

## A Tree Grows in Manhattan

When the first full genome for a microbe was published, I was teaching an evolution course, and as I read the article I was first surprised and then thrilled to learn that the discovery had such profound evolutionary significance. Along with many others, I realized that we were entering a new world, one in which evolutionary biologists such as I had new responsibility. We now could, and therefore must, build a Tree of Life. It has long been a dream of comparative biology to explain how life has evolved and what evolutionary relationships mean. It has been a personal dream to make evolutionary biology predictive. Because evolution seems to run in grooves, following avenues of least resistance, knowing something about one taxon gives one a very good sense of what a closely related taxon will be like. Why should this be so? Evidently there are rules to be discovered, generalities to be established. Genetics, especially as it relates to development, provides some inspiration. But imagine what we might learn if we knew the true Tree of Life! Such a tree would include vastly more than what I now have the courage to identify as "only" full genomic information, but even that would be a great start.

It has been nearly 20 years since my colleague Allan Wilson first told me about how it was possible to amplify and soon to sequence DNA. He thought it would be only a short time before systematists would be routinely sequencing DNA and using the data to frame and test evolutionary hypotheses. I thought he was optimistic, but he was right. About the time that these conversations were taking place, Marv

Wake and I bought our first personal computer (we actually thought it would be possible to share one!). Systematists everywhere were having such experiences, and before long we were armed with methods, techniques, machines, and most important, with an intellectual framework (coming out of the phylogenetics revolution starting with Hennig on the one hand and numerical methods on the other, in the 1960s). Rapid progress ensued, leading to the first inkling that we might try assembling a Tree of Life, envisioned in the Nobel Symposium in Sweden in 1988. But most of us toiled with our own taxa, which systematists have historically divided up so as to avoid direct confrontational competition. The organization of the systematics community into provincial societies (within the herpetological community alone there are three mainly North American societies and dozens more elsewhere in the world, most with their own journals) did not help bring groups together, but gradually, with the National Science Foundation playing a critically important role at several points along the way, we began to interact effectively, and the successful conference we have experienced is the most recent manifestation.

Not surprisingly, early attempts to develop a tree of all life began within the community of microbial biologists, not only because they had less (in the sense of organismal complexity) to work with and had to turn to molecules, but also because they already were familiar with many molecular biological techniques and were ready to move when the era of PCR (polymerase chain reaction) arrived. Perhaps more sur-

prising is how rapidly the systematics community embraced molecular methods and approaches, not as a replacement for more traditional morphological approaches (which continued to develop methodologically, with a focus on building large character-based databases and analyzing them in diverse ways), but as an exceedingly important addition to our "tool kits."

The New York meeting was an unqualified success from my viewpoint. The oral presentations were uniformly outstanding—well prepared, well delivered, and designed for effective communication with a diverse audience. Remarkably, there was no dissent from the fundamental premise—that we want, need, and *can* produce a Tree of Life. Furthermore, in a field that has experienced intellectual warfare, what controversies arose in terms of data analysis and the like were downplayed in the interests of the general good. Perhaps we were all on good behavior because of the high degree of idealism expressed so beautifully by Ed Wilson in his inspiring opening address, and the symbolism of a remarkable address by Rita Colwell, the Director of the National Science Foundation and a person who thoroughly understands and appreciates the goal we have set for ourselves. For whatever reason, there was a wonderful sense of a common purpose, as well as of duty and responsibility. And in the background of it all was the intellectual imperative that the tools are at hand to accomplish our goal.

It is amazing to me how much comparative DNA sequence is accumulating and at what a high rate! Lacking such data, we would not even be talking about a Tree of Life initiative, but for taxon after taxon we witnessed the impact of molecular data. In some instances the goal of many systematists, a "total evidence" approach incorporating morphological and molecular data, integrated with fossil evidence, is

emerging (e.g., mammals). However, large molecular databases do not assure phylogenetic resolution, as we have learned in the case of birds. For some relatively large taxa (e.g., my own group, the amphibians, with about 5500 species), it may be possible to obtain sequence information for nearly all species, so as to put the "leaves" on the tree. But for microbes (astoundingly complex in the extent of paraphyly), despite an enormous accumulation of sequence data, the number of unsampled taxa is staggering and one wonders what the impact of as yet unsampled lineages will be.

I was struck by the estimates of one after another of the specialists that the numbers of taxa in their areas were vastly greater than previously thought. We remain in a phase of discovery, as we were reminded by the very recent description of a new order of insects. The number of species of amphibians is growing more than 3% per year, and vertebrates are supposed to be well known. Certainly at the level of basal taxa we have a great deal to learn, even for our best-known groups. So, the task is large, and if we are to accomplish it we will have to modify our publication strategy and streamline the process by which we describe taxa.

There will be more Tree of Life conferences and they will become increasingly inclusive, of researchers as well as taxa. We will work together not only because we stand to benefit from the interaction, but above all because we *must*. Information about what we have in the world will improve our chances of preserving biodiversity. Just knowing the Tree of Life will not assure its preservation, but for those of us for whom taxa count and trees count, having the requisite information will, we expect, enable us to more effectively act. We live in challenging and exciting times, but they are perilous as well, and it will take more than knowledge and wisdom to preserve the main structure of the Tree of Life on this planet.