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## THE POSTULATED EVIDENCE FOR MACROEVOLUTION AND DARWINISM: DARWINIAN ARGUMENTS AND THE DISINTEGRATING NEO-DARWINIAN SYNTHESIS—PART II

W. R. BIRD\*

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### Abstract

*Part I discussed three of the eight primary lines of evidence offered for macroevolution and Darwinian mechanisms. Part II addresses the remaining arguments for macroevolution and Darwinian mechanisms. Evolutionists are cited who suggest that (1) the "facts of comparative anatomy provide no evidence for evolution," while the "attempt to find homologous genes has been given up as hopeless"; (2) the embryological argument used to center on a biogenetic "law" that has "been demonstrated to be wrong by numerous subsequent scholars," and now stands on the problem that "[a]natomically homologous parts in different related organisms appear to have quite different origins"; (3) the comparative biochemistry argument offers a "serious . . . challenge to the whole evolutionary framework" rather than support, by widespread anomalies that require "a robust rejection of a generalized molecular clock hypothesis of DNA evolution"; (4) the population genetics argument has made "no direct contribution to what Darwin obviously saw as the fundamental problem: the origin of species," and "is merely the blind leading the blind"; and (5) the artificial selection argument overlooks that "selective breeding is not analogous to the action of 'natural selection'."*

*All scientists mentioned in this article are evolutionists unless otherwise identified. All emphases in the quotes is the author's.*

### Comparative Anatomy and Physiology Argument and Difficulties

The comparative anatomy argument for macroevolution, which focuses on comparing anatomical structure (Stansfield, 1977 p. 113) is based on the similarity of structure of various organisms. Most evolutionists

interpret some, but not all, similar structure to show common ancestry. The comparative anatomy evidence that is anomalous, in the sense of indicating the unrelatedness or distinct ancestry of organisms, is treated fully elsewhere (Bird, 1987, pp. 94-8). The comparative anatomy and physiology argument is constructed on a problematic foundation that can be viewed causally and historically.

This basic problem is that similar anatomy or physiology does not necessarily indicate common ancestry and evolutionary descent. First, nearly all evolutionist

\*W. R. Bird, J. D., receives mail at 1150 Monarch Plaza, 3414 Peachtree Road, N.E., Atlanta, Georgia 30326. This article is excerpted from section 3.4 of his book, *The Origin of Species Revisited: The Theories of Evolution and of Abrupt Appearance*. Philosophical Library, New York.

scientists acknowledge that "there exists no *a priori* relation between the appearance of two structures and their relatedness," as Schwabe and Warr (1984, p. 468) state along with Cracraft (1981, p. 32), Denton (1985, p. 178), Patterson (1981, p. 217), and Macbeth (1971, pp. 13, 16). Boyden adds that:

such general resemblances in protoplasmic systems as we find in *all* living organisms *do not necessarily mean genetic relationship*. Rather, such resemblances may be fundamentally convergent, and represent only the minimum requirements or "conditions of existence" which all living systems must possess. (1973, p. 27).

Yet T. H. Morgan (1923, p. 246) acknowledged the fatal consequences if homology did not necessarily indicate ancestry:

If, then, it can be established beyond dispute that similarity or even identity of the same character in different species is *not always* to be interpreted to mean that both have arisen from a *common ancestor*, the *whole argument from comparative anatomy seems to tumble in ruins*.

There are two types of similarities that indisputably do not mean common ancestry: convergences and parallelisms, and homologous structures with nonhomologous genes.

Second, the convergences and parallelisms to which Boyden referred (anatomical or physiological similarities that do not reflect common ancestry) are strong arguments that similar anatomies or physiologies "do not imply any close biological relationship," as Denton (1985, p. 178) notes:

Then there is the problem of convergence. *Nature abounds in examples of convergence . . .* In all the above cases the similarities, although very striking, *do not imply any close biological relationship*.

Numerous acknowledgements were cited in Bird (1987, pp. 94-8) of "massive convergence"—"the bugbear of the taxonomist"—as Dawkins (1986, p. 269) describes it. So widespread are convergences and parallelisms that, Ross (1981, p. 2153) concludes, "[m]ore often than not functional comparisons turned up phylogenetic paradoxes instead of parallels."

In fact, third, the assumption that similar anatomy indicates common ancestry is generally wrong, because the genes that produce the similar anatomical structures are generally not sufficiently similar (homologous), as de Beer (1971, p. 15) points out:

It is now clear that the pride with which it was assumed that the inheritance of homologous structures from a common ancestor explained homology was misplaced; for such inheritance cannot be ascribed to identity of genes. *The attempt to find homologous genes, except in closely related species, has been given up as hopeless . . .* It is useless to speculate on any explanation in the absence of facts.

Thus Zuckerman (1970, p. 64) agreed that "relationships which are inferred on the basis of comparative anatomy may not necessarily correspond to true ge-

netic relationships," and "are in the final analysis speculations." For similar reasons, transformed cladists generally reject the alleged relation between similar anatomy and common ancestry, even though they classify organisms by some similar anatomical features (synapomorphies), because such cladists argue that similar features "need have no evolutionary implications." (Patterson, 1981, p. 208; 1982, p. 364).

Furthermore, an equally basic difficulty is that this alleged relation to common ancestry is contradicted by the history of comparative anatomy and physiology. Linnaeus, "the father of systematic biology" and a creationist scientist, established the classification system by grouping organisms that "resemble one another in body structure" (anatomy), but "did not interpret this propinquity as a consequence of common descent," Dobzhansky (1982, p. 734) observed. The anti-Darwinian scientist Owen then developed the basis of comparative anatomy, while disagreeing that it supports evolution:

The central concept of comparative anatomy is *homology*, a term introduced by Sir Richard Owen, the first director of the British Museum (Natural History), London, and a powerful anti-evolutionist (Patterson, 1978, pp. 121-2).

Therefore, the comparative anatomy argument "provides no evidence for evolution," in Denton's words (1985, p. 155):

In the last analysis the *facts of comparative anatomy provide no evidence for evolution* in the way conceived by Darwin, and even if we were to construe with the eye of faith some "evidence" in the pattern of diversity for the Darwinian model of evolution this could only be seen, at best, as indirect or circumstantial. . . .

The same deep homologous resemblance which serves to link all the members of one class together into a natural group also serves to distinguish that class unambiguously from all other classes. Similarly, the same hierarchic pattern which may be explained in terms of a theory of common descent, also, by its very nature, implies the existence of deep divisions in the order of nature. *The same facts of comparative anatomy which proclaim unity also proclaim division*; while resemblance suggests evolution, *division*, especially where it appears profound, *is counter-evidence against the whole notion of transmutation*.

Similarly, the comparative physiology argument has "not contributed much" to knowledge about macro-evolutionary relationships, in Ross's assessment (1981, pp. 2153-4):

It is an unspoken assumption that the data of comparative physiology must have implications for phylogeny. Is this realistic? . . .

Without multiplying the examples, one can safely say that the *data of comparative physiology have not contributed much to our views about phylogenetic relationships*. That is not to say that these data are irrelevant for theories of evolutionary processes . . .

It seems that *most of the stated aims and general objectives of comparative physiology in all its*

aspects have been unfulfilled. "Illusory" may be too strong a word to describe these objectives but, as I hope to show, it is not just that these objectives have been unrealized but *probably that they are unrealizable*.

The basic difficulties with the comparative anatomy argument are that similarity "may not correspond to the genetic relationships" (Denton, 1985, p. 178), and the "attempt to find 'homologous' genes has been given up as hopeless." (de Beer, 1971, p. 15). In this area, the biological theories of macroevolution and Darwinism are not compelling.

### Comparative Embryology Argument and Difficulties

The comparative embryology argument for macroevolution, which focuses on the embryology or development of tissues and organs in a particular organism, (Stansfield, 1977, p. 103), arises from the similarity of development of organs and tissues in various organisms. Most evolutionists view that similar development reflects common ancestry and descent. This argument too faces serious difficulties that many evolutionists acknowledge.

First, the "biogenetic law" was the center of the embryology argument for early Darwinists, and stated that "the embryological development (ontogeny) of an organism repeats (recapitulates) the evolutionary history (phylogeny) of its species." (Stansfield, 1977, p. 104). That biogenetic law has "been demonstrated to be wrong by numerous subsequent scholars." according to Bock (1969, p. 684):

the *biogenetic law* was widely accepted by biologists and served as the basis for the surge of embryological research that continues unabated to this day. Moreover, the biogenetic law has become so deeply rooted in biological thought that *it cannot be weeded out* in spite of its having been demonstrated to be wrong by numerous subsequent scholars. Even today both subtle and overt uses of the biogenetic law are frequently encountered in the general biological literature as well as in more specialized evolutionary and systematic studies.

Raup and Stanley (1978, p. 354) call the biogenetic law "largely in error," Ehrlich and Holm (1963, p. 66) note its "shortcomings" and yet its place in "biological mythology"; Danson (1971, p. 35) says that it is "intellectually barren"; de Beer (1965, p. 331) refers to the "evidence against the 'biogenetic law' or recapitulation in Haeckel's sense"; Bonner (1961, p. 242) calls it "probably nonsense"; Robinson (1976, p. 610) calls it "in error"; and even Mayr (1982, p. 215) describes the biogenetic law as "invalid." In fact, Haeckel, the formulator of the "biogenetic law," supported it with fraudulent drawings (Rager, 1986, p. 449; Singer, 1931, p. 487).

Second, the modern embryological argument shares the same foundational problem as the comparative anatomy argument, with which it is "very closely related," (Stansfield, 1977, p. 113): that similar embryological development does not necessarily indicate common ancestry and evolutionary descent (Bird, 1987, pp. 193-6). Oldroyd (1986, p. 154) describes one aspect of the problem:

Anatomically homologous parts in different related organisms appear to have quite different embryonic origins. This is almost *impossible to reconcile with orthodox Darwinian or neo-Darwinian theory*, and it is by no means evident at the time of writing how such problems may be overcome.

Third, the vestigial organ aspect of this embryology argument (that modern organs with no use or reduced usefulness are vestiges of evolutionary stages with former usefulness) is "invalid," as zoologist Scadding (1981, pp. 173, 175, 176) notes:

An analysis of the difficulties in unambiguously identifying functionless structures and an analysis of the nature of the argument, leads to the conclusion that '*vestigial organs*' provide no evidence for evolutionary theory. . . .

I would suggest that the *entire argument* that vestigial organs provide evidence for evolution is *invalid on two grounds*, one practical, the other more theoretical. The practical problem is that of unambiguously identifying vestigial organs, i.e., those that have no function. The analysis of Wiedersheim's list of vestigial organs points out the difficulties. As *our knowledge has increased the list of vestigial structures has decreased*. Wiedersheim could list about one hundred in humans; recent authors usually list four or five. Even the current short list of vestigial structures in humans is questionable . . . .

Similarly, for other 'vestigial organs' there is reasonable ground for supposing that they are functional albeit in a minor way. . . .

The other major objections to citing vestigial organs as evidence of evolution is a more theoretical one based on the nature of the argument. The 'vestigial organ' argument uses as a *premise* the assertion that the organ in question has no function. There is *no way however, in which this negative assertion can be arrived at scientifically*. . . .

Since it is not possible to unambiguously identify useless structures, and since the structure of the argument used is not scientifically valid, I conclude that '*vestigial organs*, provide *no special evidence for the theory of evolution*.

The alleged vestigial organs—such as human "gill slits" (which do not exist), (Langman, 1975, p. 262), male nipples, Wolffian and Mullerian ducts, tonsils, appendix, coccyx ("tail bone"), thymus, and facial muscles—almost all have been found to have functions and not to be vestigial:

A fourth category of *vestigial organs* would be those that are the *vestiges of the reproductive structures of the opposite sex*, e.g., nipples in men, vestiges (in the female) of the Wolffian duct, and (in the male) of the Mullerian ducts. These structures, however, clearly reflect the embryonic development of a sexually dimorphic organism which begins its development in a sexually indifferent condition with structures characteristic of both sexes. They certainly do *not reflect phylogenetic development*. No one supposes males evolved from females or vice versa. On the basis of

this analysis, I would suggest that *Wiedersheim was largely in error in compiling his long list of vestigial organs. Most of them do have at least a minor function at some point in life.* (Scadding, 1981, pp. 173-6).

Thus, the comparative embryology argument for biological macroevolution and Darwinism also offers little support, in the view of many evolutionists. In the embryology area, the biological theories of macroevolution and Darwinism are not compellingly established.

### Comparative Biochemistry Argument and Difficulties

The comparative biochemistry argument for macroevolution centers around "homologies at the molecular level" that evolutionists believe reflect "the degree of genetic relationship [in which] evolutionary lineages are optimally expressed" (Stansfield, 1977, p. 125). Those molecular comparisons involve the similarity of hemoglobin, cytochrome *c*, insulin, and other molecules in various organisms (Stansfield, 1977, pp. 125-7). The argument from some molecular similarities to macroevolution (common ancestry) and to Darwinian mechanisms involves several difficulties that numerous evolutionists acknowledge. First, the comparative biochemistry evidence that is anomalous, in the sense of indicating significant differences between allegedly closely related organisms, is so widespread that it may instead better support the unrelatedness or distinct ancestry of natural groups of organisms (Bird, 1987, pp. 98-103).

Those widespread anomalies lead Denton (1985, p. 291), a molecular biologist, to conclude that comparative biochemistry contradicts macroevolution:

This new era of *comparative biology* illustrates just how erroneous is the assumption that advances in biological knowledge are continually confirming the traditional evolutionary story. There is no avoiding the *serious nature of the challenge to the whole evolutionary framework* implicit in these findings.

For example, a study of cytochrome *c* by Jukes and Holmquist (1972, p. 530) reveals "anomalies" showing amphibians and reptiles to be more distant in an evolutionary sense than a bird and a fish, a mammal and a fish, or a mammal and an insect:

In either case, certain anomalies appear in certain vertebrates with respect to the magnitude of these changes and their relationship to time. Such anomalies show up on "phylogenetic trees" as apparently negative rates of evolutionary divergence, or incorrect taxonomic placement of an organism in the wrong family . . . . However, the difference *between turtle and rattlesnake of 21 amino acid residues per 100 codons is notably larger than many differences* between representatives of widely separated classes, for example, 17 between chicken and lamprey, or 16 between horse and dogfish, or even 15 between dog and screw worm fly in two different phyla.

Macroevolution and Darwinism, by contrast, involve an evolutionary sequence from invertebrates (including insects) to vertebrate fish, to amphibians, to rep-

tiles, to birds and mammals. Studies of relaxin by biochemists Schwabe and Warr (1984, p. 471) similarly "do not fit the evolutionary clock model" for comparative biochemistry:

Thus the conclusion to be drawn from the *relaxin sequence data* is that they *do not fit the evolutionary clock model*. The alternative models, those based on positive selection, depend on spurts of mutation fixation or a hypothetical gene duplication whenever a molecule does not fit into a monophyletic evolutionary tree. In fact, the neo-Darwinism of molecular evolution is used exclusively to fit molecular data into paleontologically derived evolutionary trees which in themselves are controversial. That is, the hypothesis is *not based on independent scientific reasoning* that would allow predictions to be made and tested.

Studies of DNA by Vawter and Brown (1986, p. 194) yield such anomalies that the authors call for throwing out the molecular clock hypothesis entirely:

[The] disparity in relative rates of mitochondrial and nuclear DNA divergence suggests that the controls and constraints under which the mitochondrial and nuclear genomes operate are evolving independently, and provides evidence that is independent of fossil dating for a *robust rejection of a generalized molecular clock hypothesis of DNA evolution*.

Many other anomalies, which also "do not fit the evolutionary clock model," were given elsewhere (Bird, 1987, pp. 98-103).

Second, the "molecular clock" of comparative biochemistry is conceptually flawed, as Denton (1985, p. 305) describes:

The difficulties associated with attempting to explain how a family of homologous proteins could have evolved at constant rates has created chaos in evolutionary thought. The evolutionary community has divided into two camps—those still adhering to the selectionist position, and those rejecting it in favour of the neutralist. The devastating aspect of this controversy is that neither side can adequately account for the constancy of the rate of molecular evolution, yet each side fatally weakens the other. The selectionists wound the neutralists' position by pointing to the disparity in the rates of mutation per unit time, while the neutralists destroy the selectionist position by showing how ludicrous it is to believe that selection would have caused equal rates of divergence in "junk" proteins or along phylogenetic lines so dissimilar as those of man and carp. Both sides win valid points, but in the process the credibility of the *molecular clock hypothesis is severely strained* and with it the whole paradigm of evolution itself is endangered.

There is simply *no way of explaining how a uniform rate of evolution could have occurred in any family of homologous proteins* by either chance or selection; and, even if we could advance an explanation for one particular protein family, we would still be left with the *mystifying problem*

*of explaining why other protein families should have evolved at different rates.*

In fact, the common explanation of inconvenient anomalies, as the result of different rates of molecular evolution used, for example, by Jukes and Holmquist (1972, p. 530) in connection with the cytochrome *c* results, is simply an "ad hoc argument" that resets the molecular clock whenever it is convenient to macroevolution, as Schwabe (1986, p. 280) notes:

Consider species A suddenly divided into A1, A2 and A3 by insurmountable obstacles. . .

If instead of the expected equal distribution of differences one were to observe that the insulins of A1 and A2 differ by four residues whereas the insulin of A3 differs by 25 residues from both A1 and A2 then one would have discovered *an exception to the neo-darwinian hypothesis*. There are virtually no degrees of freedom in this scenario so that *contradiction can be smoothed over only by ad hoc arguments* such as faster rates of evolution, lateral gene migration or gross errors committed by paleontologists in determining the time of branching of A1, A2 and A3.

Third, the accuracy of the "molecular clock" is unsatisfactorily poor, because the techniques for measuring molecular distance are all unsatisfactory, according to Farris (1981, p. 22):

It seems that the only general conclusion one can draw is that *nothing about present techniques for analysing molecular distance data is satisfactory*. The distance Wagner method seems to be the best available method for arriving at genealogies efficiently—certainly it is far more effective than Prager and Wilson imagined—but, at least for minimizing WSD, further improvement seems possible. But using any method that fits branch lengths to a distance matrix *presupposes* that the distances are suitable for this sort of analysis. That supposition seems *unjustified* for any distance measure now in use.

*None of the known measures of genetic distance seems able to provide a logically defensible method*, and it appears that some altogether different approach will have to be adopted for analysing electrophoretic data . . .

*Sequence data* have sometimes been analysed by way of distances, although perhaps more often they have been treated by character analysis methods (for example Goodman et al., 1979). While sequence differences do not seem to offer the severe problems of interpretability of branch lengths that plague genetic distances, *neither is there any good reason to rely on distance techniques*. Reducing character data to distances, once again, simply wastes evidence on kinship.

*Immunological distances, like genetic distances, cannot be truly clocklike*, nor can they be analysed by branch length fitting, but there is no recourse to underlying character data in this case. . . .

Farris is more qualified than almost anyone to analyze those techniques, because he developed one of the most used techniques for measuring molecular distance.

Fourth, the comparative biochemistry argument, like the other comparative arguments, in any event is based on the problematic assumption that similarities between organisms reflect common ancestry rather than engineering design or basic conditions for life:

It could be argued that the universality of much of biochemistry is *merely consistent* with the concept of a common ancestral population but does not in any sense prove it since the *same basic reaction patterns may be required for all life* (Kenyon and Steinman, 1969, p. 2154).

Therefore, the comparative biochemistry argument for macroevolution and Darwinism involves a "molecular clock" that does not work and is simply an "apologetic tautology," according to Denton (1985, p. 306):

The hold of the evolutionary paradigm is so powerful that an idea which is more like a principle of medieval astrology than a serious twentieth-century scientific theory has become a reality for evolutionary biologists.

Here is, perhaps, the most dramatic example of the principle that wherever we find *significant empirical discontinuities* in nature we invariably face great, if not insurmountable, conceptual problems in envisaging how the gaps could have been bridged in terms of gradual random processes. We saw this in the fossil record, we saw it in the case of the feather, in the case of the avian lung and in the case of the wing of the bat. We saw it again in the case of the origin of life and we see it here in this new area of *comparative biochemistry*.

What has been revealed as a result of the sequential comparisons of homologous proteins is an order as emphatic as that of the periodic table. Yet in the face of this extraordinary discovery the biological community seems content to offer explanations which are no more than *apologetic tautologies*.

Comparative biochemical information is simply "at odds" with neo-Darwinism, in the assessment of Schwabe (1986, p. 282): "One might ask why the neo-Darwinian paradigm does not weaken or disappear if it is at odds with critical factual information." Thus, at least in the area of comparative biochemistry or molecular biology, the theories of macroevolution and Darwinism are not compellingly established, in the view of many evolutionists.

#### Population Genetics Argument and Difficulties

The population genetics argument for macroevolution and Darwinism, which focuses on gene changes within a population (Roughgarden, 1979, p. 5), is founded on extrapolation of small changes in gene frequencies in a population to major transformations from a common ancestor to evolutionary descendants. It is "[p]erhaps the most important source of evidence in support of the theory of evolution," according to Stansfield (1977, p. 129) and "contains the core mechanisms of neo-Darwinian evolutionary theory," in the words of Ruse (1982, pp. 112-3). Yet that extrapolation is questionable, and the argument has failed, in the view of many evolutionist as well as nonevolutionist scientists.

First, population genetic changes (microevolution) *tell nothing about macroevolution* or even the origin of species, as Lewontin (1974, p. 159) observes:

It is an irony of *evolutionary genetics* that, although it is a fusion of Mendelism and Darwinism, it has made *no direct contribution to what Darwin obviously saw as the fundamental problem: the origin of species.*

and Grassé (1977, p. 170) notes:

To assert that population dynamics gives a picture of evolution in action is an *unfounded opinion*, or rather a postulate, that relies on *not a single proved fact showing that transformations* in the two kingdoms have been essentially *linked to changes in the balance of genes in a population. . . . [A]s for seeking in it proof of the formation of new species, there is no such hope.*

Mayr (1980, p. 11) said that "the most cogent objection against population genetics raised by Grassé" was that he "could not see any connection between changes in gene frequencies. . . and the evolutionary events. . . of species and higher taxa." Rosen (1978, p. 372) concurs that population genetics "cannot, and does not purport to, explain the origin . . . of new codons" (parts of new genes). Spiess (1977, p. x) concedes that "we are a long way from describing the origin of species . . . with methods of experimental population genetics." Saunders and Ho (1982 p. 185) add that population genetics simply "is not, however, a theory of evolution." Kempthorne (1983, p. 120), while wishfully assuming that after nearly a century "population genetics theory is in its infancy," cautions that a "real danger is that the theory is generated primarily by the mathematics we can do, rather than by the biological processes that should be included." Lambert (1984, p. 125) suggests that, because "evolution is . . . most especially not a population genetics problem," but "a problem of the origin of form," then "population genetics is not a tool to investigate evolution. Similar observations are made indirectly by all the evolutionist scientists who object to extrapolation from microevolution to macroevolution. Stanley (1975, pp. 648, 650; Bird 1987, pp. 54-64).

Second, population genetics comes perilously close to *explaining nothing*, as Lewontin (1974, pp. 11-2, 189) concludes:

The theory *explains nothing* because it explains everything. It is my contention that a good deal of the structure of evolutionary genetics comes perilously close to being of this sort. . . .

For many years population genetics was an immensely rich and powerful theory with virtually no suitable facts on which to operate. It was like a complex and exquisite machine, designed to process a raw material that no one had succeeded in mining. Occasionally some unusually clever or lucky prospector would come upon a natural outcrop of high-grade ore, and part of the machinery would be started up to prove to its backers that it really would work. But for the most part the machine was left to the engineers, forever tinkering, forever making improvements, in anticipation

of the day when it would be called upon to carry out full production.

Quite suddenly the situation has changed. The mother-lode has been tapped and facts in profusion have been poured into the hoppers of this theory machine. And from the other end has issued — *nothing*. It is not that the machinery does not work, for a great clashing of gears is clearly audible, if not deafening, but it somehow cannot transform into a finished product the great volume of raw material that has been provided. *The entire relationship between the theory and the facts needs to be reconsidered.*

Roughgarden (1979, p. 5) concurs that the assumption that by population genetics "longterm evolutionary phenomena would be explained" needs to be reassessed. And Saiff concludes:

The leading workers in this field have confessed, more or less reluctantly, that *population genetics contributes very little to evolutionary theory*. We will cite three such leaders. . . .

If the leading authorities on population genetics confess to this dismal lack of achievement and even chuckle about it, *it is altogether fitting and proper for the rank and file to take them at their word*. Therefore it seems to follow that *there is no need to teach population genetics in introductory courses on evolution*, although advanced courses may include it as a matter of history. (Saiff, 1983, pp. 71-2; cf. Hewitt, 1983, p. 73)

Finally, and related to its failure, population genetics embodies *circular reasoning* when it is used to support evolution, as Forey (1982, p. 124) argues:

The hope of many of the authors of trees is that the synthetic approach (Bock 1974) will combine the analysis of pattern with the theories of the population biologists/geneticists in mutual support. The problem is that both are ultimately derived from the theory of evolution: the fossil record being interpreted in the light of *population biology* theory and expressed as ancestor-descendent relationships (Simpson 1953). One might remark that, far from being mutually supportive, *this is merely "the blind leading the blind."*

Because the "idea of differential reproduction to explain evolutionary change formed the basis for what today is the field of population genetics" (Rosen, 1978, p. 371), the problems of natural selection in terms of macroevolutionary effect and evidence, and in terms of tautology and nonexplanatory nature. (Bird, 1987, pp. 158-65) apply equally to population genetics. In this area, macroevolution and Darwinian evolution are not compelling, in the view of many leading researchers.

#### Artificial Selection Argument and Difficulties

The artificial selection argument for macroevolution is based on extrapolation from breeding experiments (artificial selection) to natural selection and then to macroevolution. In fact, "more than almost any other single factor, domestic breeding has been used as an argument for evolution," according to Eiseley (1958, p. 223) as well as Dobzhansky *et al.* (1977, p. 97). The second extrapolation, which even many evolutionists

question, has been discussed elsewhere (Bird, 1987, pp. 155-78). The first extrapolation entails serious problems.

First, artificial selection is not *relevant* to natural selection, and thus is not a persuasive argument for it, according to Wassermann (1978, p. 235):

*Artificial selection* is often considered as a means for testing population genetic theories (cf. Lewontin [1974], p. 250). But there remain, in my opinion, *serious doubts* about the role that artificial selection could or should play. Dobzhansky ([1970], p. 201) argued that Darwin used artificial selection as a model of the natural process; a mathematical theory of selection must almost necessarily be derived from experiments on artificial selection. This belief, however (and its *doubtful* conclusion), rests on the implicit hypothesis that artificial selection necessarily simulates some natural selection process. *One could only confirm this hypothesis by studying first the natural selection process* extensively and then examine how well artificial selection simulates it. *But if one could study the natural process in the first place, then one would not need any simulation*, unless the simulation process could be better controlled (and provided the controls do not change the effects of the simulation process much from those of the natural process).

Other aspects of the irrelevance of artificial selection to natural selection are identified by Macbeth (1986, p. 194):

At the same time, however, *Darwin fell into the traps* that Fischer warns against. First, he was so enchanted with the similarities that *he paid little attention to the obvious dissimilarities* (presence of a guiding intelligence in artificial selection, plus the breeders' concentration on micro changes rather than on the big gaps). Second, he offered the analogy as a proof: see pages 14-15 and Chapter 4 of *The Origin*.

Although the analogy had nobly performed its function in stimulating Darwin's imagination, *it furnished no evidence of the correctness of Natural Selection*. It has historical interest, but it was not essential to the understanding or proof of Natural Selection. Alfred Russel Wallace did not need it to reach the same conclusion as Darwin; to the contrary, McKinney (1972, pp. 144-5) shows that he rejected the analogy . . .

Second, artificial selection is not just an irrelevant proof, but it is an irrelevant analogy, for macroevolution and Darwinism, as Russell (1962, p. 124) states:

It is important to note that in all these processes there is *no "selection"* in the proper meaning of the word. It is unfortunate that Darwin ever introduced the term "natural selection," for it has given rise to much confusion of thought. He did so, of course, because he arrived at his theory through studying the effects of selection as practised by man in the breeding of domesticated animals and cultivated plants. Here the use of the word is entirely legitimate. But the *action of man in selective breeding is not analogous to the action of "natural selection,"* but *almost its direct opposite*,

as Woltreck (1931) in particular has pointed out. Man has an aim or an end in view; "natural selection" can have none. Man picks out the individuals he wishes to cross, choosing them by the characters he seeks to perpetuate or enhance. He protects them and their issue by all means in his power, guarding them thus from the operation of natural selection, which would speedily eliminate many freaks; he continues his active and purposeful selection from generation to generation until he reaches, if possible, his goal. *Nothing of this kind happens, or can happen, through the blind process of differential elimination and differential survival* which we miscall "natural selection."

Even Dobzhansky *et al.* (1977, p. 97) join in the argument that artificial selection is too different from natural selection to be relevant. Just as human ability to construct bridges does not establish that bridges evolved without engineering, human ability to breed cows does not help establish that cows arose through macroevolution.

Third, artificial selection supports not the possibility of macroevolution but the genetic limits on viable microevolution. Those "more or less fixed limitations," and "limits to the development possible," were noted by Burbank (1939, pp. 97-9). Deevey (1967, p. 636) concurs that artificial selection faces a "species barrier." Eiseley (1958, p. 223) acknowledges that variations "cannot be selectively pushed beyond a certain point." Falconer (1960, p. 186) points out that, for breeding experiments, "only the fact that domesticated plants and animals do not live under natural conditions has allowed these improvements." Those genetic limits on viable change are analyzed (Bird, 1987, pp. 84-9).

Here, the biological theories of macroevolution and Darwinian evolution are not compellingly established, many evolutionists admit.

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## QUOTE

Hopkins labored to construct an all-encompassing ethical system. God, because of the infinite goodness of his character, deserved infinite honor. Men, as creatures made in the image of God, deserved to be treated with the great respect accorded by this high honor. Hopkins' famous ethical catchword, "disinterested benevolence," was a description of the way in which individuals should act toward men—benevolently, because of the high order of divinely created humanity, and disinterestedly, in consideration of the overarching imperative to honor the other person's inherent worth.

Noll, Mark A. 1977. *Christians in the American Revolution*. Christian University Press. Washington, D.C. p. 92.

## PANORAMA OF SCIENCE

### Formation and Rate of Growth of Stalactites

The process of stalactite formation is probably not quite as simple as the generally accepted explanation would suggest. If the deposition of the calcareous matter depended entirely upon the influence of the carbon dioxide that rain water derives from the air, it is unlikely that, when the water drips from the roof of a cave, the gas would be given off to such an extent as to result in the formation of important calcareous deposits. Emeritus Professor C. Thompson, of Cardiff, has suggested to me that, when passing through the soil, in which carbon dioxide is much more abundant than in the air, water takes up a quantity of that gas greatly in excess of what it can hold under atmospheric conditions: this increases its capacity to dissolve calcium carbonate, and, on reaching a cavity such as a cave in which the composition of the air is probably very similar to that of the outer

air, the excess of carbon dioxide is given off with comparative rapidity, with a correspondingly rapid deposition of calcium carbonate . . .

Very little is known concerning the rate of growth of stalactites. The North Bridge, Edinburgh, was erected in 1772, and after a century, stalactites an inch and a half in diameter, with the characteristic crystalline structure were found pendant from it, while in the Ingleborough Cave, Boyd Dawkins found the rate of growth to be .2946 inches per annum or nearly 30 inches in a century. This was believed to be an exceptionally rapid rate of growth ["On the Action of Carbonic Acid on Limestone," *Report British Association* (1880), p. 573]. In any case the present rate of growth in a cave like those at Cheddar or in Derbyshire is not necessarily an indication of the length of time that the pendant columns have taken to reach their present dimensions, for at times when the local water level was higher than it