

THE CASE AGAINST COMMON DESCENT

Common descent (also called 'universal common ancestry') is the hypothesis that all living species on earth are descended from a single organism that lived in the distant past.¹ By logical necessity this means, of course, that species must have undergone major evolution throughout life's history, and belief in some kind of evolution can be traced back to Ancient Greece.² Evolutionary ideas, including the idea of common descent, gathered popularity in the first half of the nineteenth century.³ One man who believed in common descent was Erasmus Darwin, the grandfather of Charles Darwin⁴ Thus, both common descent and major evolutionary change over time were familiar concepts to Charles Darwin at the time he formulated his famous theory. However, with Alfred Russell Wallace, he was the first to propose a plausible mechanism by which evolution might work.⁵

Today, Common Descent is often regarded as a 'proven fact' because of the 'overwhelming' evidence in support of it. But is the evidence as really as strong as most people think? This essay will examine some common lines of evidence used in its favour and show why they fail, before looking at some additional lines of evidence to show that common descent is an unworkable hypothesis.

ARGUMENTS FOR COMMON DESCENT

The argument from comparative morphology

Evolutionists have long argued that the similarity of structures in living things (homology) is a sure sign of common ancestry. Erasmus Darwin put it this way: "when we revolve in our minds the great similarity of structure, which obtains in all the warm-blooded animals, as well quadrupeds, birds, and amphibious animals, as in mankind; from the mouse and bat to the elephant and whale; one is led to conclude, that they have alike been produced from a similar living filament".⁶ Charles Darwin was similarly convinced that morphology showed common descent: "the several classes of facts which have been considered in this chapter, seem to me to proclaim so plainly, that the innumerable species, genera, and families of organic beings, with which this world is peopled, have all descended, each within its own class or group, from common parents, and have all been modified in the course of descent, that I should without hesitation adopt this view, even if it were unsupported by other facts or arguments".⁷

In response, Creationists have pointed out that homology does not necessarily point to common descent, because there is an equally compelling possibility – a common designer.⁸ It then becomes a simple question of the worldview within which one frames the evidence. But there is another reason to question the inference to common descent drawn from comparative morphology which does not rely on belief in a supreme designer. That reason is the phenomenon, ubiquitous in biology, of convergence. The term 'convergence' is used when the same or similar structures are found in organisms not believed to be closely related by common descent. Since orthodox biologists accept the truth of evolutionary theory, the phenomenon is usually referred to as 'convergent evolution', and is assumed to happen either as a result of common environmental or developmental constraints.⁹ If Darwinian evolution were correct, this might conceivably be so; but it undercuts the supposed proof of common descent from comparative morphology. If homology cannot always be ascribed to common descent, even by evolutionists¹⁰, then it cannot be used to prove common descent in other circumstances.

Now, it might be argued that a few isolated examples of convergence should not be enough to overturn the much more prominent pattern in nature of homology due to common descent. Also, if form follows function¹¹, we should not be surprised if evolution confers fish, seals and porpoises

with streamlined bodies for swimming, or provides two different desert-dwelling plant families with similar leafless, succulent stems.¹²

However, convergence is anything but rare¹³, and often much more profound than a streamlined body shape. For example, the katydid *Copiphora gorginensis* has been shown to process sound in much the same way as mammals, collecting sound with a tympanic membrane, passing it through the middle ear, and analysing its frequency through the movement of waves across a fluid, as in the cochlea: that's despite the katydid having one of the smallest ears of all animals.¹⁴ Then there is the

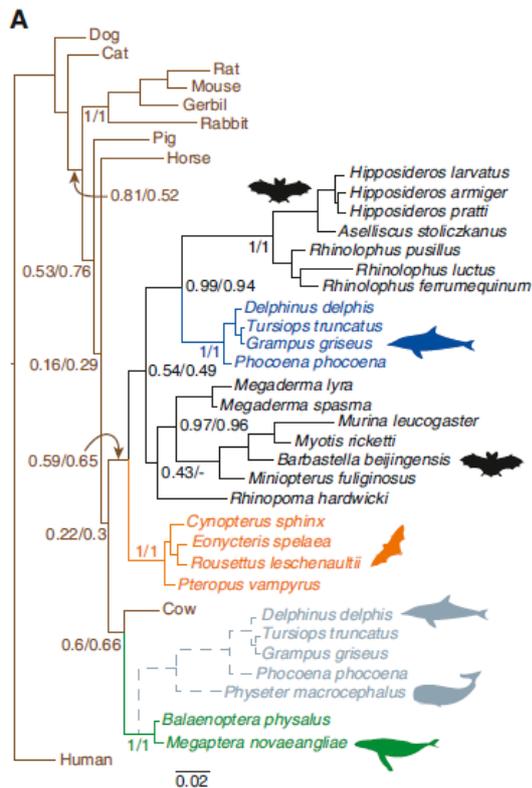


Figure 1: Phylogenetic tree based on the amino acid sequence of the Prestin gene. Liu Y, Cotton JA, Shen B, Han X, Rossiter SJ and Zhang S (2010). *Current Biology* 20(2), R53-R54

compound eye of arthropods, which evolutionists think must have evolved many times over: “arthropod compound eye evolution has remained controversial, because one of two seemingly very unlikely evolutionary histories must be true. Either compound eyes *with detailed similarities* evolved multiple times in different arthropod groups or compound eyes have been lost in a seemingly inordinate number of arthropod lineages” [emphasis mine].¹⁵

The pattern of convergence occurs at all biological level, from organ systems right down to the molecular level.¹⁶ One example involves bats, whales and dolphins, which all use sonar pulses for orientation and finding prey (echolocation). This “spectacular example of phenotypic convergence”¹⁷ extends to a mammalian gene (called *Prestin*) involved in the perception of high frequency tones; one study found a convergence in the amino-acid sequence coded by the gene in bats and dolphins. In fact, when they constructed a phylogenetic tree based on amino acid sequences, one group of bats were found to be more closely related to dolphins than they were to other bats (Figure 1).¹⁸ Another example can be found in squid, which ‘evolved’ a complex bioluminescent organ in two unrelated

lineages, with almost identical gene expression in both groups.¹⁹ A most remarkable convergence has also been discovered in the brains of humans and songbirds, which both have specialised neural networks dedicated to vocal learning. These specialised brain networks are not found in other birds, nor are they found in the higher apes, only in humans and songbirds. And yes, the convergence extends to molecular changes within the genes.²⁰

The pattern of convergence is common enough that taxonomists are well aware it can – and has – complicated the process of constructing evolutionary trees.²¹ In both birds and orb-weaving spiders, molecular evidence has overturned the previous trees based on morphology. Orb-weavers are no longer considered a monophyletic group (where all members are related by common descent), meaning that the trait of web-weaving had to evolve several times.²² An extensive study of 48 bird species found pigeons and flamingos to be closely related, and that the trait of vocal learning arose independently several times.²³ The examples here are a drop in the ocean. Suffice it to say that convergence is a remarkable pattern in nature, leading us naturally to infer design. As stated in one evolutionary paper, “Convergent evolution is a potent indicator of optimal design”.²⁴

The argument from embryology

The argument from embryology can be regarded as a special case of the argument from comparative morphology. The difference is that animals are much more alike at the embryo stage, and are believed to show the pattern of common descent more clearly than the adult animal forms. As Richard Dawkins has said, “every individual animal has a developmental history. It starts as an embryo and grows, by disproportionate growth of different parts of the body, into an adult. Evolution is not a genetically controlled distortion of one adult form into another; it is a genetically controlled alteration in a developmental program”.²⁵

Ernst Haeckel, a prominent early Darwinist, was the first to popularise the argument from embryology. He coined the phrase “ontogeny recapitulates phylogeny”, which summarised his theory that embryos develop in ways that resemble their evolutionary history.²⁶ He famously

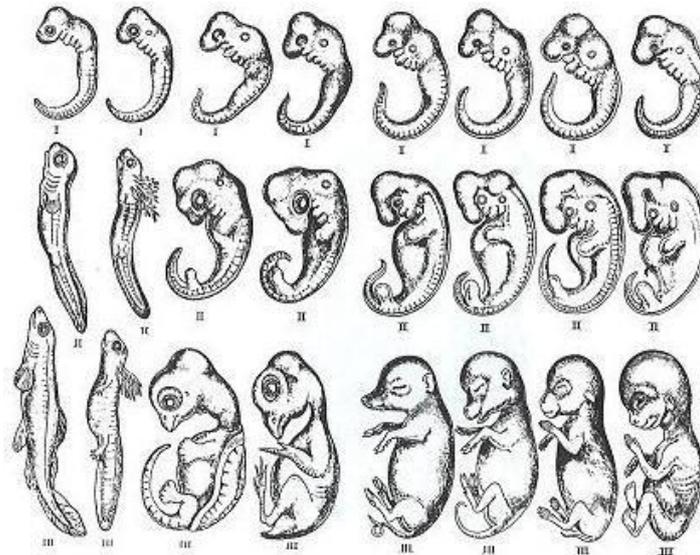


Figure 2: Embryo drawings by Ernst Haeckel. http://www/evolutionnews.org/2007/05/the_textbooks_dont_lie_haeckel003663.html

illustrated a series of embryo drawings, purporting to show how similar human embryos were, at various stages, to animal embryos (figure 2). These drawings are known to be fraudulent, but this has not prevented their use in textbooks as evidence for evolution.²⁷

Haeckel’s version of recapitulation has been discredited, but the version postulated by Karl von Baer is still put forward as evidence for evolution; he suggested that general characteristics shared by an animal’s group appear first in its development, followed later by more specialised characteristics.²⁸

Table 1: A morphological comparison between embryos at the talibud stage. Never = trait never expressed. Yes = present at talibud stage. No = not present at talibud stage. Partial = structure faintly indicated. Adapted from Richardson *et al* (1997). *Anatomy and embryology* 196(2), 91-106. Internal citations omitted.

Species	Somites	Pharyngeal arches	Limb or paired fin buds	Lens buds	Liver tube	Heart
Lamprey	40	4	Never	Yes	Yes	Yes
Dogfish	44	4	No	Yes	Yes	Yes
Platyfish	12-13	3	Yes	Yes	No	No
Queensland lungfish	30-32	2	No	No	No	Yes
African clawed toad	19	1	No	Partial	Yes	No
Caecilian	65	6	Never	Yes	No	Yes
Lizard	32	3	Partial	Yes	Yes	Yes
Chicken	23	2	No	Yes	Yes	Yes
Scaly anteater	28	3-4	Partial	Partial	Yes	Yes
Mouse	30-34	3-4	Yes	Yes	Yes	Yes

Von Baerian embryology was later modified into the hourglass model, in which early and late stages of embryo development are divergent, but there is a conserved stage in the middle where the embryos are most similar.²⁹ However, even at the talibud stage, where embryos are considered most alike, close observation has shown major structural differences between different groups (Table 1).³⁰ Thus embryology, like comparative morphology, fails to establish a pattern of common descent. There is another problem: macro-evolutionary change requires mutations expressed very early in an animal's development.³¹ Unfortunately for the evolutionist, it is these very mutations which are the most harmful and least tolerated by natural selection.³²

The argument from molecular biology

Emile Zuckerkandl and Linus Pauling were early advocates of using molecular evidence to establish phylogeny, seeing the potential it had to provide support for evolution: "There is yet an ultimate reason, of a more philosophical nature, for interest in the paleogenetic approach... it will be determined to what extent the phylogenetic tree, as derived from molecular data in complete independence of the results of organismal biology, coincides with the phylogenetic tree constructed on the basis of organismal biology. If the two phylogenetic trees are mostly in agreement with respect to the topology of branching, the best available proof of the reality of macro-evolution would be furnished. Indeed, only the theory of evolution, combined with the realisation that events at any supramolecular level are consistent with molecular events, could reasonably account for such a congruence between lines of evidence obtained independently".³³

If Zuckerkandl and Pauling's two lines of evidence were indeed congruent, it would certainly give strong support for common descent. The logical corollary is that when those two lines of evidence turn out to be contradictory, it cannot help but weaken the theory. I have already referred to two studies (on birds and orb-weaving spiders respectively) in which the molecular evidence painted a

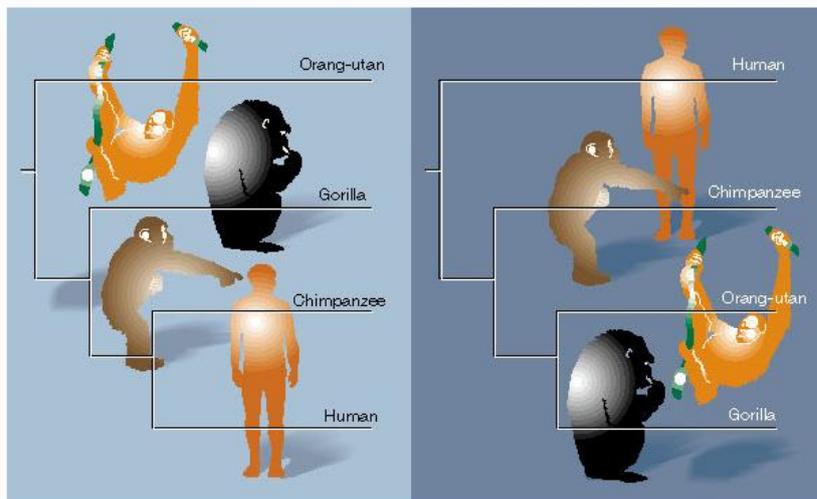


Figure 3: Two phylogenetic trees based on molecular evidence (left) and morphological evidence (right). From Gura T (2000). Bones, molecules...or both? *Nature* 406, 230-233.

different story from the morphology. These are not isolated examples – so common are the conflicts between molecules and morphology that there is a spirited debate between taxonomists as to which line of evidence is more reliable.³⁴ The evidence on the phylogeny of higher apes is conflicting (see figure 3).³⁵ Furthermore, the phylogenetic tree for placental mammals based on microRNAs is radically different from the traditional tree based on morpho-

logy.³⁶ A review of invertebrate phylogeny put it this way: "taken together, modern re-evaluations of traditional evidence support different and *mutually exclusive* subsets of relations... this must lead to reduced confidence in the neat dichotomous phylogenetic trees that textbooks display" [original emphasis].³⁷

Similar to Zuckerkandl and Pauling, Richard Dawkins thinks the congruence between molecular phylogenetic trees using different genes provides powerful evidence for evolution: "...you can take any pair of animals you like – kangaroo and lion, horse and cat, human and rat – any pair of animals you

like, and count the number of differences in the letters of a particular gene, and you plot it out, and you find that it forms a perfect branching hierarchy. It's a tree, and what else could that tree be, but a family tree. And then you do the same thing for another gene. Having got the family tree for *FOXP2*, you then do the same thing for another gene, and another, and another. You get the same family tree... This is overwhelmingly strong evidence. The only way you could get out of saying that that proves evolution is true is by saying that the intelligent designer, God, deliberately set out to lie to us, deliberately set out to deceive us."³⁸

Unfortunately for Dawkins, different trees made from different genes *do* conflict, despite his claims. One study commented on the uncertainty of the relationships between the five major metazoan groups: "In the last few years, this debate has been fuelled by a plethora of conflicting phylogenetic hypotheses generated using molecular data".³⁹ Some researchers hoped that whole-genome studies would resolve these problems.⁴⁰ However, a study of bats noted that the problem has only become *greater* with whole-genome data sets, such that "phylogenetic conflict is common, and frequently the norm rather than the exception".⁴¹ In the light of so much conflicting evidence, how can we say that universal common descent is proven beyond reasonable doubt?

The argument from the genetic code

In the minds of some, the fact that every species on earth is built from instructions coded within the same DNA molecule is proof, in itself, that we are all descended from one original life-form (figure 4). George McGhee wrote, "All life on earth evolved from a single common ancestor. We know this because all life on Earth used the exact same coding molecule, DNA, and the exact same molecular construction: DNA codes for RNA, and RNA codes for the same 20 amino acids that are assembled to produce proteins, the building blocks of life".⁴² The inimitable Richard Dawkins put it this way: "The DNA code is invariant across all living creatures, while the individual genes themselves vary. This is a truly astounding fact, which shows more clearly than anything else that all creatures are descended from a living ancestor... what varies is what is written in the code, not the code itself."⁴³

		Second letter				
		U	C	A	G	
First letter	U	UUU } Phe UUC } UUA } Leu UUG }	UCU } UCC } Ser UCA } UCG }	UAU } Tyr UAC } UAA Stop UAG Stop	UGU } Cys UGC } UGA Stop UGG Trp	U C A G
	C	CUU } CUC } Leu CUA } CUG }	CCU } CCC } Pro CCA } CCG }	CAU } His CAC } CAA } Gln CAG }	CGU } CGC } Arg CGA } CGG }	U C A G
	A	AUU } AUC } Ile AUA } AUG Met	ACU } ACC } Thr ACA } ACG }	AAU } Asn AAC } AAA } Lys AAG }	AGU } Ser AGC } AGA } Arg AGG }	U C A G
	G	GUU } GUC } Val GUA } GUG }	GCU } GCC } Ala GCA } GCG }	GAU } Asp GAC } GAA } Glu GAG }	GGU } GGC } Gly GGA } GGG }	U C A G

Figure 4. The standard Genetic code. DNA is read in three-nucleotide blocks called codons, of which there are sixty-four. Sixty-one codons between them code for twenty amino-acids. The remaining three are 'stop' codons which tell the ribosome to end the translation process.

Of course, immediate objections to this line of reasoning can be raised. Shakespeare's sonnets and the King James Bible share a common code – the English alphabet – but they do not share common ancestry. Moreover, if all life was created together by a wise designer, why should he not use the same code in all his works? But there is an even more basic flaw in Dawkins' reasoning: his facts are wrong. The genetic code is not 'invariant across all living creatures': the National Centre for Biotechnology Information lists twenty-four known variants of the genetic code, in addition to the standard code.⁴⁴ Richard Dawkins himself recognises that any evolution in the genetic code is problematic: "Any mutation in the genetic code itself (as opposed to mutations in the genes that it encodes) would have an instantly catastrophic effect, not just in one place but throughout the whole organism".⁴⁵ He is absolutely right; even a single mutation in the genetic code would alter every single protein in every single cell, something no living creature could survive. With this in mind, how did these variations in the genetic code arise? (We might ask where the genetic code came from in the first place). Thus the genetic code generates problems, not proof, for the theory of common descent.

The argument from Human-chimpanzee similarity

The similarity of humans and chimps is an argument for common descent on a small scale, and is susceptible to all the same weaknesses as common descent in general. If universal common descent as a whole cannot be demonstrated, what basis do we have for assuming that humans and chimpanzees have a common ancestor? Few people would argue that while mankind and monkeys have a common ancestor, other species were specially created. Likewise, not many would argue that common descent was true for all life on earth except for humans and chimps. Nevertheless, the issue of whether humans and chimps had a common ancestor is the most hotly debated of all the questions relating to common descent, because this is where it gets personal. It is also where the theory of evolution most comes into direct conflict with Biblical teaching. Therefore it seems appropriate to deal with it in isolation here.

Human and chimpanzees are often said to have genomes that are close to identical. Depending on the source, slightly different values are claimed, but the figure is usually between 96 and 99 percent.⁴⁶ The figure is difficult to pin down, as it varies depending on the method used; one geneticist has estimated a much lower figure of 70 percent.⁴⁷ Another study states that "for about 23% of our genome, we share no immediate genetic ancestry with our closest living relative, the Chimpanzee".⁴⁸ Whatever the true figure, it seems clear that human and chimpanzee genomes have significant similarities. This surprises nobody, be they creationist or evolutionist. The similarity between human and chimpanzee body plans is obvious to a child, and it would be surprising if there were *not* significant genetic similarities. A better question to ask is this: what accounts for the profound differences, physical, intellectual, emotional and spiritual, between humans and chimps? It is worth noting in passing the inability of the Neo-Darwinian mechanisms of mutation and natural selection to account for the differences that must have appeared between the two species since they diverged. In a paper designed to disprove the arguments of the Intelligent Design advocate Michael Behe, the authors admitted that, by their own calculations, it would take 200 million years for a single instance of two coordinated mutations to become fixed in the human population.⁴⁹ It takes at least three mutations to convert even a single protein to a highly similar one that performs a slightly different function.⁵⁰ There simply isn't time.

Francis Collins has outlined a somewhat subtler argument for common ancestry between humans and chimps: "The human has twenty-three pairs of chromosomes, but the chimpanzee has twenty-four. The difference in the chromosome number appears to be a consequence of two ancestral chromosomes having fused together to generate human chromosome 2... the sequence at that location – along the long arm of chromosome 2 – is truly remarkable. Without getting into the technical details, let me just say that special sequences occur at the tips of all primate chromosomes. Those sequences generally do not occur elsewhere. But they are found right where evolution would

have predicted, in the middle of the fused second chromosome. The fusion that occurred as we evolved from apes has left its DNA imprint here. It is very difficult to understand this observation without postulating a common ancestor”(Figure 5).⁵¹ Collins does not say what his ‘special sequences’ are, but the most likely candidate is something called “Interstitial Telomeric Sequences” or ITSs. Unfortunately for Collins, they are not located at the exact breakpoints between chromosomes, and “were present before the reorganisations occurred”.⁵² Speaking of chromosomes, one study found ‘radical’ differences between human and chimp Y chromosomes both in gene content and overall structure.⁵³ Simplistic comparisons between human and chimpanzee chromosomes may look convincing, but as the saying goes, ‘God is in the details’.⁵⁴

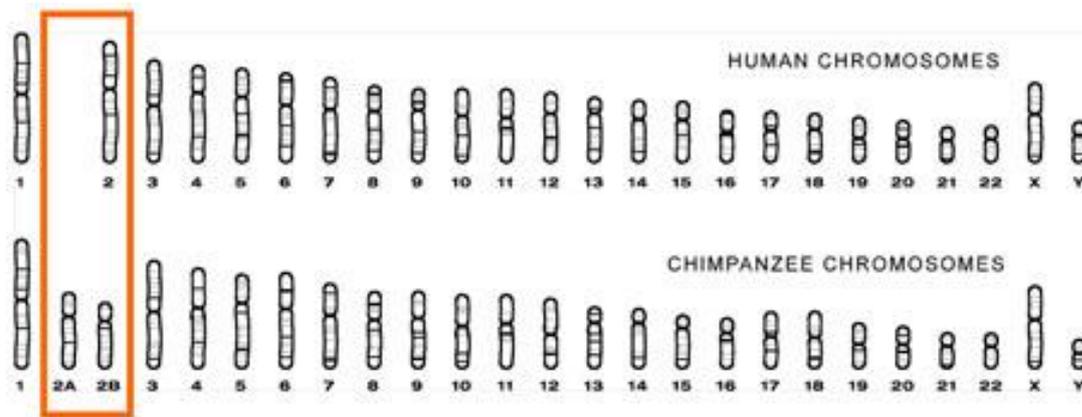


Figure 5: A comparison of human and chimpanzee chromosomes, with Collins’ hypothetical fusion highlighted. http://scienceasworship.hostoi.com/img_chimp_chrom.jpg

EVIDENCE AGAINST COMMON DESCENT

Germ Cell formation

In the germ line of animal embryos, a group of cells called Primordial Germ Cells (PGC’s) must first be produced, from which the gametes form.⁵⁵ There are two modes of germ cell formation; *pre-formation*, in which the cells generate inherited internal signals from within their own structure to become germ cells, and *epigenesis*, in which the signals are received externally from surrounding tissues.⁵⁶ These cells are essential to an organism’s ability to reproduce, and mutations that disrupt the development of PGC’s always have a deleterious effect on reproduction.⁵⁷ Unfortunately for common descent, the two modes of PGC are randomly distributed throughout metazoan lineages.⁵⁸ This requires that the mode of PGC formation, which for obvious reasons is strongly resistant to change, had to arise anew on many occasions for common descent to be true.

Orphan Genes

Orphan genes, also called taxonomically restricted genes (TRGs), are genes that are unique to a particular taxonomic group, having no recognised homologs (similar genes) with other species. Every taxonomic group studied so far has a genome at least 10 percent made up of orphan genes.⁵⁹ A study of the leafcutter ant (*Atta cephalotes*) revealed over 9000 proteins that are unique to that species, more than half its predicted proteome.⁶⁰ An analysis of the Argentine ant (*Linepithema humile*) found that 45 percent of its genome was unique compared to the three other species they analysed.⁶¹ The human genome also contains many orphan genes that had to have arisen ‘de novo’ since our divergence from the apes.⁶²

Where did these genes come from? Common descent cannot account for them. An evolutionist must assume that large parts of the genome arose from scratch during every major speciation event⁶³ – something that boggles the mind. Alert readers may have thought of a potential objection: orphan genes may only be orphans due to incomplete knowledge; not all genomes have yet been sequenced, and homologs for them may eventually turn up. However, this appears not to be the

case, as the discovery of orphan genes has so far kept pace with new information.⁶⁴ Orphan genes remain a problem for the theory of common descent.

Patterns in the Fossil Record

Charles Darwin saw the lack of a finely graduated series of transitional fossils as the most serious difficulty with his theory. Another problem was the abrupt manner in which radically different forms of life appear in the fossil record, particularly in the rock layers we know today as the Cambrian. The reason, he said, was that the fossil record is imperfect.⁶⁵ Since Darwin, multitudes of new fossils have been found all over the world in finds like the Burgess Shale, and statistical studies have shown that enough is now known for the fossil record to be considered reliable.⁶⁶ Despite this, the problem Darwin identified is as sharp as ever. The abrupt appearance of life forms that Darwin noted is now known as the “Cambrian explosion”; twenty out of the twenty-seven known phyla in the fossil record first appear in the Cambrian.⁶⁷ Even under evolutionary assumptions, many of these phyla must have evolved in less than five million years, and in some cases within one million years, leading palaeontologists James Valentine and Douglas Erwin to admit that “neither microevolutionary, species selection, nor rapid macroevolutionary jumps will adequately satisfy the data”. They therefore concluded that evolution must have operated differently in the past than it does today.⁶⁸

The rapid appearance of new forms is not the only challenge posed by the fossils. If all life evolved from a common ancestor, the fossil record should show a ‘bottom up’ pattern, in which small differences, such as those between closely related species appear first, building up to large differences such as those between different phyla. The fossil record instead shows a ‘top down’ pattern, where the large-scale differences between phyla and classes first occur, followed only later by a diversity of different genera and species.⁶⁹ This fits with what we know about the inventions of intelligent minds – the overall design is first produced, followed downstream in time by variations on a theme. For example, the blueprints of a house are drawn up before the light-fittings or the colour scheme is chosen.

CONCLUSION

We have seen that the evidence usually put forward for common descent is not as strong as evolutionists might wish, or that popular writers would have us believe. In fact, there are good reasons for doubting that common descent is even possible, especially by naturalistic mechanisms. The physicist Lee Spetner has observed that it is not necessary for a theory of evolution to explain how common descent occurred, since it has never been observed to occur – it is sufficient for a scientific theory that it can explain those facts that can be observed.⁷⁰ Ultimately, of course, only the God of the Bible can reliably tell us about the unobserved. It seems a pity that He did not tell us, in the Bible, whether Common Descent were true or not. If I had written the Bible, I would make it clear that many kinds of plants and animals were created, all reproducing after their own unique types.

Oh wait... it does say that?

GLOSSARY

Convergence. In Biology, the phenomenon in which the same structure or trait is observed in two species that are not directly related by common descent.

Homology. Sameness in general structure or type. In evolutionary literature, used to denote similarities believed to arise due to common descent.

Interstitial Telomeric Sequences (ITSs) Repetitive DNA sequences associated with DNA breakage and repair.

Metazoan. Any animal that has cells differentiated into different types of tissues.

Monophyletic. A taxonomic group in which every member is directly related through common ancestry.

Morphology. The study of shape and form in living things.

Ontogeny. The developmental history of an organism.

Paleogenetic. Pertaining to the study of preserved genetic material from ancient organisms.

Phenotype. The set of observable characteristics of an individual resulting from the interaction of its genotype with the environment.

Phenotypic. Pertaining to the phenotype.

Phylogenetic tree. A branching diagram showing an inferred evolutionary relationship between species or other groups.

Phylogeny. The evolutionary divergence of a species or group of organisms.

Proteome. The complete set of expressed proteins within a cell, tissue or organism.

Supramolecular. Pertaining to structures above the molecular level; for example, morphology.

Taxonomy. The branch of biology that seeks to classify living things.

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