SPEECH BY DR. COLIN PATTERSON

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[Colin Patterson (deceased) was a senior paleontologist and editor of the journal of the British Museum of Natural History in London.]

My title is "Evolutionism and Creationism.". I can tell you that title was laid on me by Don Rosen. I'm speaking on it to gratify this old friend of 700 years. I've never spoken on it before and I hope I never have to speak on it again. It's true that for the last eighteen months or so I've been kicking around non-evolutionary or even anti-evolutionary ideas. I think always before in my life when I've got up to speak on a subject, I've been confident of one thing that I know more about it than anybody in the room, because I've worked on it. Well, this time it isn't true. I'm speaking on two subjects evolutionism and creationism, and I believe it's true to say that I know nothing whatever about either of them.

One of the reasons I started taking this anti-evolutionary view, or let's call it a non-evolutionary view, was last year I had a sudden realization for over twenty years I had thought I was working on evolution in some way. One morning I woke up and something had happened in the night and it struck me that I had been working on this stuff for twenty years and there was not one thing I knew about it. That's quite a shock to learn that one can be so misled so long. Either there was something wrong with me or there was something wrong with evolutionary theory. Naturally, I know there is nothing wrong with me, so for the last few weeks I've tried putting a simple question to various people and groups of people.

Question is: Can you tell me anything you know about evolution, any one thing, that is true? I tried that question on the geology staff at the Field Museum of Natural History and the only answer I got was silence. I tried it on the members of the Evolutionary Morphology Seminar in the University of Chicago, a very prestigious body of evolutionists, and all I got there was silence for a long time and eventually one person said, "I do know one thing - it ought not to be taught in high school."

Well, maybe someone here know a more convincing answer than. that - something they know about evolution. The other answer, apart from the high school answer, I've had from anybody, and I've had this from several people in conversation - yes, they do know something, Convergence is everywhere, that's what they've learned.

Well, I'll come to convergence later but it does seem that the level of knowledge about evolution is remarkably shallow. We know it ought not to be taught in high school and that's all we know about it.

My second subject is creationism and what do we know about that? We know that it ought not be taught in high school too.

... I want to talk about evolutionism and creationism as applied systematics... The text of my sermon will be from Gillespie's book, Charles Darwin and the Problem of Creation, California University Press...I want to consider the way in which these two alternative world views-evolutionism and creationism have affected or might affect systematics and systematists.

Gillespie's book is a historian's attempt explain the amount of space that Darwin gave to combating the creationist arguments. Gillespie shows that what Darwin was doing was trying to replace the creationist paradigm by a positivist paradigm, a view of the world in which there was neither room nor necessity for final causes. Of course, Gillespie takes it for granted that Darwin and his disciples succeeded in this task. He takes it for granted that a rationalist view of nature has replaced an irrational one and of course, I myself took that view about eighteen months ago. Then I woke up and realized that all my life I had been duped into taking evolutionism as revealed truth in some way.

From my new viewpoint, some of Gillespie's comments on pre-Darwinian creationism seem to be strikingly apt, but they are apt because when I transposed them from the period he is talking about (1850s to today) - Here is one quote from Gillespie's book:

"The old scientific epic scene has sanctioned, or so it appears from the new perspective, a pseudo-paradigm that was not a research governing theory. This is hard to explain with only verbal, but an anti-theory, a void that had the function of knowledge but as naturalists increasingly came to feel, conveyed none."

Here Gillespie is characterising the old pre-Darwinian creationist paradigm. But I feel that what he says could just as well be applied to evolutionary theory today.

Now, of course, it must seem to you that I'm either misguided or a malicious to suggest that such words could be applied to evolutionary theory. But I hope to say that there is something at least as far as systematics is concerned. Gillespie says first that creationism can't be a research governing theory since its power to explain is only verbal. Now today evolution certainly seems to be a research governing theory. Most of us think that we are working in evolutionary research. But is its explanation power any more than verbal when in systematics the research governing aspects of evolution is common ancestry or descent with modification or divergence?

Those of you who were at the meeting last month may have heard that both Rob Brady and I without any prior collusion both quoted the same statement. This was the statement:

"Explanatory value of the hypothesis of common ancestry is nil."

We attributed that statement to T.S. Russell's 1916 book, Form and Function. In thinking about it since then, I feel that the effects of hypotheses common ancestry in systematics has not been merely boring, not just a lack of knowledge, I think it has been positively anti-knowledge. I'll come back to that later anyway.

Gillespie also said that creationism is an anti-theory, a void that has the function of knowledge but conveys none. Well, what about evolution? It certainly has the function of knowledge but does it convey any? Well we're back to the question that I've been putting to people. "Is there any one thing you can tell me about evolution?" The absence of answers seems to suggest that it is true, evolution does not convey any knowledge or if so, I haven't yet heard of it.

Well, here we all are. We all have shelves of books on evolution. We've all read tons of them and most of us have written one or two. How could it be that some Donald Black had read these books and learned nothing from them? How could I work on evolution twenty years and learn nothing from it? Gillespie's comment: "a void that has the function of knowledge but conveys none" seems to me to be very precise, very apt.

But in systematics there are pieces of evolutionary knowledge that all our heads are stuffed with, from the :most general statements like eukaryotes evolved from prokaryotes, vertebrates evolved from. invertebrates, down to specific ones like I evolved from apes. I imagine by now this group does appreciate that such statements exactly fit Gillespie's description - voids that have the function of knowledge but that convey none.

To analyze all such things saying that there is a group, a real group of characters, eukaryotes, vertebrates, Homo sapiens, whatever, and opposed to is a non-group, prokaryotes, invertebrates, apes. These are abstractions that have no character of their own; they have no existence in nature and therefore they cannot possibly convey knowledge, though they appear to when you first hear such statements.

So, in general, I'm trying to suggest two themes. The first is that evolutionism and creationism seem to have become very hard to distinguish, particularly lately. I've just been showing how Gillespie's bitterest characterization of creationism seems to be, as I think, applicable to evolutionism - a sign that the two are very similar.

Now as you all know thee is somewhat of a revolution going on in evolutionary theory at the moment. It doesn't concern the fact of evolution or things general theory of evolution, descent with modification. It concerns possible mechanisms that are responsible for transformations. Well, natural selection is under fire and we hear a raft of new and alternative theories. I've heard four in the last six weeks.

Well, here's Gillespie again on creationism in the 1850s. He says:

"Frequently, those holding creationist ideas could plead ignorance of the means and affirm only the facts."

That seems to summarize the feeling I get in talking, to evolutionists today. They plead ignorance of the means of transformation but affirm only the facts, knowing that it's taken place. Again the two points do seem hard to distinguish.

Here are a couple more quotes from Gillespie. Again, he's saying things on creationism that seem to be just as applicable to evolution today.

"The supposed credibility of the theory was merely the result of familiarity."

Here's a second quote:

"Too much of the contents of the old science was the result of intuition that was in principle unverifiable either directly or indirectly."

Now those two may have a familiar ring. We hear that sort of thing in evolutionary theory all the time.

Here's another quote on the changing world view associated with the spread of evolutionary thinking in the 1860s.

"Just as science shifted from a theological ground to a positive one so religion among many scientists and laymen influenced by science shifted from religion as knowledge to religion as faith."

So I think many people in this room would acknowledge that during the last few years if you had thought about it at all, you've experienced a shift from evolution as knowledge, to evolution as faith. I know that's true of me and I think it's true of good many of you in here.

So that's my first theme. That evolution and creation seem to be sharing remarkable parallels that are increasingly hard to tell apart.

The second theme is that evolution not only conveys no knowledge but seems somehow to convey anti-knowledge, apparent knowledge which is .... to systematics.

I want to illustrate that with a couple of parables. These parables concern a diagram that I expect to be immediately familiar to all of you when I put it up. Do you recognize it? It is a diagram that Ernst Mayr has used in his repeated explanations of the true method in systematics that exists in evolutionary systematics.

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Fig. 1 Cladogram of taxa A, B, and C. Cladists combine B and C into a single taxon because B and C share the synapomorph character b. Evolutionary taxonomists separate C from A and B, which they combine, because C differs by many (c through k) autapomorph characters from A and B and shares only one (b) synapomorph character with B.

My first lesson with the diagram - the first parable - looks like that. (See Figure 1). That is the version that came out in Science (October 30, 1981) last week. The marks along the lines are all autapomorphies of A, B, and C except. for that one which is a synapomorphy of B and C. In Mayr's paper in Science last week C is man, B is the chimpanzee, our sister group according to Mayr and A is not named but I would assume it is the gorilla, Here's what Mayr said:

"The main difference between cladists and evolutionary taxonomists, thus, is in the treatment or autapomorph characters. Instead of automatically giving sister groups the same rank, the evolutionary taxonomist ranks them by considering the relative weight of their autapomorphies as compared to their synapomorphies (Fig. 1). For instance, one of the striking autapomorphies or man (in comparison to his sister group, the chimpanzee) is in the possession of Broca's center in the brain, a character that. is closely correlated with man's speaking ability. This single character is for most taxonomists of greater weight than various synapomorphous similarities or even identities in man and the apes in certain macromolecules such as hemoglobins and cytochrome c. The particular importance of' autapomorphies is that. they reflect the occupation of new niches and new adaptive zones that may have greater biological significance than synapomorphies in some of the standard macromolecules."

There are several things one might say about that statement but not all of them would be polite so I'll just point out that both the statement and the diagram are intended to convey knowledge of evolution. The diagram in the different angles of the lines there and the statement in reference to things like new niches and new adaptive zones, etc. When I first read that passage in Science it immediately reminded me of something - an episode in the history of evolution that many of you may recall; something called "The Great

Hippocampus Question." The Great Hippocampus Question is recorded in fiction in Charles Kingsley's novel, his children's book, The Water-Babies, In fact, not in fiction, it was a controversy that lasted through 1861 and 62 between Richard Owen and T.H. Huxley. Owen was a creationist and Huxley an evolutionist. Owen, the creationist ; insisted that man was quite distinct from the apes. He couldn't be related to them by descent or any other physical link because the brain of man contained a certain centre, the hippocampus, that was absent in apes. T.H. Huxley insisted that man was related to the apes because the ape's brain, so he said, contained a center that was homologous to the hippocampus. The row went on for two years and eventually a usual, Huxley won.

Here we are 120 years later and we have Ernst Mayr, the evolutionist, insisting that man is quite distinct from the apes because the brain of man contains a certain center Broca's center, that is absent in apes. Mayr even goes on to cite Julian Huxley, grandson of T.H. Huxley and with some approval of his kingdom for Psychozoa. You remember that? It all begins to sound very familiar, doesn't it? Yet notice how the roles have been reversed. The part of Owen, the creationist, with hippocampus now taken by Mayr, the evolutionist and Broca's center. The part of T.H. Huxley, the evolutionist, is now taken by the cladists, who most people now cite as anti-evolutionists, many do.

Bev Halstead, who I'm sure needs no introduction here published a paper called, "A Debate with the Creationists" in which he called me a devoted disciple of Sir Richard Owen. So be it. The wheel has gone right the way around. The evolutionist is now taking just the stand that the creationist took 120 years ago- Broca's center equals the hippocampus .This parable reinforces the point I was making earlier that evolutionists and creationists are now hard to distinguish.

I want to use it to make another point about evolution being an anti-theory that conveys anti-knowledge. It is harmful to systematics. What is Mayr recommending? He recommends that man be maintained in a taxa of high rank, distinct from the apes. Look at what prompts him to that recommendation. It is his apparent knowledge of evolution - that man has evolved at an exceptional rate... Those evolutionary facts justify a taxa of high rank. Then look at the consequence of his recommendations. Man is removed in a taxa of high rank and apes are left to the character of the group, a group without characters and therefore with no individuality or reality and therefore an abstraction that is beyond criticism.

...Man evolved from the apes. That must say something about evolution. Seems to me we have another statement that has the appearance of knowledge, but, in fact, contains none, a piece of antiknowledge derived from the evolutionary theory. Rather than comment further on this I'll quote what T.H. Huxley said of Owen in 1861, again referring to the hippocampus question:

"I do not believe that in the whole history of science there is a case of a man of reputation putting himself in such a contemptible position."

SECOND PARABLE

Now I'd like to go on to the second parable and return again to this same diagram but I'd like you now to think of the way in which it was previously used by Ernst Mayr in his 1969 book with his 1974 paper on "Systematics." At that time it looked like this:

15%
10%
70%

Now, that's how Mayr tried to put some precision into evolutionary systematics. Then he said, "Let A be the common ancestor of BCD and suppose the genome of B is diverged from the ancestral genome by l5%, that of C diverged by 10%, and D has moved off rapidly into some new adaptive zone diverged by 70%." Then he said we should be quite wrong to classify C with D which appears towards its nearest relative by common ancestry because relationship means inferred amount of shared genotype not the inferred recency of common ancestry. Here is the very simple sum:

B and C share 75% of the ancestral genotype
C and D share only 30%

..... show the kind of mistakes that might be made, Mayr said that systematists might group crocodiles with birds rather than other reptiles or might group African ape with man rather than with the orangutan. So Mayr in his knowledge of evolution is making predictions about the genotype of crocodiles and African apes.

In the first example crocodiles, birds, and reptiles, he predicts that the proportion of genotypes shared by C, the crocodile and B, another reptile be greater than proportion shared by C, the crocodile and D, the bird. He predicts that in some shared genotypes BC will be greater than CD.

Now next is Mayr ..... demonstrating the explanatory power here of a hypothesis of common ancestry, something that I've [said] scarcely had zero explanatory power. He is also demonstrating a knowledge of evolution, writes a theory, makes a prediction and is going to test it.

Last month in Ann Arbor, a student of Morris Goodman gave me the amino acid sequences for alpha and beta hemoglobin of 3 crocodilians: a caiman, a Nile crocodile the Mississippi alligator. We already knew the alpha and beta hemoglobin sequences of 2 birds, a chicken and a goose but the problem is finding another reptile. As far as I know the only other reptile available at the moment is the alpha hemoglobin sequence of a snake, the viper. Alpha hemoglobin is 143 amino acids long so there 3 times that or 429 nucleotides long. That is a very small part of the genotype but at least it is worth checking. The prediction is that the amino acids common to B the viper, C the crocodile and D the chicken, that BC would be greater than CD. And here of course are his findings:

BC	8 out of 143	5.6%

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CD =	25 out of 143	17.5%
BD =	15 out of 143	10.5%

Here we are. The theory makes a prediction, we've tested it and the prediction is falsified precisely. CD far outweighs BC so something is wrong with the prediction. Something is wrong with the theory. But, of course, we know that falsification is never absolute, for you're never sure what it is you have falsified.

And here we see only three possibilities. First, we've falsified the data; there is something wrong with alpha hemoglobin. Second, we've falsified the diagram; there is something wrong about the physical relationships of the snake, bird and crocodile. And third, we've falsified Mayr's knowledge of evolution, either the particular stuff about rates and adaptive zones or something more general.

We can check one of those pieces of data by taking another sample of the genome: a crocodile, bird including chicken and two other reptiles a lizard and turtle. Myoglobin is 153 amino acids long.

BC	16 out of 153	10.5% (B is lizard)
CD	13 out of 153	8.5% (C is crocodile)
BD	16 out of 153	10.5% (D is chicken)

This time the BC proportion of the genotype is larger than the CD, slightly larger, as Mayr predicted. What happened here? What fits BD? It ought to be by far the smallest proportion of the genome, yet it is exactly the same as the BC. Something has gone wrong again. Again there are 3 possibilities: data, diagram or the theory

In fact, when you think about the diagram and this data but yet a different diagram BC same as BD, and possibility of dichotomy, like that. Perhaps the diagram is wrong.

Let's check again with the turtle, turtle myoglobin. B is the turtle (terrapin as I remember), C is crocodile and D is chicken.

BC	11.8% (B is turtle)
CD	5.2% (C is crocodile)
BD	5.9% (D is chicken)

Now we're getting closer to what Mayr expected. BC is much larger than BD here. Again there is another problem. The BD portion (turtle-bird) should be tiny [but] is larger than the CD. Again, something is wrong. This data suggests a different diagram like this where BC go together, D is separate.

So it seems with these three examples, either we get the right diagram as we did with the first sample .... with the viper and alpha hemoglobin but we had the wrong proportion, or we get the right proportions as here but the wrong diagram or we get a set of data that is just agnostic that gives us a trichotomy. So what is it we are falsifying? There aren't any more lizard sequences available, no more reptile sequences.

Two things we might do: One is to accept Mayr's assumption that reptiles are a group and to sum up the data and take averages. You add together 3 kinds of beings: the turtle, viper or the lizard; 3 kinds of crocodiles; 3 kinds of chickens - when you do that, the 3 summations are for BC you get 27.9, for CD you get 30.9 and BD 26.9. They are virtually identical...

The creationist makes one assumption - that there are some groups in a set of data. The evolutionist, I think, has to make another assumption - that there some groups in there and that the groupings tell us something about the history of groups.

Someone from audience says: "Which creationist?"

Patterson: "Alright, me."

Audience member: "You don't mean Duane Gish?'

Patterson: "No, I don't. I mean a creationist systematist."

Audience member: "Duane Gish doesn't make any assumptions."

Other member: "Oh, yes he does."

Patterson continues lecture

I think I am able to treat that DNA .... data, taking all of it as saying something, but I only find two signals in it. In order to get a tree out of it, you have to infer that some of it is good data - the stuff that gives you that (at board) and some of at is bad data - the stuff that gives you that (at board). Sounds like [in] this case the stuff that gives you BC and AB is more than twice as numerous as the stuff that gives you BC is inferred. Now what is it that is being paired here? These are all identities at the nucleotide level, the ones that gives you AB are identities. The ones that give you .... - they are all identities at the nucleotide level. Yet somehow you'll have to say that some of those identities are ...... the same. Some of them are not the same, because the theory demands that. It seems to me somehow nonsensical.

There is one more problem with homology at the DNA level and that is this business of plurality, or inferred duplication. There is a similar problem coming in beside ...A. A couple of weeks ago Roger Lewin had a piece in <u>Science</u> (Oct. 23, 1981) on globin genes and in it he touched on a model of DNA that is now factual among molecular geneticists. He called it the "Vesuvian" model and a simple description of it by Roger Lewin and others is that every gene is constantly bombarding the rest of the genome with pseudogenes which are more or less perfect copies of itself. Now if this is so, and the model does have empirical support, then the problem of plurality of duplication of DNA is even more pressing.

In order to do DNA sequencing, you mix up the genome and clothe [clone?] a bit that you think is right that you can get out. If there really are all these bombarding pseudogenes lying, around I see no possible way of knowing whether you've got the right one or not.

Well, I'm sorry to have on so long about that and the point of it is that I think it has something to say about evolution because of all the discussion in the last few years whether evolution is tastable, and by evolution here I mean the general theory, the descent with modification, that species are mutable and related by descent rather than a specific theory about mechanisms.

If the general theory of evolution is testable, it must have some function ...... that can be confronted with reality. In other words, it must make some predictions. As far as I know only one sensible prediction has been offered. Niles Eldredge put it like this in a letter to <u>Science</u>.

"If evolution is descent with modification, the hierarchical array of organisms defined by nested sets of evolutionary novelties must result. This is evolution's grand prediction."

Then Niles went on to say that whatever organism you look at, whatever aspect of it you study, you find the same hierarchy. I've heard this same point made repeatedly, at meetings. There really is a hierarchy and there can be no hierarchy without history and therefore the prediction of evolution is met.

The first thing that strikes me about this is that it seeps [steps?] inside of evolution as a deductive inference from the systematic hierarchy. The people like Cuvier, Linneus, Hooker and a thousand other pre- Darwinians were merely fore- thinkers but they failed to see the necessary...

The second thing concerns the prediction of whatever aspect of organisms you look at, you find the same hierarchy. Not everyone wants to agree with that. Here's Ernst Mayr again in <u>Science</u>. Different types of characters: morphological characters, chromosomal differences, enzyme genes, regulating genes, and DNA matching made these a rather different groupings. Different stages in life cycles result in different groupings.

Here's Arnold ...... with the conclusion of his cladistic study of apes and men. His study denotes a clear lack of congruence between molecular and other more traditional kinds of data. Notice they are both saying the same. Mayr is saying that molecular data or whatever level you look at it, it doesn't seem to matter, morphology and Arnold are saying the same thing.

Now, the prediction. of evolution, according to Niles is that hierarchy and congruent hierarchy is what we'll find no matter what aspect of the species you look at. ...... the experience of Mayr and Arnold that there is no such thing as congruence. In particular, molecular data are incongruent with morphology.

Well, is that so? I'm not sure but I think there are other signs of it among protein sequences. For example, that cladogram that I was building up earlier is one of the congruents with everything that we know about morphology. Now there are published cladograms that have bird with sister group of mammals, Nile crocodiles, snakes and sister groups of all other amniotes. Never mind the details of it.

Let me put the question at the most basic level. How is it you recognize a hierarchy? At the level of the phenotype I think you have no real problem. We have a fairly rational concept of homology and I agree with Gary that the organizing principle is ontogeny and Von Baer's* law in particular. And as Gary suggested we can analyze phenotypification that way and get a hierarchy by a method that has no evolutionary implication at all. There is a history ahead but the history is on the genetics. The history is a what gives you the direction in Von Baer's law. We don't have to infer anything more about the geological [genealogical?] history, for example.

So what about this molecular level or the level of protein and DNA sequences? How do we recognize a hierarchy there? First of all, the concept of homology is estimates of the old autapomorphies we derived. The gibbon has 66 autapomorphies, 53 orang, 21 gorilla, chimp 19 and man has only 14. Notice that is the exact reverse of Mayr's prediction... So we get no useful grouping out of that.

The next set of characters is the one that picks out 3 of the 5.

ABC	30
ABD	11
ACD	10
CDE	10
ADE	9
ABE	7
BCD	7
BDE	4
ACD	3
BCE	3

One signal here - ABC form a group. Since there are 10 ways of picking 3 species out of 5, the probability of a repetition by chance in that sort of data is 1 in 10. This group has 19 repetitions over its nearest competitor, so far as I understand it; you can't be getting a signal like that. The probability of getting a signal like that purely by chance is 10^{-18}.

The last set of characters pick out 2 from the 5. Again there are 10 of them. I won't list them all. There is only one that gives a signal .... E. The rest of them are grouped very much like this with as far as I can see no distinguishable differences between them and here the probability according to my calculation is 10^{-17}.

So as I understand this data, the information that is in there, is there are 2 groups ABC ... DE; together they form a larger group and that's all the data says. It also gives an estimate of the number of autapomorphies to be grouped...

So what about the tree here and the numbers on the branches? As Steve said, it is produced by a program. Those numbers don't pop out of the data in any way, so I suppose those come from massaging the data with evolutionary theory. It is a program that assumes evolution to be true and tells the computer to find a tree. So my question will be: What is the tree telling us about? Is it telling us something about nature or something about evolutionary theory?

One last thing, at this level of DNA, the level of DNA, we also have a problem of homology. What does homology mean in terms of DNA? The alignment procedure is the same with protein sequences, its a purely statistical business but because in DNA we only have 4 possible nucleotides in any one position, we expect a 25% match by chance alone. Amongst these 5 very closely related species there is only a 7% match, that leaves a 45% variation to accommodate all other eukaryotes. I think that the problem with aligning DNA...will be extremely...

Then in the level of individual nucleotides we have to assume that a match of one position, say an adenine in the same position of all these, is homology. A mismatch is a non-homology. So bearing that notion in mind, let's look again at the tree. The tree tells us that - no, I'm going to forget all that. I was going to talk about the effects of putting data through a tree generation program.

The other thing we might do is accept Gary Nelson's optimistic view that every set of data is a glimpse of the truth. We might combine the 3 cladograms. Try that and let's see what we get. Comes out like this...(works on board) This is the cladogram we get with nice data. You like it? You don't. So what do a do? I'll take one more of these....and than I'll drop it. We have no more reptile sequences but we have plenty of mammal sequences. Let's try mammals, I think if we were to put mammals with birds and crocodiles in Mayr's diagram again I still do him no injustice if I assume that the diagram would look like this - that 3 is a mammal; C is a common ancestor, mammals that diverge very far in one direction, crocodiles a little in the other one and birds like that; B mammal, C crocodiles and D birds. B is a man, C is a crocodile and D is a chicken again. If we use the alpha hemoglobin data, this what we get.

BC	7.7%	(man-crocodile)
CD	7.7%	(crocodile-bird)
BD	14.7%	(man-bird)

What's going on? BC should be smaller than CD if the diagram is roughly right. In fact, they are both the same. BD should be the smallest of all, the 2 are miles apart. Something is wrong.

Well, I don't know what an evolutionist would do with this but I could guess. When I ask them about evolution the only answer I get from them is, "Convergence is everywhere." Well, I'm pretty sure they would take this as an example of convergence and they would read off the diagram: After all, birds and mammals converge into the endothermic adaptive zone.

This hemoglobin data might have given you another instance of convergence. Here the BC and CD proportion of the genotype are the same. What am I talking about? Haven't the faintest idea, not the faintest. I'll ask you what I mean. Yes. First time I put it up I meant to put it like this but that wouldn't do because these are both the same distance from C so you have to do it like this- they converge until the bird now converged until they are identical. But then the problem is they are each different from the turtle by 7.7%. Those 7.7%s are entirely different. They have to be apart by 15% whatever you do with it, convergence won't explain it. There is something funny in there.

So, after all, the question does seem insoluble. There is one more thing we can do with this. This data does give a diagram. It's not the diagram that is there (another diagram). The birds and mammals appear together and crocodiles and lizards so we follow Gary's recommendation and combine the cladogram and add mammals here. There's the cladogram we get with all this playing around. Do you like this any better? No, I'm sure you don't. So, what do we do? Well, luckily I don t have to keep asking you rhetorical questions because I'm talking about Mayr's example and I know what he did.

You remember Mayr published his original diagram in talking about the fortunes of genomes in 1974, when there very few samples of the genome available in the form of proteins or amino or nucleic acid sequences. And the two examples he offered to conform to his example were birds and crocs and apes. Well, far from matching his scheme, they all said the same thing that.... genome. So Mayr's prediction was falsified there.

As I said before, falsification is never absolute and in this case, I suggested that there 3 possible things that might be false: genome data, diagram, or the claims about evolution. Well, with man and ape Mayr still believes in the diagram, and he still believes he knows about evolution so all he counted on is his data. So he dropped the genome and returned to morphology and so last week we got Broca's center and the hippocampus question all over again or its equivalent.

There are two points. to be made there. The first concerns another of the parallels between evolutionism and creationism. Back in 1974, Mayr appealed to the genotype as the holder to true knowledge. At that time the genotype was still very much a mystery. Now that we have samples of a genotype from a wide variety of organisms it's no longer quite so mysterious, its dropped and a new mystery is proposed, Broca's center and that long list of unspecified autapomorphies of man. It seems that just like creationists, evolutionists are liable to appeal to mystery.

The second point is a much more important one and it concerns the levels at which we can investigate characters in systematics. The traditional level is morphology, and we're all pretty familiar with morphology. We feel at home with morphological data and competent to handle it just by its complexities. We have a good grasp of what homology means at the morphological level and we have the transformations of ontogeny as a guide in ordering characters into transformation series.

Back in 1978 Gary Nelson suggested, "The concept of evolution is an extrapolation or interpretation of the orderliness or ontogeny." So far as I know, at the morphological level, that is at all true. As Gary said it's Von Baer's* law that ontogeny goes from the general to the particular, that it's behind the transformations we invoke in morphology and behind the systematic hierarchy being built on those morphological characters.

Of course, all the transformations we invoke are not directly observed in ontogeny but I think you'll find that every transformation that is inferred is congruent with Von Baer's* law. So at the morphological level we have a sound concept of homology and we have ontogeny to help us in ordering homology. Morphology or in the most general terms, the phenotype, is the highest level of investigation in systematics.

The next level down is the level of gene products- proteins. Here the concept of homology becomes very general. In the first place we have the problem of plurality. Plurality is what the people who play with protein sequences call the relation between gene products that we think are the results of the duplication. So plurality is the molecular version of serial homology in morphology. The difference is that in morphology you can be fairly sure that you've struck the serial homolog because you have ontogeny in which to observe whether they really are duplications or something new. But with protein sequences and this question of plurality and inferred gene duplication, the inferred duplication is somewhat ... there is no way to investigate them. It does seem to me gene duplication is often invoked simply to explain away all the data.

When you are comparing two protein sequences as a whole rather than amino acid by amino acid, homology for a molecular biologist is a purely statistical concept. You compare the two sequences and if the masses between them pass certain statistical tests, they're homologous. There was a paper by Doolittle in Science two weeks ago explaining this concept.

Well, having decided that two sequences of the whole are homologous, you can then align them and compare them to specify position, and that is to say amino acid is a homology of a finer level. But here the problem is whether the amino acid is really the same, the same in .... because of the redundancy of the genetic code, they are only two amino acids out of the 20, tryptophan and methiamine, that are coded by a single triplet. All the rest are coded by two or more. So there are only two amino acids that are always the same in terms of the triplet that coded them and they are the rarest amino acids. They account for less than 2% of the average sequence. All the other amino acids coded by two or more triplets, so that the amino acid level, the protein level, the gene-product level and that can never be treated or hardly ever be treated as a homology at the DNA level. You're making a guess.

So at the gene product level, homology becomes a a pretty vague concept. And also we don't have ontogeny of the gene product level with which to help us to help us order the homology for the transformation series.

Now, I used to think that because there is no ontogeny in proteins, yet somehow we seem to need the notion of transformation to order sequences, that they provided some sort of proof of evolution. And I'm no longer sure that follows because the homology ..... that we infer and the transformations that we infer in ordering them are subject to the uncertainty because of the ambiguity of the genetic code. So the real molecular homology must lie further down than the level of DNA. Below the level of DNA we know virtually nothing because there is hardly any comparative data in the form of sequences that can be aligned and compared.

Last Saturday up in Ann Arbor I was lucky enough to meet Arnold... and talk to him about the first sets, of the datas - DNA sequences. This is mitochondria ... DNA of man, chimpanzee, gorilla, orangutan and gibbon. The work was done by Prager and Wilson and their group. The sequences are each: (works on board) (mitochondria of DNA) 896 nucleotides, of those 612 are invariant and the rest variant. This is the most parsimonious tree that the Berkeley people got out the data.

A = man
B = chimp
C = gorilla
D = orang
E = gibbon

This their tree. The numbers on here are the evolutionary events, lineages. This tells us lots of things about evolution. For example, it says gorilla has evolved fastest and man slowest. It says that the mitochondria of DNA evolved about times as fast as nuclear DNA. It says that sibling substitutions are several times as likely as coding substitutions and that being. the result of every comparison of DNA sequences that has yet been done. OK. That's what, the evolutionists made of the data.

Will you permit me to show you what a creationist makes of it? We've got 5 taxa, B, C, D, E there, so the first set of characters that we need to look at are the ones that pick 4 out of every 5. There are ... characters. That's the same nucleotide in every 4 and a different one in ..... ABCD there are 53, ABDE there are 21, ACDE 19, ...DE 40. There are 2 strong signals here - 53 (ABCD) and 66 (ABCE) but unfortunately those 2 groups are incongruent. The 2 strong signals are congruent one with the other so its best to treat these rather than groupings of 4 as much hazier at those levels and we don't have ontogeny and Von Baer's* law to guide us. Now I suggested it and commented on the DNA data that the hierarchy is recognized by massaging the data with evolutionary theory. Put it through a program based on evolutionary theory and that will .... get a hierarchy out. I wonder if the data is hierarchical without massaging of that sort? I don't know. At the protein sequence level where I have played about a lot, my impression is that it is very strongly hierarchical when you have a few sequences for when you take selected them so that you are just doing 5 or 6 problems but when you take a complete set of data, like the myoglobin that is now available, my experience is that the hierarchy can be melted away and this forces it by massaging it with evolutionary theory...

I think I'll stop and go into some quotes. This one is by Darwin the Origin.

"When the views entertained in this volume are generally admitted, systematists will be able to pursue their labors as at present.

By "present" Darwin means as in pre-Darwinian times, as in pre- evolutionary biology. He is saying don't let the theory get in the way of systematics.

The last quote is from Gillespie again and it concerns Hooker. If you think about it, Hooker was the only professional systematist amongst the Darwin coterie. He was also Darwin's oldest confidant in reading all of Darwin's manuscripts and talking to him solidly since 1840 and yet he remained unconverted to evolution until 1859. Here is Gillespie on the reason Hooker was not converted.

"Hooker adopted a view that species were immutable and each descended from a single parent. It was not necessarily his belief but a methodological postulate to make classification possible...Hooker believed that a taxonomist, who was an evolutionist, must ignore his theory and proceed as if species were immutable."

In other words, evolution may very well be true but basing one's systematics on that belief will give bad systematics.

(Patterson C., "Evolutionism and Creationism," Transcript of Address at the American Museum of Natural History, New York NY, November 5, 1981, p.14)