

**Quote:** “He [Darwin] proposed that living species are descended, with modification, **from common ancestors.**”  
“To illustrate this idea, he drew the very first evolutionary tree. (Fig 16-12) . ... .All species are descended from ancient common ancestors.”

**Question:** Wouldn't the genome of the Last Universal Common ancestor, if it existed, have to be **indefinitely large** to account for the ubiquitous unique genes (the so-called ORFan genes) that have been discovered, beyond anything that could be biologically plausible? Doesn't that mean that Darwin was wrong about common descent, as reported in *New Scientist Magazine*?



What the Experts say:

Stephen Gould, Harvard Paleontologist

“The [neo-Darwinian] synthesis, as a general proposition, is effectively dead, despite its persistence in textbook orthodoxy.”

Paleobiology, V. 6, p.121, 1980

*New Scientist*, January 21, 2009

## Darwin Was Wrong About Common Descent\*

The first thing you learn as a student of evolutionary biology is its foundational proposition, the theory of Common Descent (CD): “The diverse living species we find in the modern world are descended from a single common ancestor that lived in the remote past.” Normally, this is illustrated as a tree, with the claim that all life falls somewhere on that tree, and it is a *universal* domain. CD is enormously attractive to scientists, but they need to separate their attraction from the theory’s possible truth or falsehood. That unified domain is abbreviated as LUCA, the Last Universal Common Ancestor, the first member of the set of your ancestors. In neo-Darwinism, it is not to be questioned, any more than an astronomer would question whether the earth goes around the sun.

Some biologists have argued that Common Descent is properly held as an *axiom* of biology, but in doing that one insulates the theory from empirical challenge--You make it invulnerable to testing. But if we are to have healthy science, the evidence has to be able to talk back; which raises the question, “*If the theory of common descent were false, how would we know it?*” Darwin addressed this question as follows: “ If any organ [or *biological character*] existed that could not have been formed by numerous, successive slight modifications, my theory would break down.” That means there must be some natural pathway of change, which has become known as the *Principle of Continuity (PC)*. If a hypothesis of evolutionary transformation posits a natural pathway from A to B, then every point on that pathway must be biologically plausible. For example, Orgel argued from PC: “It is very difficult to see how a totally different biological organization could have undergone a continuous transition to the nucleic acid system with which we are familiar.” Likewise, PC was used to rule out a simple larval organism as the ancestors of invertebrates having larval states, because the pathways of transformation that are implicated by that are not biologically viable.

This PC principle has the power to test Common Descent, but there is a logical problem: The very formulation of Common Descent places every living thing within the domain-- there is nothing outside [by definition?]. But unique genes and proteins, if widely distributed, would lie outside the domain. With the invention of automated DNA sequencing equipment, in the last 15 years, we have been able to really see what the genetic composition of life looks like; and, we’ve seen an explosion of information, with millions of genes sequenced. And one of the puzzles that’s been revealed by whole genome sequences, is called **ORFan genes**. The problem with “orphans” is when they are initially noticed, all of them have no associated functions. This is a great surprise to biologists. These are genes with **no molecular parents**; but CD requires that new genes come from old, with a large similarity. Extant genes and proteins [must] derive from the set present in the last universal common ancestor, LUCA. If everything lies in the Great Tree of Life (TOL), we ought to be able to trace a history of genes in any group back through evolutionary time to the set that was present in the last universal common ancestor. The ubiquity of orphan genes is radically transforming the way biologists think about the history of life, and the result is that CD is increasingly being challenged by evolutionary biologists.

Dr. Nelson proved his point with many examples, beginning with the discovery of a consistent 10-15% of genes in bacteria that are unique, with no homologues in any relatives. The most extreme example is the topo-isomerase V [enzyme], which is found in **only one** archaean species on earth, but is essential for life. In an analysis of 573 bacterial genomes, the orphans turn out to be far more numerous than shared sequences; only 8% were shared, and 28% unique.

CD would predict that all nested life should inherit them—False. This implies the genome of the LUCA for this group of organisms would be (if it existed) “**indefinitely large**” to account for the unique genes, beyond anything that could be biologically plausible. We have millions of unique sequences, which are accumulating much, much faster than the shared sequences, without evolutionary antecedents. As a result, the TOL is under attack. Even Craig Venter, Mr. Human Genome himself says, “I don’t buy it—I think we have thousands of recent common ancestors.” One biologist in France dared to call the puzzle: “**gene creativity**.” The findings have consequences, one being a cover story in *New Scientist*, Jan. 2009, entitled “Darwin was Wrong,” which started a firestorm of controversy, not within the creation/evolution debate, but because of what’s happening in evolutionary theory in light of the unexpected data.

So what about animals? Comparison of just two morphologically similar mollusks reveals that they use totally different biochemistry to construct their shells, with only 19 % similar proteins, which are essential. The **anatomy** of the hydra is specified by a set of ORFan genes. Taking an average across the genomes of six ant species, we find about 10% unique genes. Extrapolating this to the 5800 species of ants in this family, we get almost ten million unique genes that its LUCA must have had to provide support for the theory of CD (not plausible).

Bottom line: if you give the *Principle of Continuity* the power it should have, you could overturn Common Descent today. And this [universal] domain is going to go away, because of the evidence.

---

\* Abstracted from a lecture by Dr. Paul Nelson at the August, 2013 Int’l Conference on Creationism; see <https://www.youtube.com/watch?v=gH2Gu-07ps8>