



OXFORD
BIOLOGY



the **TIMETREE** *of* **LIFE**

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Foreword

I first began to appreciate the variety of living organisms when I went bird watching with my father, in Jackson Park, Chicago. My father had been a devoted bird-watcher since his high school days, and it was not just to escape Mass that I began to join him on Sunday morning visits to the park. I much enjoyed learning to distinguish birds that to the uninitiated were merely differing shades of brown. My appreciation of the diversity of the living world was further enhanced by visits to the wonderful Field Museum of Natural History, named in honor of Marshall Field. (I have reason to like Marshall Field. His grandson, Marshall Field III, played an important role in the history of Cold Spring Harbor Laboratory, hosting a 1932 fund raising gala at his 1750 acre estate on Long Island.)

While I knew that evolution was at the bottom of it all, it was still a source of wonder to me that naturalists were able to make sense of, and name, all of these creatures. Then, and for many years after, the naming of species and determining their relationships, was based on observable characters—the number of bones in a skull, the structure of genitalia, and so on. This began to change in the 1950s with the use of paper, followed by starch and acrylamide gel, electrophoresis to examine proteins. But a key step was taken in 1962, when Emile Zuckerkandl and Linus Pauling introduced the “molecular clock,” bringing together the relationships between organisms and the times of their divergence. By the 1970s, analysis had moved away from proteins and to using DNA hybridization methods which provided genome-wide data. However, these methods were not without problems, and there were some celebrated (or infamous) controversies.

It was the development of DNA sequencing in the 1970s, but especially the invention of automated DNA sequencing that heralded a new phase in the study of biological processes. For the first time, it was possible to produce large amounts of DNA sequence and so comparisons could be made between many genes across many organisms. The latest sequencing techniques can generate gigabases of nucleotide sequence, as Craig Venter and I know from seeing the complete sequences of our own genomes. One can only hope that the cost of sequencing will continue to decline so that all biologists can sequence their favorite organism.

Now, I look in wonder at *The Timetree of Life*, at the breadth of life that it covers, and the extraordinary data presented in it. Darwin himself drew trees, most famously the sketch (Fig. 1) that appears in what is known as Notebook B, on “Transmutation of Species” (1837–1838). The branching pattern illustrates how Darwin thought

species arose by descent with modifications from an ancestral species, and explained the relationships between existing and extinct species. How thrilled he would be to know how his insights continue to be the foundation of all that we do in biology.

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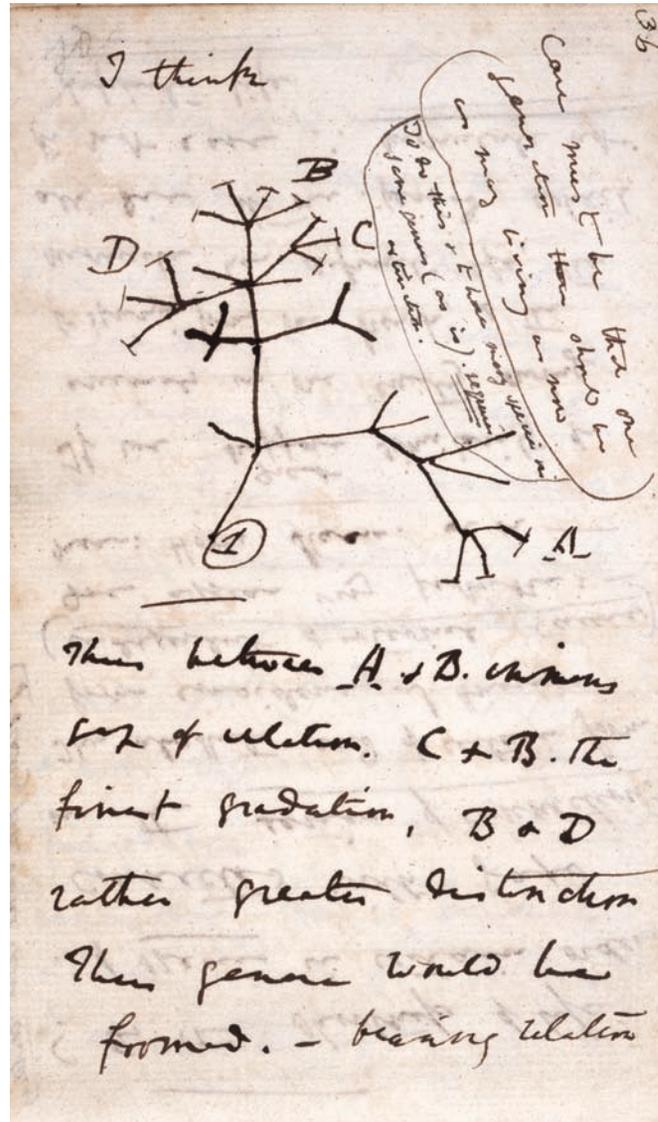


Fig. 1. A page written by Charles Darwin in a notebook in 1837, at age 28, showing a phylogenetic tree and collecting his early thoughts about the evolution of species. He writes "I think. Case must be that one generation then should be as many living as now. To do this & to have many species in same genus (as is) requires extinction. Thus between A & B immense gap of relation. C & B the finest gradation, B & D rather greater distinction. Thus genera would be formed—bearing relation [next page] to ancient types—with several extinct forms for if each species an ancient (1) is capable of making 13 recent forms, twelve of the contemporaries must have left no offspring at all, so as to keep number of species constant" (page 36 of "Notebook B," reproduced by kind permission of the Syndics of Cambridge University Library).