

CHAPTER 9

EVIDENCE FOR PLANT AND ANIMAL EVOLUTION

GENETIC DIVERSITY WITHIN SPECIES

Another piece of evidence for common ancestry comes from the genetic diversity within each species. Diversity can be measured by determining the number of *alleles* which the species has for various genes. An *allele* is one of several different codings that a gene might have. A species might have many different alleles for one gene (lots of genetic diversity) and just a few alleles for another gene (less genetic diversity). The pattern of this genetic diversity tells scientists something about the history of that species. Here's an illustration of how it works, using a familiar species—the dog.

Like all animals, a dog has two copies of most genes, one from its father and one from its mother. Suppose a particular dog received a black-fur gene from its father and an identical black-fur gene from its mother. That dog would be said to have only one allele for that fur color gene. But if it received a black-fur gene from its father and a white-fur gene from its mother, it would be said to have two alleles for that fur color gene.

Now imagine, in an attempt to create a new breed of dog, taking one male and one female dog to an island. For some of their genes, both the male and the female will have a single allele, the same allele. All of their offspring will have just a single allele of that gene. But for some of their genes, the male and the female together will have two or three, but at most four alleles between them (at most two alleles in the male and two different alleles in the female). Unless a mutation occurs, all of their descendents' combined—the entire dog population of the island—will have *at most* four alleles for any gene. If the dogs live and breed on the island for enough generations, eventually a few mutations will happen, so eventually some genes will come to have five or six alleles in the dog population.

Now imagine discovering an island with a population of several hundred dogs. Genetic samples are taken from every dog on the island. Three dozen different genes are studied to determine how many different alleles are found in the dog population for that gene. Suppose that for every gene tested, the entire dog population has between one and four alleles but never more than four. We would conclude that, most likely, the island was originally settled by a single pair of dogs not that long ago. An alternate model, one that fits the available data just as well, is that the island was settled long ago by many dogs, but fairly recently a disease or natural disaster reduced that population down to a very small number of dogs, perhaps just a single pair. This “population bottleneck,” as it is sometimes called, reduced the number of alleles of every gene down to four or fewer. The dog population has been increasing since the bottleneck, but not enough time has passed for mutations to increase the number of alleles to more than four.

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Suppose, instead, that for several of the genes tested, the dog population has five, six, seven, or even eight alleles. We would conclude that, most likely, either the island was originally settled by more than a single pair of dogs or that it was settled by a single pair of dogs very long ago and enough time had elapsed for mutations to increase the number of alleles.

Finally, imagine discovering two islands, each with a population of dogs. The islands are separated by hundreds of miles of ocean, so the two populations cannot now interbreed. Testing the genes of both populations, we find a gene in which the dog population of the first island has eight alleles and the dog population of the second island has nine alleles. Seven of the alleles are identical between the two populations. It is extremely unlikely that identical mutations would happen independently on both islands to produce identical alleles. We would conclude that, most likely, these two dog populations share a common ancestry. At some point in the past, the groups of dogs that originally settled on each island shared a set of ancestors that is the source of the seven identical alleles. The one or two unmatched alleles on each island could have been separately produced on each island through mutations.

This illustration is analogous to what scientists see when they look at the genetic diversity within each species and compare it to closely related species. For example, they can select a particular gene in house cats that has many different alleles and compare them to the alleles of that same gene in lions and tigers. They will find some of the alleles are the same in all three species. Again, this is consistent with common ancestry and the theory of evolution.