Some Proposed Tests of Evolutionary Theory

As found on the IDEA Center website at http://www.ideacenter.org

Test 1: Testing a particular supposed evolutionary transition.

"*If numerous species, belonging to the same genera or families, have really started into life all at once, the fact would be fatal to the theory of descent with slow modification through natural selection.*" (Charles Darwin, The Origin of Species: A Facsimileof the First Edition, Harvard University Press, 1964, p. 302.)

(A) Key fossils documenting the transition must be found.

It is realized that the fossil record is incomplete, and one would not always expect to find fossils of all extinct species. However, the use of a collectors curve and other statistical techniques can be used to determine if it is likely whether or not the "missing" links are really missing, or if the fact that they haven't been found indicates that they never actually existed. Every effort must be made to take a complete sampling of the strata which might contain the fossil intermediate, and the likelihood of the fossilization of the given transitional organism should also be taken into account. This wouldn't be too difficult, for if fossils of similar organisms are available, then it could be established that fossils of the alleged transitional organism are indeed fossilizeable. Only if no similar organisms have left any fossils, could it most strongly said that one would not expect to find fossils of the transitions.

(B) The numbers must add up.

The amount of biological change necessary must be mathematically possible within the supposed time allowed for the transition in the fossil record. The rate of change would be a function of the mutation rate (and gene duplication rate), size of population, reproduction rate of population, and selection pressures upon the "evolving" population according to the rules of population genetics. Some of these factors may be dependent upon one another, but the bottom line is that after taking everything into account, the numbers must add up. For example, the fossil record supposedly documents that a rodent-like animal turned into a whale in less than 10 million years. Regardless of whatever transitional fossils might be claimed to have been found, the numbers in this case do not add up, especially given the fact that whales are a long-lived globally distributed species--the exact opposite of what a geneticist needs to model punctuated equilibrium. Natural limits to biological change must also be taken into account.

(C) Intermediate Morphologies must be functional.

All stages of intermediate macro- and micro- morphology of the transitional organisms must be testably and conceivably functional. This goes not only for macromorphology, but also for any biochemical adaptations which must have occurred along the way to make the change possible. Obviously one cannot expect that the absolute biochemical evolutionary pathways can be rediscovered, but plausible pathways must be provided. If no explicit and specific plausible pathways can even be imagined, then it is likely that the claimed "biochemical evolution" did not take place.

We're really sorry, but unless criteria A, B, and C are all met for any given alleged natural evolutionary transition, then it cannot be said that the evolutionary transition took place. If any of the tests are failed, then according to the explanatory filter, there is no valid naturalistic explanation for the origin of the species in question. Criteria A could only be dismissed if the species would in all cases NOT be expected to form a fossil, and could only be failed if thorough searching of the fossil record failed to turn up the necessary fossil intermediates and if statistical analysis of the collection process then showed that the fossil should have been found if they had actually lived. Criteria B could easily be tested through

simple mathematical modeling to see if the alleged amount of could take place in the given amount of time. Criteria C is admittedly bit more difficult to fail, for one could always claim to "imagine" functional intermediates in a "just-so" story of how it evolved. However, such "just-so" stories are falsifiable, and rigorous experimental testings, computer modeling, and honest evaluation of these "just so stories" could in the end render many of them, well, ludicrous. If the "new" biological functions in question turns out to defy any conceivable intermediate morphology, then criteria C could be conclusively failed. Honesty is the key here folks, not philosophy. If a single one of these criteria is clearly failed, then the alleged evolutionary transition did not take place through natural means, and barring any philosophical close-mindedness certain theories, the proper inference is Design.

Test 2: Did gene duplication really lead to higher complexities biological organisms.

One of the major arguments used by evolutionists to hurdle complexity problems is the idea of gene duplication. In fact, in order to explain the observed level of complexity in the genome, gene duplication must be employed so much that evolution predicts that the genome should be full of an array of ancient gene duplications that would be nonfunctional.

This test is quite simple. If gene duplications have really occurred to help build "alleged" irreducible complexity, then there should be evidence of old duplicated-but-unused genes all over the genome. In other words, if gene duplications really solve all of our problems for building complexity, then surely they happen often, or at least sometimes, and thus the evidence of such past gene duplications which were incorporated into the genome and later discarded ought to be all over the place. Statistically speaking, the vast majority of duplicated genes will not get hijacked or reused, and will get shuffled back into the genome as some remnant unused part of the genetic code. If these supposed gene duplications have really been occurring all throughout time and are responsible for the evolutionary construction of many complex biochemical functions, then one should find old unused duplicated genes everywhere.

Old unused duplicated genes could be recognized by sequence analysis. If genes have really been duplicated throughout life's random history, you would expect to find the genome in a very disorderly state, rather than the predictably ordered state it is in today. Furthermore, since gene duplication isn't always a perfect process, it duplicates parts or small portions of genes. One would expect to find little pieces of duplicated genes all over the place, perhaps even some stop codons and upstream or downstream controlling regions. The reason you'd expect to find so much of this is because there's no selection pressure to get rid of old unused "junk DNA". Once it becomes useless genetic baggage it is like a neutral mutation that has no adverse effects. Thus, these should be all over the place. Instead, the so-called "junk DNA" has regular patterns, and many biochemists are sure it has some function. Biochemists may not fully understand exactly what it does or what it is, but they do understand that its sequence looks nothing like old unused remnant coding regions, i.e. old unused duplicated genes. A good understanding of molecular biology may be necessary to really understand a lot of this, but the point is that the genome doesn't seem to exhibit the sort of tattered random appearance it ought to have if these so-called gene duplications have been happening throughout life's history.

Additionally, there must not be "too many" gene duplications in the allowable time. Evolutionists estimate that the average gene duplicates about once every 100 million years. Furthermore, the vast majority of duplicated genes do not acquire a new function and are eventually silenced. If too many duplications are needed, perhaps, once again, the numbers aren't adding up.

3. The Punctuated Equilibrium Theory Test

This test is essentially an experimental test of the supposed biological mechanism which drive the rapid speciation predicted by the theory of punctuated equilibrium. The theory of punctuated equilibrium basically states that given the right selection pressures and population sizes, species can evolve

extremely rapidly. By saying the evolution was too rapid to form fossils, this theory attempts to explain away why there are not the predicted fossil intermediates of evolutionary theory. However, according to the fossil record, this change is often so rapid that it ought to be quite visible within, say, 1000 or even fewer generations!!! Given that punctuated equilibrium states that the changes occur most rapidly in small populations in environments with very strong selection pressures, this evolution ought to be possible to observe under the properly controlled conditions.

Put a bunch of small populations of say, rodents, or small animals with high reproduction rates into small enclosed controlled environments with strong selection pressures, and see what you get! Perhaps even the aid of selective breeding might help quicken the process. If there really is a biological mechanism which allows for the rapid speciation called for by the "punc eq" model, then eventually you ought to see your guinea pigs adapt to their strange new environment and perhaps actually form a new species!

Of course it is realized that this experiment might need to be done a thousand times before it could really be said, "punc eq" is, biologically speaking, a garbage theory. However, punc eq enthusiasts boast of how adaptable life really is and how quickly it will change given the proper conditions. Just open up a few niches and change the environment, and whalla, you're supposed to get about 30 new orders of mammals with a relatively short evolutionary time period! Something at least beginning to approach such changes should be observable given the right conditions.

We've done a little bit of thinking over here to come up with some possible "weird" environments to choose from. Perhaps a computer could randomly select the variables to allow for large and random selection pressures.

4. Phylogenetic trees.
It can be tested if similarities between morphological characters, gene sequences, or protein sequences are really indicative of common ancestry. When a phylogeny is given, it must maximize parsimony. However, if many unnecessary evolutionary steps are required by the character distribution (i.e. too much convergent evolution), then nice neat Darwinian trees cannot be drawn? What if convergent evolution pops up all over the place regardless of how you shape your tree? Is this a good evolutionary tree? According to the evolutionist, the answer is yes, and no.

Evolutionary theory both allows for convergent evolution and for inheritance of characteristics through ancestry. Thus, it can explain 2 predictions which are often mutually exclusive:

1. That character distributions will reflect inheritance of characteristics through ancestry.
2. That character distributions will reflect novel inventions through mutation and selection.

While on the surface this seems to make evolutionary theory seem powerful, in reality, it makes it weak. The theory that can explain anything, really explains nothing, for a theory which makes mutually exclusive predictions actually has very little predictive power, and cannot really be tested. Though a tree which has perfect hierarchical nesting, no convergent evolution, and reflects only inheritance of characteristics through ancestry is perhaps compelling evidence for common ancestry, such trees are rarely, if ever found. The fact is that convergent evolution is always required to explain large portions of tree data, the question must be asked, "Are the observed character distributions really indicative of common ancestry?" Sometimes, it doesn't seem like that.

At the heart of systematics (the science of classification and tree-building) is a long-standing methodological debate which highlights one of the fundamental evidences which contradicts Darwinian predictions. The two methods, "cladistics" and "phenetics", are different methods of classifying

organisms. Cladists believe that classification of organisms should reflect only evolutionary history (which, mind you, is alleged) such that characteristics of organisms which are most complex and similar ought to define evolutionary relationships. Pheneticists say that a simple statistical analysis of the number of similarities should define the classification. Phenetics and cladists often come up with different classification schemes. From an evolutionary perspective, a major prediction would be that the more similarities, the closer the relationship. But what does it mean when that prediction fails and highly similar complex features are said to have evolved independently? In a simple Darwinian world, cladistics and phenetics wouldn't contradict one another. In a complex one like ours, they wouldn't contradict one-another so often or in such striking ways if Darwinian evolution were really responsible for life.

For example, both kangaroos and thylacines (a marsupial animal similar to a wolf) rear their newborns in external pouches on the underside of the stomach. For this reason, their complex method of birthing classifies them both as "marsupials" a subdivision (called an infraclass) of the taxonomic class mammalia. A cladist would classify a thylacine as a marsupial, yet in body structure and behavior it is almost identical to the placental wolf. (And the story is the same for the marsupial and placental rodents, marmot & wombat, and marsupial and placental cats, and many other non-mammalian examples as well). We are said to have observed "convergent evolution" but what we really mean is that two almost identical animals allegedly evolved independently from a small primitive mouse-like mammal over 120 million years ago. The chances of the two evolving to such a degree of similarity is almost nil under and evolutionary scenario, and this might be better explained by the common design of a designer. Thus, whenever phenetics and cladistics contradict one another (which they often do as seen in the many still-raging debates today) - we see an example of an alleged evolutionary tree which common ancestry didn't predict very well, and a taxonomic scheme which is perhaps better explained by common design. And there are many many examples not just from macro-morphological data, but also from genetic and molecular data which show that the "trees constructed" don't fit the expected Darwinian trees from common ancestry.

What about protein similarities, or gene sequence similarities, often called "protein homology" common ancestry is assumed. But wait, what's the evidence for common ancestry? The similiarites? Similarities themselves only provide circumstantial evidence--there's no real proof that the similarities are due to common ancestry. How can we test if these similarities are due to common ancestry or gene duplication? Whoops, this can't be done! Whenever common ancestry is claimed due to genetic it must be assumed, and can't really be tested.

In fact, looking at similarities, one could use the same methods used in protein trees construct a tree for anything--even a totally meaningless tree. Just go around your office and pick things off the shelves, write down their characteristics, and you could construct a tree. Does that mean that these items have some sort of genetic history? Not at all, they were designed for similar, though still quite different purposes, and perhaps we could say the same for various forms of life on earth.