of the gene? And for those differences within coding regions, why are the majority of substitutions silent? This bias is best explained by selection. Most mutations that occur in coding regions will alter the amino acid specified, disrupting proper function; hence, these mutations will be removed by selection. The reason we do not see more variation in the coding regions of genes is that the organisms carrying such mutations die (or have greatly reduced fitness). *It appears that the major role of selection at the molecular level is that of a conserving, not transforming, force.*

This conclusion is supported by a wealth of other molecular data. Clarke (1970) observed that for a particular protein, substitutions (in a variety of species) which were accompanied by small chemical changes were much more common that those associated with large chemical changes. Bogardt *et al.* (1980) looked at mammalian myoglobins; by making a residue-by-residue comparison and considering various physico-chemical properties of amino acids, they found that differences which are compatible with the retention of the original conformation of the protein appear to be favored. Kimura (1983) looked at the relationship between physico-chemical differences and the relative frequency of amino acid differences among various `homologous' proteins. He found a convincing negative correlation between the two: the greater the physico-chemical difference associated with a particular amino acid substitution, the smaller the rate of occurrence of such events.

This theme is repeated from other perspectives. Molecules which are functionally important show less dissimilarity between types of organisms when compared to functionally less important molecules. Extreme examples might include the fibrinopeptides and histones. Fibrinopeptides, which have little known function after they become separated from fibrinogen in the blood clot, demonstrate significant differences between types. In contrast, histone proteins--which play an essential role in DNA packaging--demonstrate little variability between types. In fact, when the histone H^4 (approximately 100 amino acids) of pea plant and calf thymus are compared, only two amino acid differences are seen (Isenburg, 1979). This is in spite of the fact that plants and animals supposedly diverged 1.2 billion years ago.

Different parts of the same molecule also demonstrate this same theme. Amino acid sequences which play a crucial role in the function of a particular protein demonstrate a rather stringent conservation when compared to amino acid sequences which do not. For example, Jukes (1971) looked at the amino acid sequences of vertebrate hemoglobins spanning a supposed evolutionary history of 500 million years. When he surveyed the position of the two histidines which bind to the heme molecule (and thus function importantly in the molecule), he found an almost complete invariance.

Among different types of organisms, functionally important molecules and functionally important parts of molecules demonstrate remarkable homogeneity: these molecules cannot tolerate significant change. If such change occurs, selection will work to prevent it from being propagated. As Fristrom and Clegg (1988: 689) explain:

> [T]he great majority of mutations in genes whose products play a central role in metabolism may disrupt function and lead to deleterious conditions. Such mutations are rapidly eliminated by selection and do not become part of the evolutionary record of nucleotide substitutions.

In other words, the indirect effects of selection seem to indicate that it works at the molecular level not as a force of major transformation, but as a force of stasis. Obviously, the selection pressure remained rather constant over time for all these important proteins.

One might argue that if selection pressures had changed, it is possible that these proteins could have evolved away from their basic types. To argue along these lines, however, is to place the cart before the horse--for the data indicate that selection pressures have *not* changed throughout nature and over hundreds of millions of years. Yet if numerous macroevolutionary events are behind the diversity of the living world, surely many important molecules must have changed radically. This seems unlikely, for randomly changing the very things which are most resistant to change does not translate into a very successful formula. At least that is what the molecular data are telling us.

Gene Duplication

How can an important molecule or structure change when the molecular data indicate that such transformations are doomed to failure? How is one gene transformed into another gene, if such changes will most often result in the loss of that gene, and thus the reduced viability or death of the organism "experimenting" with such changes? The most common explanation is the hypothesis of gene duplication (Markert *et al.*, 1975). Suppose that a particular gene which encodes for protein A is duplicated. If a functioning protein A is essential for the life of an organism, random changes in the gene for that protein will be lethal. But if there are now two copies of the gene, the situation is different. The ancestral gene can continue coding for protein A and thus important processes are maintained. The duplicate gene, howver, is free to accumulate mutations which might ultimately transform it into a different, functioning protein. Such a hypothesis seems plausible. Three lines of reasoning, however, suggest that this mechanism is probably insufficient to generate enough new genetic material to account for all the transformations which must have occurred.

First, consider the larger perspective. A common example of putative gene duplication concerns the oxygen transport molecules myoglobin and hemoglobin. Myoglobin is assumed to be the ancestral molecule (where did it come from?). About 650 million years ago, the myoglobin gene was supposedly duplicated, and the new

gene for [alpha] hemoglobin was formed. Subsequent duplications and divergences led to the addition, in this gene `family,' of [beta]-hemoglobin, [gamma]-hemoglobin, and [delta]-hemoglobin.
Yet even if this hypothesis is correct, not much change has really occurred. Lester and Bohlin (1984: 91) comment:

> After 650 million years of duplication and subsequent mutation, the various genes have not escaped their basic function of oxygen transport. Once an oxygen transporting gene, always an oxygen transporting gene.

If such a transformation did occur, it was still constrained by some form of stasis. What mechanisms of stasis might exist to constrain these types of molecules from transforming into something really different? I would now like to suggest two possible mechanisms which cast doubt on the efficacy of gene duplication.

Protein Degradation

One mechanism which may counteract gene duplication is protein degradation. Inside a cell, proteins do not exist in static pools. Instead, they are in a dynamic state of constant turnover. New proteins are made to replace old proteins (which are broken down). Hershko and Ciechanover (1982) define several classes of cellular proteins in terms of their degradative properties. Long-lived proteins, which constitute the majority of cellular proteins, have a slow turnover rate. Short-lived proteins have an exceptionally high turnover rate. Abnormal proteins, which may arise from mutations or errors in RNA/protein synthesis, are broken down more rapidly than short-lived proteins.
The rate of degradation of abnormal proteins is impressive. In *E. coli*, normal [beta]-galactosidase is completely stable, but if incomplete chains are synthesized, they are broken down in a few minutes (Zubay, 1988). Hemoglobin is a remarkably stable molecule which lasts the life span of the red blood cell. However, if a synthetic analog for the amino acid valine is incorporated into the newly forming hemoglobin, the resulting polypeptide is broken down with a half-life of about ten minutes. According to Zubay (1988: 968), cells have "very efficient mechanisms to recognize and quickly degrade the damaged proteins."
One polypeptide thought to play an important role in eukaryotic protein degradation is ubiquiton (Zubay, 1988: 968). Ubiquiton has been detected in all eukaryotes examined and its amino acid sequence is remarkably conserved (Hershko and Ciechanover, 1982). It works by covalently linking, in an ATP-dependent series of reactions, to the lysine residues of abnormal proteins. This linking marks the protein for rapid degradation by other cellular proteases.
Another protein involved in prokaryotic protein degradation is protease La (Swamy and Goldberg, 1981). This enzyme degrades nonsense polypeptides, missense proteins, and other abnormal proteins.

Although such processes are just beginning to be elucidated, it is quite apparent that they play a crucial and finely controlled role in the life of the cell. Their significance is obvious: by preserving the status quo, these processes seriously challenge notions of transformation at the molecular level.

If gene duplication is to have any relevance, novel proteins ultimately had to be formed. For example, the duplicated gene may be copied in such a way that it is no longer expressed. At this point, it would accumulate mutations at the rate of a pseudogene. Some time later, the gene may then be `reactivated,' resulting ultimately in the production of a novel protein. Although the protein degradation processes would be irrelevant while the gene is actually mutating, once the product is finally expressed their role becomes evident. Since the duplicated gene mutated without being expressed, selection could not edit this process. It is highly likely that the gene product would be chaotic in structure and thus be recognized by the protein degradation processes. And even if the new protein were to escape those processes, it is unlikely to be functional simply because it was "redesigned" randomly.

I should also mention that there are difficult problems associated with reactivating a silent gene. Li (1983: 29) argues:

> [T]he probability of reactivation would still be very small...because a pseudogene often contains multiple major defects such as frameshifts, which cannot be easily corrected.

These problems seem to negate the effectiveness of this method of gene duplication. Another route is to allow the duplicated gene to continue expressing its product constitutively as it undergoes mutation. Although this route would bypass the problems associated with random changes and reactivation, the gene product would be opposed constantly by protein degradation processes. Most proteins exist in a three-dimensional, globular state. But to change one form of protein into another form would include a significant amount of gradual unfolding and refolding. This process of unfolding and refolding is likely to cue the degradative processes.

The protein degradation processes constitute a selective force to constrain molecular structure and therefore function. Selection would work to maximize the resistance to these proteases. And how is this accomplished? Simply by minimizing the change in protein structure. The less a protein changes, the lower the likelihood that that protein will encounter degradation processes.

One should also note that these processes of protein degradation use energy (Ciechanover *et al.*, 1984). Any organism "experimenting" with the production of abnormal proteins as a result of gene duplication and mutation would be investing huge amounts of energy, just to degrade these proteins during the long intervening period between functional states. Any organism experimenting with protein modification is likely to be at an energetic disadvantage compared to organisms which minimized such "experiments."

It seems implausible that a new functional protein could form randomly over thousands of years, when abnormal proteins are degraded in minutes. Do abnormal proteins--usually degraded rapidly--really constitute the raw materials of gradual evolution?

Gene Conversion

If gene duplication is to be a source of new functional proteins, it must also overcome the DNA repair processes expressed in gene conversion. To better understand the significance of gene conversion, one should consider an interesting property of multigene families.

Many essential intracellular molecules are encoded for by multiple copies of a gene. One example concerns the rRNA genes (Fristrom and Clegg, 1988: 677). Approximately 600 copies of the rRNA genes are found in the frog *Xenopus*, arranged on the chromosome as tandem repeats. When the genes were mapped and seqeunced, a striking discovery was made: *the multiple copies within the species were nearly identical*.

How could this be? Surely mutations should have accumulated in these multiple copies, creating significant differences among them. What forces are at work to maintain the homogeneity of 600 copies of a particular gene?

Since rRNA genes are essential to the life of the organism, changes are likely to be detrimental; selection, then, might appear to be an obvious candidate. Given the great multiplicity of these genes, however, it is hard to see how selection could work to eliminate new mutations. For example, a mutation in one gene is unlikely to have a perceptible effect because the non-functional gene product is greatly outnumbered by the hundreds or thousands of wild type, functional gene products.

The most widely accepted mechanism for maintaining this homogeneity of multiple gene copies is *gene conversion* (Li *et al.*, 1985). Gene conversion is the consequence of heteroduplex formation and DNA repair (see Figure 1). In essence, two sequences from two different strands of DNA interact in such a way that one is converted by the other. Where once there was diversity, there is now homogeneity. Gene conversion works to maintain the homogeneity of repeated sequences (see Figure 2, which illustrates only one round of gene conversion). It should be obvious that this process would continue until the mutation either spreads or is lost.

Now consider the process of gene duplication. Two identical copies of a gene are made. This means that a multigene family is being created! The door is now open for gene conversion to work, in opposition to the functional divergence which the theory of gene duplication assumes will follow. In other words, if one copy of the duplicated gene undergoes mutation, gene conversion will work to eliminate the resulting diversity. As Li *et al*. (1985: 72) write:

> [I]f there are only two repeats on a chromosome, a single intrachromosomal gene conversion will lead to homogeneity of the repeats on the chromosome.

Quantitative data exist to support this hypothesis. When the mutation rate--which generates diversity--is compared to the rate of gene conversion--which generates homogeneity--one finds that the frequency of gene conversion is "clearly much higher than the frequency of mutation" (Klein and Petes, 1981). Douglas Futuyma (1983: 141) notes that an average gene mutates at a rate of 10 -5 per generation. On the other hand, experimental evidence demonstrates that the frequency of gene conversion is approximately 10 -2 per generation (Klein and Petes, 1981; Klein, 1984). It is important to emphasize that such frequencies were obtained by studying the interactions of only two copies of a particular gene. This makes it possible to validly extrapolate such frequencies to the post-gene duplication state (where two copies of a particular gene exist). The evidence indicates that gene conversion occurs one thousand times more often than the mutation rate. Thus, it is highly improbable that on its way to a novel function, a duplicated gene could continually escape gene conversion processes.

It seems clear that gene conversion will maintain the original allele. If gene conversion worked to spread the mutation to both alleles instead of eliminating it, selection would likely eliminate such changes. Remember the attractive feature of gene duplication is that one gene can continue to produce its essential gene product while the other is free to accumulate changes. But if gene conversion spreads the mutations, this feature is lost. We are back to suggesting that essential molecules can tolerate random changes.

Given the homogeneity of multigene families in spite of mutations, gene conversion seems to be at work. And not only would it work to maintain this homogeneity, it would oppose the divergences which supposedly follow gene duplication, and thus would constitute a mechanism of stasis.

Other Possible Mechanisms of Stasis

We have seen that stasis is evident in the fossil record and in the molecular data. We have also seen that the popular notion of gene duplication inadequately explains significant molecular transformations. When all this is added to the absence of a working mechanism for macroevolution, the case for continuity seems weak. Perhaps it is time to consider seriously possible mechanisms of stasis.

I propose that mutational changes must travel through several levels of stasis before becoming fixed in a population. When these mechanisms are considered *in toto*, it is unlikely that theories of continuity can account for the diversity of body plans and molecules we observe.

A battery of DNA repair enzymes and pathways make up the first level of post-replicational stasis. Through a variety of mechanisms, mutations are recognized and corrected to restore the original nucleotide sequence (Kornberg, 1980: 607-624). Although these mechanisms cannot drive the mutation rate to zero, they are finely tuned to minimize it (Haynes, 1988: 577-584). The processes involved in gene conversion are part of this level of stasis.

The second level of stasis is post-translational. As we have already seen, a variety of protein degradation systems recognize and eliminate abnormal proteins. For one type of organism to transform into another type, some new proteins would have to be formed through gradual mutation. Yet these biochemical reactions would serve as a powerful force oppposing novel change.

The third level of stasis is nuclear-cytoplasmic. Regulatory molecules which interact with the DNA may serve as a process which prevents radical change and further retards the extremely slow process of neo-Darwinian transformation. Experimental research with nuclear transplants (which remove the nucleus from one cell, and replace it with the nucleus from another cell) suggest this.

One illuminating experiment involved the removal of the nucleus from the egg of the frog *Xenopus laevis laevis* (Gurdon, 1962). This enucleated egg then received the nucleus from the embryo of *Xenopus tropicalis*. The resulting egg never developed beyond the late neurula stage. If it received the nucleus from an embryo of *Xenopus laevis laevis*, however, it developed into an adult frog.

Other researchers conducted similar experiments with two protozoans, *Amoeba proteus* and *Amoeba discoides* (Yudin, 1979). When the nucleus from *A. proteus* was transplanted into an enucleated cell of the same species, 90% of the cells survived. However, if the nucleus from *A. discoides* was transplanted into the enucleated cell of *A. proteus*, only 1% of the cells survive. This phenomenon is known as transplantation incompatibility (Yudin, 1979: 66).

Experiments like these clearly suggest that DNA alone is insufficient to guide the development of an animal, or insure the survival of protozoans. Cytoplasmic regulatory molecules probably exist to decode the DNA. It is possible that there must be a correct distribution of such molecules and/or the correct affinity for the DNA if proper gene expression is to occur. What might be happening is this: when the nucleus from species A is placed in the enucleated cell of species B, the regulatory molecules in the cytoplasm of B cannot properly decode the DNA of A. From such results, J.M. Barry (1986) concludes:

> The possibility is often overlooked that each generation of organisms must inherit not only DNA from the previous generation but also other cell components peculiar to that species.

This phenomenon would seem to preclude macromutations. For example, if the DNA of an egg undergoes a major mutational reconstruction which might now encode for a novel protein and/or pathway, it is highly improbable that simultaneous mutations would produce the necessary regulatory molecules to express these new features properly. Yet if these unlikely mutations are not simultaneous, the embryo will not develop successfully.

Barry (1986) argues, however, that this phenomenon does not preclude neo-Darwinian evolution. He writes:

> In the development of new species, mutations in DNA produce changes in the structure of other cell components which in turn allow the survival of further mutations in DNA.

Although this may look plausible in principle, when one considers the extreme rarity of advantageous mutations in general, it certainly appears that such a mechanism will be unable to generate the great diversity of form and function found in nature. After all, you can slow down a gradual process only so much before it becomes undetectable.

The fourth level of stasis is populational. Assume that a mutation occurs, somehow bypasses the DNA repair mechanisms and protein degradation processes, and does not interfere with the cytoplasmic regulatory mechanisms. Unless this mutation is advantageous, and has a very high selective coefficient (rare events in themselves), its frequency in a population will remain very low. Thus, these alleles are likely to be lost by random drift (where the probability of being lost is 1-1/2N, where 2N = the number of genes in a diploid population).

Even if the mutation bypasses the cellular mechanisms of stasis, spreads to a significant percentage of the population, and is advantageous, major transformations still appear improbable. This is because *microevolutionary changes* may be yet another process that maintains stasis.

This may seem paradoxical. But a commonly cited example of microevolution--industrial melanism--will illustrate the point. As a result of strong selective forces, the melanic forms of the moth *Biston betularia* almost completely replaced the non-melanic forms. Had *Biston betularia* lacked the requisite genetic variability for color, the species may have become extinct. Too much stasis is deleterious to a species. Limited variability, on the other hand, works to allow the species to continue to exist as that species under adverse conditions. After all, *Biston betularia* responded to environmental challenges, and changed, *as Biston betularia*. Microevolution works as a force of stasis *by allowing a species or type to continue to exist as that species or type under modified environmental conditions*.

Another example may be helpful. Bacteria exhibit remarkable homogeneity in both morphology and biochemistry. Yet, on a lower level, one may observe a striking amount of plasticity. Consider antibiotic resistance: a bacterial colony normally sensitive to an antibiotic may become resistant to that antibiotic. The antibiotic streptomycin, for instance, interacts with bacterial ribosomes, disrupting normal protein synthesis. Ordinarily, this disruption will kill the affected bacteria. Yet some bacteria have mutations in the genes for their ribosomal proteins, which allow their ribosomes to function, unhindered by streptomycin (Zubay, 1988: 957).

Yet note that the mutated ribosome is still typically bacterial. If the bacterial ribosome had become eukaryotic-like, streptomycin resistance would also be observed--but bacteria change *as bacteria*, not by transforming into another type. The minor biochemical changes associated with such bacterial 'evolution' work to preserve the bacteria type. Transformations to non-bacterial characteristics are not observed.

Microevolutionary changes do not modify basic types; rather, they serve to adapt organisms *within* their types. Change is subservient to stasis on a higher level.
One could argue at this point that such 'minor' changes, extrapolated over millions of years, could result in macroevolutionary change. But the observational evidence will not support this argument. In the bacterial example just given, the ribosome did not deviate from the prokaryotic type to which it belonged. In fact, even the novel metabolic capabilities discovered by Barry Hall's research with *E. coli* (Hall, 1983) cannot be said to have transformed these bacteria into a new species. And certainly, the boundaries of the bacterial type to which *E. coli* belong have not been violated. Thus, the changes observed in the laboratory are not analogous to the sort of changes needed for macroevolution. Those who argue from microevolution to macroevolution may be guilty, then, of employing a false analogy--especially when one considers that microevolution may be a force of stasis, not transformation.
The fifth level of stasis is natural selection. For purposes of clarity, Kimura (1983: 118) classifies natural selection into two distinct types, positive and negative selection. Positive, or directional, selection works to spread an advantageous mutation or trait throughout a population. Kimura notes that:

> Despite its biological importance, positive selection is seldom observed at work in nature.

Negative, or stabilizing, selection is much more common in nature. It works to eliminate deleterious mutations or traits. Kimura notes that when compared to positive selection, examples of negative selection are much more abundant. Studies of mutations in *Drosophila*, for example, have "shown beyond a doubt that the majority of these mutant genes are unconditionally deleterious both in homozygous and heterozygous states" (Kimura, 1983: 118).
It should come as no surprise that natural selection works like this most of the time. Complex organic designs are composed of interdependent structures, most (or all) of which must be present simultaneously to offer any selective advantage. Natural selection acts to eliminate the useless incipient stages through which any major structural or functional innovation must pass. In so doing, it inhibits major evolutionary change and promotes stasis. Soren Lovtrup (1987: 274) reminds us that this criticism of Darwinism is longstanding:

> Darwin complained that his critics did not understand him, but he did not seem to realize that almost everybody, friends, supporters and critics, agreed on one point, his natural selection cannot account for the origin of the variations, only for their possible survival. And the reasons for rejecting Darwin's proposal were many, but first of all that many innovations cannot possibly come into existence through accumulation of many small steps, and even if they can, natural

> selection cannot accomplish it, because incipient and intermediate stages are not advantageous.

For those who must describe the history of life as a purely natural phenomenon, the winnowing action of natural selection is truly a difficult problem to overcome. For scientists who are content to describe accurately those processes and phenomena which occur in nature (in particular, stasis), natural selection acts to prevent major evolutionary change.

This aspect of selection correlates well with the fossil record. Fossil evidence indicates that phyla stopped appearing first, followed by classes and then orders. All modern phyla, for example, can be traced to the early Cambrian, and no new phylum has arisen in over 500 million years. One explanation for this pattern holds that novel body plans are excluded by competition and the lack of open adaptive space; thus, natural selection prevents major evolutionary change and promotes stasis.

Conclusion and Prospects for Research

I have suggested possible mechanisms to account for the stasis observed in fossil and molecular data (see Table I). These mechanisms work at different levels, from gene sequences at one end to populations on the other (Figure 3). As a mutation travels through each level of stasis, less and less real transformation is likely to be realized. When one considers the already extemely slow process of neo-Darwinian evolution, macroevolution--which requires novel structures and functions--seems unlikely.

Given the overwhelming preoccupation with demonstrating change, it is remarkable that possible mechanisms for stasis are relatively easy to find. One can only wonder how our theoretical and explanatory landscape would appear, if even a small fraction of the energy spent on supporting theories of continuity were instead spent on examining the various phenomena of discontinuity.

Perhaps the most exciting point about hypotheses of stasis is that, unlike theories of macroevolution, *they are all testable and subject to experimental falsification.* Site-directed mutagenesis can be used to test notions of functional constraint in proteins, to determine whether supposed evolutionary transformations are possible. The exact relationship between mutations and the protein degradation systems can be examined. The cytoplasmic regulatory molecules can be sought experimentally, and their role in gene expression studied. One could even predict that certain genes may be more resistant to mutation than other genes. It has already been determined that actual mutation rates appear to differ among different genes (Wolfe *et al.*, 1989). The list can go on, but it is clear that there is much room for genuine scientific research into the possible mechanisms of stasis.

It is time to take stasis seriously, regardless of its philosophical implications, and attempt to account for it through rigorous scientific research.

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