

CHAPTER 9

EVIDENCE FOR PLANT AND ANIMAL EVOLUTION

GENETIC EVIDENCE FOR EVOLUTION

Genes are segments of a special molecule called DNA that serves as a sort of instruction manual for cells. DNA tells each cell how to manufacture the chemicals it needs. If we think of an organism as a building, then the genes are like the blueprint for the building. Each gene is like one page of the blueprint, describing some particular details of the organism.

The most dramatic evidence for common ancestry and the theory of evolution comes from the modern study of genetics. Scientists are now able to make detailed comparisons of the genes across different species, something Darwin could not have anticipated. The genes in lions, tigers, cougars, bobcats, and house cats are more similar to each other than to the genes in rats, horses, or other mammals. The genes in different species of rats, bats, and mice (all rodents) are more similar to each other than they are to genes in other mammals. This pattern of nested similarity matches the predictions of common ancestry and the theory of evolution.

This pattern of similarity extends beyond the genes themselves to include genomic organization, introns, and pseudogenes.

Genomic Organization

One evidence for common ancestry comes from what scientists call genomic organization. If we think of genes as pages of the blueprint for a building, then genomic organization refers to the order in which these pages are stacked up. Lions and tigers and house cats have genomic organizations that are very similar. If you compare one species of cat to another, the blueprint pages are almost always in the same order, with just a few small sections flipped into different orders. Cats and dogs have less similar genomic organizations. Mammals are more similar to each other in genomic organization than they are to fish and so on.

Introns

Genes tell the body how to build molecules. Introns are sections of genes not actually used to build molecules. If genes are the blueprint and instruction manual for building a house, then introns are like accounting records, notes, and scratch paper stapled onto the blueprint pages—things that are ignored by the carpenters. When a mutation happens in an intron, that mutation almost always has no positive or negative effect on the organism because the intron is usually ignored when the body builds molecules. If the genes in different species were similar to each other only because they share a *common function*, rather than sharing a *common ancestry*, there

would be no particular reason why the introns in different species show a pattern of similarity across species. On the other hand, common ancestry predicts that introns should show the same nested pattern of similarity that we see in ordinary genes—and that is exactly what scientists see.

Sweet Receptor Genes

Pseudogenes are broken or non-functional genes. Mammals have sweet receptor genes that allow them to taste that certain foods are sweet. It was recently discovered that in cats one of these sweet receptor genes is a pseudogene. Because cats have a pseudogene instead of a functioning gene, cats cannot taste sweet flavors. For most mammals the inability to taste sweets would be a bad thing because foods that taste sweet are high in energy. But since different cat species mainly eat meat, they are not particularly harmed by the inability to taste sweets. Scientists believe that long ago a common ancestor of lions, tigers, house cats, and other cat species had a mutation that turned their sweet receptor gene into a pseudogene, but this did not harm them because they were already eating mostly meat. This pseudogene was then passed down to all their offspring. If cats were created separately, without common ancestry with other mammals, there would be no particular reason for cats to have a sweet receptor pseudogene. But if God created cats using the mechanisms of evolution and common ancestry with other mammals, then it makes sense that they might have such a pseudogene.

All of this is strong evidence for common ancestry and is consistent with the theory of evolution. When scientists construct family trees of different species based on similarities of genomic organization, introns, and pseudogenes, they get a tree that matches the family tree built by comparing similarities in ordinary genes, and this in turn matches the family tree built by studying fossils.