Disclosure

of things evolutionists don't want you to know

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FOR THE BIRDS

How can anyone read last month's set of articles in Science *about the genetic comparisons of birds, and still believe in evolution?*

This is the 232nd issue of *Disclosure*. It might be the most important issue we have ever published because it reviews the eight major articles produced by the Avian Phylogenetics Project published in the December 12, 2014, issue of the journal *Science*. It is so important we are devoting 8 of the 9 pages in our monthly "six-page newsletter" to it.

A consortium of 200 scientists from 80 labs used an incredible amount of supercomputer time to compare the whole genomes (that is, the complete DNA molecules) of selected species representing nearly every kind of living bird. Those 200 scientists tried their best to present their results in such a way as to support the theory of evolution; but when one looks at the facts they presented, one has to wonder how they could have reached the conclusions they did. That special report in *Science* gives an amazing look behind the scenes, which shows the extreme measures that evolutionists take to ignore the obvious conclusion.

TAXONOMY

The special report attempts to establish evolutionary history through taxonomy (that is, hierarchical biological classification). There are two things you need to know about taxonomy.

First, there is an invalid assumption that taxonomy has something to do with evolution. The underlying assumption evolutionists erroneously make is that similar creatures are similar because they have inherited those similarities from a close common ancestor. Therefore, the taxonomy of living things is assumed to represent the mythical Tree of Life.

Second, classification is entirely arbitrary. Consider this statement about a classification of birds called Accipitriformes from Wikipedia:

> **Accipitriformes** is an order that has been proposed to include most of the diurnal [active during the day] birds of prey: hawks, eagles, vultures, and many others, about 225 species in all. For a long time, the majority view has been to include them with the falcons in the Falconiformes, but some authorities have recognized a separate Accipitriformes. A recent DNA study has indicated that falcons are not closely related to the Accipitriformes, being instead related to parrots and passerines [perching birds].
>
> Since then the split and the placement of the falcons next to the parrots in taxonomic order has been adopted by the American Ornithologists' Union's South American Classification Committee (SACC), its North American Classification Committee (NACC), and the International Ornithological Congress (IOC). The British Ornithologists' Union (BOU) already recognized the Accipitriformes, and has adopted the move of Falconiformes. [1]

This statement tells us that it made sense to some authority to create a new, arbitrary biological category called Accipitriformes, and four important groups dedicated to the study of birds decided it was a good idea to say that falcons are more like parrots than hawks. Falcons didn't suddenly become more like parrots than hawks. Falcons didn't change at all. What changed was the academic opinion about which characteristics are most important when guessing their evolutionary origin.

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[1] http://en.wikipedia.org/wiki/Accipitriformes

Hawks have eyes set close together, giving them binocular vision, which gives them depth perception. They need depth perception because they are birds of prey, which swoop down on poor defenseless animals and eat them.

Parrots have eyes on the sides of their head, giving them great peripheral vision (so they can see predators coming), but no depth perception. They eat seeds, and nuts, and berries, but not other animals. Parrots know how to mimic the sounds of other animals.

Unlike parrots, but like hawks, falcons have binocular vision. Unlike parrots, but like hawks, falcons eat other animals. Unlike parrots, falcons cannot mimic the sounds of other animals. Clearly, falcons are more like hawks than parrots. But, DNA analysis says falcons are more like parrots, so common sense goes out the window.

The point of this long introduction is to establish the fact that evolutionists think that if they can figure out the "right" biological classification of every species of bird, they can trace their evolutionary history. With that in mind, let's see what they found out.

The Avian Phylogenetics Project

Unlike previous studies of bird DNA, this study examined the whole genome (the whole DNA molecule), rather than just certain parts. Here is their summary of what they did.

> To study evolution across a major vertebrate class, dissect the genomics of complex traits, and resolve a centuries-old debate on the avian species tree, we formed a consortium focused on the sequencing and analyses of at least one genome per avian order. The resulting data set of 48 consistently annotated bird genomes spans 32 of the 35 recently proposed avian orders, including all 30 neognath orders, and thus represents a wide range of avian evolutionary diversity. Our consortium's analyses have resulted in eight papers published today in *Science*, as well as 20 papers in other journals [avian.genomics.cn/en]. These include two flagship papers: one exploiting genomic-scale data to generate a highly supported avian order phylogeny that resolves many debates on the timing and topology of their radiation; the other a comparative genomic analysis exploring avian genome evolution and the genetic basis of complex traits. Other studies in *Science* describe convergent brain regions and gene expression for avian song learning and human speech, the singing activated genome in songbirds, complex evolutionary trajectories of avian sex chromosomes, a single loss of teeth in the ancestor of modern birds, the genomes of their closest extant outgroup (crocodilians) and inferred dinosaur ancestor, and computational methods developed for large-scale genomic analyses. [2]

The six things we want to address are: (1) The centuries-old debate on the avian species tree and the 35 recently proposed avian orders. (2) The evolutionary problem regarding song learning. (3) The evolutionary problem regarding sex. (4) The evolutionary problem about teeth. (5) The evolutionary problem about the relationship between dinosaurs, birds, and reptiles. And (6) the questionable techniques they invented to do the analysis.

Avian Orders and Species Tree

There has been a centuries-old debate on the avian species tree, with changing avian orders [groupings] because the mythical biological Tree of Life is not like the real chemical Periodic Table of the Elements. The Periodic Table is based on fact, not opinion. That's why there are never any debates about whether carbon should be next to nitrogen or oxygen. The Periodic Table doesn't change from year to year, based on some chemist's whim. The Table only changes when a new element is discovered. When a new element is discovered, it always fits perfectly in the table without causing any changes to the rest of the table, just like Dmitri Mendeleev predicted it would. Mendeleev was able to discover the order of chemical elements because that order really exists in nature. Biologists and geologists can't discover the evolutionary sequence because the evolutionary sequence they are searching for doesn't exist. They can't find it because it didn't happen. That's not just true of birds—it's true of all living things.

That's good for evolutionists because they can always pubish papers showing the old species tree was wrong, and species evolved sooner or later than previously believed, and their new analysis always "resolves the debate." Evolutionists don't have to make any real discoveries, like chemists do. ☺

In an attempt to be less subjective about the grouping of species, DNA analysis has been used in recent years. The fundamental idea is that the more similar the DNA of two species is, the more closely they are related. There are two problems with this.

The first problem is that it is hard to decide

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[2] Guojie Zhang, *et al.*, *Science*, 12 December 2014, "Introduction to Special Issue—A flock of genomes", pp. 1308-1309, http://www.sciencemag.org/content/346/6215/1308.full

how to make the comparison. That is, which parts of the DNA are significant, and should be compared, and which parts are not? How does one line up the parts of the DNA from two different species if the corresponding genes are in different places on the chromosomes? What if they don't have corresponding genes?

The second problem is that DNA comparisons often imply relationships that vary from slightly ridiculous to totally absurd. The conclusion that a falcon is more like a parrot than a hawk is just one of many examples. We first noted the inconsistencies between DNA analysis and common sense in July, 1999, [3] and have continued to do so over the years in various other essays.

Song Learning

Song learning presents a problem for evolutionists because it strikes at the very core of evolutionary thought. Richard Dawkins wrote,

> Darwin made it possible to be an intellectually fulfilled atheist. [4]

He said that because Darwin proposed an apparently plausible explanation for the vexing problem of how there could possibly be so many diverse life forms in the absence of a creator. The apparently plausible explanation was that a really unlikely, but useful, variation happened once, and that unlikely variation was inherited by its descendants. It replaced belief in an infinite number of miracles with belief in a very large, but finite number of miracles. ☺

Darwin thought that characteristics acquired through diet, exercise, or climate could be inherited. This made his theory plausible in the 19th century. We now know that acquired characteristics can't be inherited. (Baby girls aren't born with smaller versions of their mother's tattoos.) The neo-Darwinian explanation is that random mutations to DNA cause the evolutionary innovations which can be inherited. Neo-Darwinian evolution depends on something very unlikely happening by chance very often.

Since it is very unlikely that a marvelous innovation would happen accidentally once, it is much more unlikely that it would happen more than once. This has led to the assumption that all creatures with the same remarkable characteristic must have inherited it from the same common ancestor. This assumption is more "intellectually fulfilling" than the notion that miraculous biological innovations happen by chance all the time.

Given this fundamental assumption (that all species with a common characteristic evolved from a common ancestor) it had been widely assumed that all singing birds have a common ancestor. After all, the notion that birds could accidentally learn to produce variations in sound which could be used to convey information is highly unlikely. Therefore, all singing birds must have evolved from a common ancestor. At least, that was the conventional wisdom on this subject.

> We focused on vocal learning, which given our phylogenetic analyses is inferred as having evolved independently, either twice, in hummingbirds and the common ancestor of songbirds and parrots, or three times. All three groups have specialized song-learning forebrain circuits (song nuclei) not found in vocal nonlearners. [5]

Their phylogenetic analysis is shown on a diagram that is too big and complicated to reproduce here, [6] so we will just tell you about it. Their species tree has 42 horizontal branches, each branch representing a species grouping. At the top (let's call it Branch 1) are the songbirds, and the bottom branch (Branch 42) has an ostrich sitting on it. Going down to Branch 4 we find the parrots. There are just two branches between Branch 1 and Branch 4, so they aren't too distantly related. That's why they are unsure whether songbirds and parrots evolved vocal learning independently, or from the mythical common ancestor of branches 1 through 4 (and vocal learning was lost in branches 2 and 3).

Going on down the tree we see falcons on Branch 5, woodpeckers on Branch 8, owls, eagles and vultures on Branches 13, 14, and 15 respectively (more than 7 branches from falcons), assorted water birds on branches 16 through 26, and we finally get to hummingbirds on Branch 28. Because Branch 28 isn't anywhere near Branch 1 or Branch 4, they assume that hummingbirds independently evolved the ability to communicate vocally.

How do they explain the conclusion that birds evolved vocal communication two or three times independently?

> The fact that convergent neural circuits for vocal learning are accompanied by convergent molecular changes of multiple genes in species

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[3] *Disclosure*, July 1999, "The DNA Dilemma", http://scienceagainstevolution.info/v3i10f.htm

[4] Richard Dawkins, The Blind Watchmaker (1986), page 6

[5] Zhang, *et al.*, *Science*, 12 December 2014, "Comparative genomics reveals insights into avian genome evolution and adaptation", pp. 1311-1320, http://www.sciencemag.org/content/346/6215/1311.full

[6] http://www.sciencemag.org/content/346/6215/1320/F1.large.jpg

> separated by millions of years from a common ancestor indicates that brain circuits for complex traits may have limited ways in which they could have evolved from a common ancestor. [7]

In other words, if a problem only has one solution, everyone searching for the solution will find the same one. These three diverse groups of birds have similar genes for vocal learning because those are the only genes that can produce this ability. Therefore, all three groups of birds accidentally stumbled on the only genetic solution to the problem of how to communicate with others of the same species.

But, **if distantly related species have similar genes, how can the similarity of genes be used to infer a close relationship?** They can't. But they are—when they confirm evolutionary bias.

SEX

We've mentioned the problems that sexual reproduction poses for the theory of evolution in passing many times, and devoted three longer essays to the subject. [8]

Sex chromosomes are different for birds than they are for mammals. Mammals use male heterogamety, in which males are XY and females are XX. Birds are the opposite because they use female heterogamety in which females are ZW and males are ZZ. That's why the quotes below use Z and W for the sex chromosomes instead of X and Y.

The complete article about bird sex chromosomes [9] is so long it wasn't actually printed in the journal. It is available only on-line. The printed journal simply contained a shorter summary, part of which said:

> **INTRODUCTION:**
>
> Sex chromosomes originate from ordinary autosomes. Ancient sex-specific W or Y chromosomes, like that of female chicken or those of male mammals, usually have lost most functional genes, owing to a loss of recombination with their former homologs, the Z or X chromosomes. Such a recombination restriction occurred in a stepwise manner along most of the sex chromosomes in parallel in birds and mammals (creating so-called "evolutionary strata"), apart from small pseudoautosomal regions (PARs) that maintain recombination. Sex chromosomes of some basal birds like ostrich and emu have exceptionally large recombining PARs, but little is known about the genomic composition of most bird species' sex chromosomes.
>
> **RESULTS:**
>
> Surprisingly, we find that more than half of the studied species have a W chromosome that is not completely degenerated.
>
> **CONCLUSION:**
>
> Our study uncovered an unexpected complexity of avian sex chromosomes, due to the lineage-specific recombination suppressions and different tempo of W degeneration. In contrast to mammals, some birds never experienced global recombination arrest, or differentiate at a very low rate between Z/W even after the recombination loss. This may relate to different intensities of sexual selection across bird species and explain their lack of a general chromosome-wide dosage compensation mechanism. [10]

Whenever evolutionists don't find what they expect, they blame it on "loss." The "missing links" were there—but they got lost in the fossil record somehow. The male Y chromosome is smaller than the X chromosome, so they assume some unnecessary parts of it got lost through degeneration. They expected the same to happen for the W chromosome—but that's not what they found. But rather than admit that they were wrong, they try to come up with a convoluted explanation for how something they don't understand happened.

TEETH

The article about bird teeth also appears only on-line. [11] The journal contained just a summary, which said this (in part):

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[7] Andreas R. Pfenning, *et al.*, *Science*, 12 December 2014, "Convergent transcriptional specializations in the brains of humans and song-learning birds", http://www.sciencemag.org/content/346/6215/1256846.full

[8] *Disclosure*, February 2003, "Birds and Bees", http://scienceagainstevolution.info/v7i5f.htm
Disclosure, February 2004, "Sex and the Single Bacterium", http://scienceagainstevolution.info/v8i5f.htm
Disclosure, February 2010, "Sex and Violets" http://scienceagainstevolution.info/v14i5f.htm

[9] Qi Zhou1, *et al.*, *Science*, 12 December 2014, "Complex evolutionary trajectories of sex chromosomes across bird taxa", http://www.sciencemag.org/content/346/6215/1246338.full

[10] http://www.sciencemag.org/content/346/6215/1246338.full.pdf

[11] Robert W. Meredith, *et al.*, *Science* 12 December 2014, "Evidence for a single loss of mineralized teeth in the common avian ancestor", http://www.sciencemag.org/content/346/6215/1254390.full

> **INTRODUCTION:**
> The absence of teeth or edentulism has evolved on multiple occasions within vertebrates, including birds, turtles, and a few groups of mammals (anteaters, baleen whales, and pangolins). There are also mammals with enamelless teeth (aardvarks, sloths, and armadillos). All toothless/enamelless vertebrates are descended from ancestors with enamel-capped teeth. In the case of birds, it is theropod dinosaurs. Instead of teeth, modern birds use a horny beak (rhamphotheca) and part of their digestive tract (muscular gizzard) to grind up and process food. The fossil record of early birds is fragmentary, and it is unclear whether tooth loss evolved in the common ancestor of all modern birds or convergently in two or more independent lineages.
>
> **CONCLUSIONS:**
> We postulate, on the basis of [“fragmentary”] fossil and molecular evidence, a two-step scenario whereby tooth loss and beak development evolved together in the common ancestor of all modern birds. In the first stage, tooth loss and partial beak development commenced on the anterior portion of both the upper and lower jaws. The second stage involved concurrent progression of tooth loss and beak development from the anterior portion of both jaws to the back of the rostrum. We propose that this progression ultimately resulted in a complete horny beak that effectively replaced the teeth and may have contributed to the diversification of living birds.[12]

How can anybody read this and take it seriously? Enamelless teeth evolved from enamel-capped teeth? What is the evolutionary advantage in that? Sadly, I can tell you from personal experience that losing teeth is not a good thing! ☺

They said, “Instead of teeth, modern birds use a horny beak (rhamphotheca) and part of their digestive tract (muscular gizzard) to grind up and process food.” That’s why you have to put gravel in the bottom of your parakeet’s cage. The gravel acts like teeth inside the bird’s gizzard as it contracts and expands. Of course, the gravel is eliminated along with the indigestible parts of the food they have eaten, so they have to keep eating gravel on a regular basis.

Did you ever wonder how birds learned that they need to eat gravel to digest their food? If they have some compelling urge to eat gravel, why do they eat anything else? Why don’t they just eat gravel and starve to death? Back when they had teeth, they presumably didn’t eat gravel because they didn’t need to. So the muscular gizzard, and the urge to eat gravel, must have evolved at exactly the same time as the birds lost their teeth. What a lucky coincidence! ☺

But, as foolish as it is, the evolutionists are perfectly serious when they say that evolution made birds better suited for survival by losing the teeth they inherited from dinosaurs.

Speaking of dinosaurs …

Dinosaurs

They start with the ridiculous assumption that birds evolved from theropod dinosaurs.

> Birds originated from a theropod lineage more than 150 million years ago during the Jurassic and are the only extant descendants of dinosaurs.[13]

Of course, if the assumption is wrong, all the conclusions will be wrong. Their absurd conclusions should give them a clue they are wrong.

> Although many fishes and some amphibians have smaller genomes than birds, among amniotes, birds have the smallest. The genomes of mammals and nonavian reptiles typically range from 1.0 to 8.2 Gb, whereas avian genomes range from 0.91 in the black-chinned hummingbird (*Archilochus alexanderi*) to a little over 1.3 Gb in the common ostrich. A number of hypotheses have been proposed for the smaller avian genome size. Here, we document key events that have likely contributed to this smaller genome size.[14]

What are those likely, key events?

> The proliferation and loss of transposable elements (TEs) may drive vertebrate genome size evolution.[15]

> The condensed genomes may represent an adaptation tied to rapid gene regulation required during powered flight.[16]

In other words, they don’t have a clue. But, they have to write something.

> Although gene loss is a common evolutionary process, this massive level of segmental deletion has not been previously

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[12] http://www.sciencemag.org/content/346/6215/1254390.full.pdf

[13] Guojie Zhang, *et al*., *Science,* 12 December 2014, “Comparative genomics reveals insights into avian genome evolution and adaptation”, pp. 1311-1320, http://www.sciencemag.org/content/346/6215/1311.full

[14] *ibid.*

[15] *ibid.*

[16] *ibid.*

> observed in vertebrates. Over 77% of the 1241 genes present in the large segmentally deleted regions have at least one additional paralog in the green anole genome, a level higher than the overall percentage of genes with paralogs in the green anole genome or avian genomes (both at ~70%). This suggests that birds may have undergone functional compensation in their paralogous gene copies, reducing selection against the loss of these segmental regions. We predict that the loss of functions associated with many genes in the avian ancestor may have had a profound influence on avian-specific traits (table S11). [17]

The green anole is a little lizard I used to catch in Florida in the 1950's. Circus performers used to catch them, too, and sell them as "chameleons" up North when the circus came to town. Like real chameleons, they changed color (green when active, brown when sedentary). In 1955, I could catch any lizard I saw. But the last few years whenever I've tried to catch a lizard, I haven't even come close. They must have evolved to be much quicker than they were 60 years ago! ☺

They assume that comparisons of bird DNA with green anole DNA is meaningful because they assume that birds and lizards have a close common ancestor. Therefore, the massive differences are the result of losses of large segments of DNA in birds, which have been compensated for by evolution of smaller, but functionally equivalent genetic material. They want to believe that just as much as I want to believe lizards are quicker than they used to be! ☺

ANALYSIS

We've saved the best for last!

Usually we give the quote first and explain it in plain English second so our explanation won't prejudice your reading of the quote. Unfortunately, their description of their analysis is so inscrutable, you might be tempted to skip it. So, we are going to break with tradition and give you the summary first to help you understand it, and then let you read it for yourselves in the evolutionists' own words.

There are two main things to understand about their analysis.

First, they tried several different computer programs to analyze the whole genome, and got several different results. So, they published their report using the "best" analysis. How do they know which program is best? Obviously, the best program is the one that gave the "right" answer, which they already knew in advance. The "right" answer is the one that is most consistent with evolutionary prejudice.

Second, they analyzed the data by sorting it into lots of small bins. They examined each bin for inconsistent data, and discarded the inconsistencies. Then, after purging all the little bins of inconsistent data, they combined all the data and it was consistent! What a surprise! ☺ In their words,

> Within core landbirds, we found 100% BS. [18]

They use the abbreviation BS to mean, "Bootstrap Support;" but we think the more common meaning is more accurate. ☺

Here's the paragraph that summarizes how they cherry-picked the data analysis program, and introduces the notion of sorting the data into bins.

> We found that the SATé iterative alignment program yielded more reliable alignments than other algorithms for large-scale data, and we developed alignment-filtering algorithms to remove unaligned and incorrectly overaligned sequences (SM3 [Supplemental Material 3]). We developed ExAML, a computationally more efficient version of the maximum likelihood program RAxML, for estimating species trees from genome-scale concatenated sequence alignments (SM4). We also developed a statistical binning approach that improves multispecies coalescent analyses for handling gene trees with low phylogenetic signal to infer a species tree (SM5). [19]

A large portion of the report is spent justifying their choices.

They studied all Neoaves—that is neo [new] aves [birds]. Neoaves are modern birds (as opposed to extinct birds).

> To better determine the history of modern birds, we performed a genome-scale phylogenetic analysis of 48 species representing all orders of Neoaves using phylogenomic methods created to handle genome-scale data. We recovered a highly resolved tree that confirms previously controversial sister or close relationships. We identified the first divergence in Neoaves, two groups we named Passerea and Columbea, representing independent lineages of diverse and convergently evolved land and water bird species. Among Passerea, we infer

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[17] *ibid.*

[18] Erich D. Jarvis1, *et al.*, *Science*, 12 December 2014, "Whole-genome analyses resolve early branches in the tree of life of modern birds", pp. 1320-1331, http://www.sciencemag.org/content/346/6215/1320.full

[19] *ibid.*

> the common ancestor of core landbirds to have been an apex predator and confirm independent gains of vocal learning. Among Columbea, we identify pigeons and flamingoes as belonging to sister clades. Even with whole genomes, some of the earliest branches in Neoaves proved challenging to resolve, which was best explained by massive protein-coding sequence convergence and high levels of incomplete lineage sorting that occurred during a rapid radiation after the Cretaceous-Paleogene mass extinction event about 66 million years ago. [20]

It seems like every month we have to explain "convergence," in case there are new readers. "Convergence" means that completely different evolutionary paths just happened to end up in the same place.

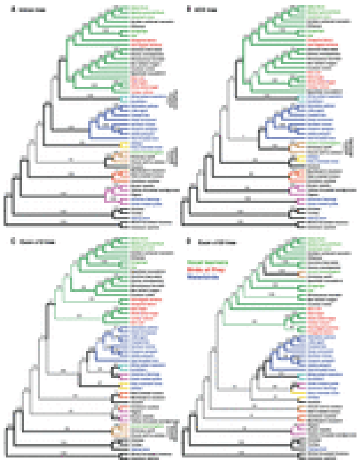
"Incomplete lineage sorting" is the technical term for "missing links." They can't figure out how some modern birds are related because (they assume) the intermediate forms went extinct 66 million years ago. If they just had those missing links, it would all be perfectly clear! ☺

In the next paragraph it says they found that evolution happened rapidly—except when it happened slowly. A lot of evolution happened 66 million years ago—unless it actually happened 80 to 125 million years ago. They don't really know because they get different answers depending upon what computer programs they use, or what data those programs analyze.

> The diversification of species is not always gradual but can occur in rapid radiations, especially after major environmental changes. Paleobiological and molecular evidence suggests that such "big bang" radiations occurred for neoavian birds (e.g., songbirds, parrots, pigeons, and others) and placental mammals, representing 95% of extant avian and mammalian species, after the Cretaceous to Paleogene (K-Pg) mass extinction event about 66 million years ago (Ma). However, other nuclear and mitochondrial DNA studies propose an earlier, more gradual diversification, beginning within the Cretaceous 80 to 125 Ma. This debate is confounded by findings that different data sets and analytical methods often yield contrasting species trees. Resolving such timing and phylogenetic relationships is important for comparative genomics, which can inform about human traits and diseases. [21]

As you will see in the following quotations, they admit that every DNA analysis method gives a different result. They, of course, think that their result (the Total Evidence Nucleotide Tree, "TENT") is the right one. In the past, introns [any nucleotide sequence within a gene that is removed by RNA splicing], exons [any nucleotide sequence within a gene that isn't removed], and UltraConserved Elements (UCEs) have been analyzed, and gave different results. (The UCEs are parts of the DNA molecule that don't show any variation, presumably because any variation would be fatal.)

They show this in the diagram below [22] comparing four different avian species trees obtain using different genetic comparisons. (We don't have space to print it big enough for you to read—but here's a small version just to show you it exists.)



Nor do their results square with analysis of "morphological characters" (that is, distinguishing physical features having to do with shape, such as appearance or physical ability), or with analysis of mitochondrial DNA.

> The avian biological gene trees have very low average BS. Of the three types of genomic markers—exons, introns, and UCEs (ultraconserved markers) analyzed—the exons have the least signal (average BS 24%), the introns have the most (average BS 48%), and the UCEs are intermediate in support (average BS 39%). The longest introns (with at least 10,000 bp) have the highest average BS (59%) but represent a very small fraction of the total set of gene trees examined (only 638 of 14,446). [23]
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> **All estimates of gene trees differ from our candidate species trees**

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[20] *ibid.*

[21] *ibid.*

[22] http://www.sciencemag.org/content/346/6215/1320/F4.large.jpg

[23] Siavash Mirarab, *et al.*, *Science*, 12 December 2014, "Statistical binning enables an accurate coalescent-based estimation of the avian tree", http://www.sciencemag.org/content/346/6215/1250463.full

> No single intron, exon, or UCE locus from our TENT data set had an estimated topology identical to the ExaML TENT or MP-EST* TENT (fig. S10, A and B). The top three loci (all introns) with the closest inferred topologies differed from the two versions of the TENT on more than 20 to 30% of their branches. Average topological distance with the ExaML species tree was 63% for the introns, 66% for the UCEs, and 80% for the exons. To test whether our total evidence data set missed some genes with the TENT topologies, we constructed a more comprehensive collection of genes trees with phylomeDB, which assigns orthology using maximum likelihood analyses (http://phylomedb.org) [see SM8 and (68)]. For ~13,000 (low-coverage genomes) to ~18,000 (high-coverage genomes) annotated genes across avian species, phylomeDB inferred orthologs for 94.58% of them and these agreed with the synteny-based orthology of the 8251 protein-coding genes of the TENT by 93%. This more complete set of protein-coding genes still did not have a single estimated gene tree that was fully congruent with the ExaML or MP-EST* TENT trees (fig. S10, C and D), and there was overall low congruence with the species trees (http://tol.cgenomics.org/birds_v1) (fig. S11, A and B). The conflicting nodes largely reflected branches with low statistical support (approximate likelihood ratio test < 0.95), which primarily corresponded to the short successive deep branches of Neoaves. These findings can be explained by both a low amount of phylogenetic signal in individual loci (figs. S24 to S26 and SM4) and a high amount of ILS during the neoavian radiation. [24]
>
> **Comparisons of TENT with previous studies**
>
> The TENT contradicted some relationships in avian phylogenies generated from morphological characters, DNA-DNA hybridization, and mitochondrial genomes. [25]

CONCLUSION

How does one disprove the theory of evolution if all these contradictions with evolutionary expectations don't do it? How can it be falsified? If the findings of this study don't disprove the theory of evolution, what will? The facts clearly don't support the evolutionary hypothesis. There is "overall low congruence with the species tree." They cherry-picked the data and got (in their words) "100% BS." ☺

Unfortunately, their obsession with evolution caused them to overlook the obvious. They discovered the communication genes that songbirds, parrots, and hummingbirds have which other birds don't have. They found,

> Song-learning birds and humans share independently evolved similarities in brain pathways for vocal learning that are essential for song and speech and are not found in most other species. Comparisons of brain transcriptomes of song-learning birds and humans relative to vocal nonlearners identified convergent gene expression specializations in specific song and speech brain regions of avian vocal learners and humans. The strongest shared profiles relate bird motor and striatal song-learning nuclei, respectively, with human laryngeal motor cortex and parts of the striatum that control speech production and learning. Most of the associated genes function in motor control and brain connectivity. Thus, convergent behavior and neural connectivity for a complex trait are associated with convergent specialized expression of multiple genes. [26]

The next step should be to look for those same genetic characteristics in dolphins, whales, and bats. Communication depends upon pattern generation and pattern recognition, which are fundamental to information transmission and information processing. Therefore scientists should try to learn more about those genes because they are instrumental in mental development. They should pay special attention to the differences in the genes in people with Down's syndrome and other mental disabilities. This could lead to effective gene therapy for mental disorders.

We have no doubt that someday, some scientist will use this information to cure mental illness. We also believe the scientist will be a creationist, not an evolutionist, because he isn't Hell-bent on massaging the data in an attempt to disprove the Bible, and will instead honestly evaluate the data to discover ways to put that data to good use.

If we could just cure mental deficiencies, nobody would believe in the theory of evolution any more! ☺

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[24] Erich D. Jarvis, *et al.*, *Science*, 12 December 2014, "Whole-genome analyses resolve early branches in the tree of life of modern birds", pp. 1320-1331, http://www.sciencemag.org/content/346/6215/1320.full

[25] *ibid.*

[26] Andreas R. Pfenning, *et al.*, *Science*, 12 December 2014, "Convergent transcriptional specializations in the brains of humans and song-learning birds", http://www.sciencemag.org/content/346/6215/1256846.full

Web Site of the Month – January 2015

by Lothar Janetzko

PRESENTING THE CREATION MODEL

http://cavern.uark.edu/~cdm/creation/presentation.htm

Creation Insights

This month's web site review looks at a site which seeks to provide evidence for the supernatural origin of the universe, life and species. The particular article for discussion is the main web page for the *Creation Insights* website.

The author, Patrick Briney, Ph.D., provides some background into his own experience regarding creation and evolution. He was an evolutionist until his third year of college. He switched positions after gaining insights about the subject of origins. He states that "I am excited about creation science as a field of study because it offers a cohesive model of everything that exists, consistency with scientific laws, and a wide open field for pioneering investigators…The purpose of this presentation is to show why creation models are reasonable and credible models of science."

In the introduction of the article he also states the "Science is a tool and is not inherently theistic or atheistic. It should be used to discover truth not to censor unpopular models. Recognizing the important role science plays in verifying and offering credibility to systems of thought, science is the very tool needed to resolve the debate between natural and supernatural models of origins."

After the introduction, the web site author discusses scientific models. He believes that "legitimate scientific models fulfill four qualifications, namely, 1) Explain data, 2) Are supported by data, 3) Do not contradict data and 4) Predict discoveries. Credibility of an origin model should be based on its ability to logically explain data, its consistency with known facts, and its reliability to make accurate predictions." [Editor's note: This month's feature article shows how the Avian Phylogenetics Project fails to fulfill these four qualifications.]

An outline is then presented to serve as a tool to use in the study of origins. The outline contains the following topics: 1) Origin by Design, 2) Origin of Universe: 3) Origin of Life: 4) Origin of Species: and 5) Origin and History of Earth.

These topics are then presented in some detail and observations are made that the creation model "offers a consistent and relevant explanation for observed phenomena… while the evolution model cannot dissociate itself with obvious bias."

There is much to explore on this web site so just follow topics of interest as there are many links to additional material.

Disclosure, the Science Against Evolution newsletter, is edited by R. David Pogge.

All back issues are on-line at **ScienceAgainstEvolution.info**.